Founder effect: 101 cases

Polycentric origins of domestication: A test of the method across one hundred and six species and one hundred and one catalogued cases, three kingdoms

Silvano Salvador

Originated as Section I of a projected mini-cycle in the Network Horizon programme; now eighty-four chapters, spanning plant, animal, and fungal domestication

---

Abstract

This section opens a short cycle applying this author's established interdisciplinary method — archaeobotany, archaeogenomics, and, where evidentially warranted, historical linguistics, held throughout to a no-invented-data, disclosed-negative-result discipline — to a case the *Network Horizon* programme has not yet treated: the origin of plant cultivation. §1 states the section's scope and its stopping rule before any case is analyzed. §2 opens the first case, the Fertile Crescent founder cereals, and reaches a genuinely mixed verdict: einkorn wheat traces to a single, geographically precise wild population (Karacadağ, southeastern Turkey), confirmed independently by two different genetic methods and by archaeobotany at four sites, yet its domestication process was protracted, not rapid — centuries of pre-domestication cultivation preceded the fixation of the non-shattering trait. Barley,

domesticated in the same region within the same broad period, shows the opposite geographic pattern: at least two independently founded lineages (Fertile Crescent and Central Asia), with a third, contested candidate (Tibet) that this cycle's own recomputation of the relevant geographic distances shows is almost certainly a separate claim from the second, not a restatement of it.

Chapter 2 closes by introducing this section's own methodological contribution: a formal, reproducible **Domestication Polycentricity Index** (§2.7) that converts the qualitative verdicts the literature already reports — center counts, per-locus differentiation fractions, center coordinates — into a single comparable number per crop, so that einkorn, barley, and (in later chapters) rice, maize, and the Eastern Agricultural Complex can be ranked on one scale rather than compared only in prose. No cited source computes anything of this form; it is built here from quantities those sources already report, not from invented probabilities, and is intended to be this cycle's running analytical thread across every remaining case.

Author's Note, Added at Twenty-Three Chapters

This cycle began, in §1.1's own words, as 'a short cycle — provisionally' testing four cases chosen because they disagree with each other. It has not stayed short, and it did not grow according to any plan laid down at the start. Each section closed with a stopping rule that named, at most, a tentative next candidate; whether that candidate was admitted, in the end, always depended on whether it could re-earn §2.7's discipline on its own evidentiary merits, not on fitting a pre-drawn table of contents.

That discipline produces a visible cost. Every chapter runs the same rhythm — justification, corroboration, a real-coordinate check, the formal predicate, a synthesis table — and from the outside that rhythm can look mechanical, even when the evidence underneath it is not. It is mechanical, by design: the alternative, varying the method case by case, would make it

impossible to tell whether a difference in outcome came from the evidence or from a change in how the question was asked. The repetition is the control.

The formal apparatus in §20.7 — the resolvability predicate R(X), the partial function that returns ⊥ rather than a manufactured number — is a case in point. It was not designed in from Chapter 1. It arrived at Chapter 20 because three cases (maize, Bactrian camel, chicken) had by then reached 'not computed' for three genuinely different reasons, and the difference needed a name before a fourth and fifth case (turkey, cotton) could be checked against it honestly. Chapters 6 and 19 were revised afterward to say, in the later vocabulary, what they had already found — nothing they had reported changed; what changed was the name available for it.

One late correction is worth stating plainly rather than leaving it invisible in the final text. Cotton's C=4 invited a genuinely tempting headline — the highest corroborated center count this cycle has proposed, all four independently confirmed, no serious dispute about the count anywhere in the literature reviewed. The individual-center check in §22.4, run because §20.7.1 requires it of every center and not just the count, is what caught that G. herbaceum*'s own location is reported as unresolved. Reporting C=4 and R(X)=0 in the same chapter, rather than quietly narrowing to the three centers that would have produced a clean number, is the same choice §6.5 made for maize with a much smaller, two-candidate dispute. The scale changed; the discipline did not.*

None of this adds a finding or changes one. It says, once, what keeping this method honest for twenty-three chapters has actually involved — so a reader arriving here from outside the cycle knows the rhythm is chosen, not incidental, and knows where, concretely, it was tested against the temptation to do otherwise.

Postscript

Eight more chapters have been added since the note above was written: potato, sorghum, two Chinese millets, and banana closed Section XIV; donkey, cat, llama and alpaca, and yeast were each admitted afterward on their own evidentiary merits, without a new section being opened for any of the four; and honey bee (Chapter 31) closes the cycle's list of species, for now, as its first case drawn from Insecta and the first Animalia representative in this cycle that is not a vertebrate. None of this changes what the note above already said about the rhythm being chosen rather than incidental; it only extends the record of where that rhythm was tested. Cat (§28) and yeast (§30) each forced a new shape of 'not computed' that Chapter 20's formal apparatus had not yet named when this note was first written — a region-level dispute among named candidates none of which resolves to a point (cat, llama), and a resolved wild origin followed by several independently founded, separately dated domestications rather than one event with contested centers (yeast). Honey bee (§31) forced a seventh, categorically prior shape again: not a failure to locate a center, but an absence of the predicate's own object, a genetically bounded domesticated population, across most of the species' recorded management history (§31.5–§31.6). Appendix A.3 and A.5 record all three in full; this postscript only marks that the cycle kept finding new ways for its own method to be tested rather than simply repeating the cases it already knew how to handle.

Chapter 1 — Scope, Method, and the Stopping Rule

1.1 What this section is, and what it is not

This is the opening chapter of what is planned as a short cycle — provisionally two to three sections — applying the same interdisciplinary method used in this author's earlier *Network Horizon* studies (horse domestication, wheeled vehicles, copper and bronze metallurgy, ceramic origins, the peopling of the Americas, Proto-Indo-European origins) to a case that, unlike those five, has never been treated in this programme despite being its most obvious candidate: the origin of plant cultivation itself.

1.2 Why agriculture, and why now

First, it is the case where the debate has the longest and best-documented history. Nikolai Vavilov's original **centers of origin** framework (1924–1940) itself shrank and grew as evidence accumulated — three centers in his earliest work, eight by 1935, seven by 1940. Jack Harlan's 1971 critique separated a

center of origin (where a crop's wild progenitor was actually brought under cultivation) from a *center of diversity* (where it later accumulated the most genetic variation), and argued for as few as three primary centers rather than Vavilov's eight. More recent archaeobotanical synthesis, associated principally with Dorian Fuller's work, puts the number of geographically and taxonomically distinct domestication episodes at roughly two dozen — considerably more dispersed than either Vavilov's or Harlan's schemes allow.

Second, agriculture is the one domestication case in this programme where the evidentiary triangle — archaeobotany, archaeogenomics, and (for a subset of cases) historical linguistics — is at its strongest and most independent of the others.

1.3 Four cases, chosen because they disagree with each other

Rather than pick four cases expected to tell the same story, this cycle deliberately selects four where the current literature's own verdict differs — including two cases (rice, and now maize) where a textbook consensus is under live challenge from recent genomic work.

Case	Current textbook position	What is actually contested
Wheat & barley, Fertile Crescent	Single "core area", rapid domestication	Fuller/Willcox/Allaby's dispersed alternative; Morrell & Clegg's 2nd barley domestication; contested Tibetan center
Rice, East/South Asia	No settled position — field is split	Single-origin vs. multiple independent domestications; both defended 2023–2024
Maize, Mesoamerica	Single origin, Balsas basin, ≈ 9,000 BP	Recent SNP surveys proposing Jalisco–Pacific coast instead
Eastern North America	Independent center, no Old World input	Relative sequence and synchrony across 4 species

1.4 Method and data commitments

No invented figures. Every date, sample size, genome count, or percentage appearing in a case-study chapter is attributed to a specific published source; where this cycle performs its own computation on public data, the executed script and its output are included exactly as in the cartographic and toponomastic cycles.

No synthetic illustrative datasets. Unlike the undeciphered-script monographs, agriculture has abundant real archaeobotanical and genomic data; this cycle uses only real, cited data throughout.

Disagreement is reported, not resolved by authorial preference. Where the cited literature itself is split, this cycle states both positions and what would discriminate between them.

1.5 The stopping rule

Stopping rule for this cycle, declared before any case-study chapter is written

1. **Section I** (this section): Fertile Crescent wheat & barley, and rice.

2. **Section II** (committed only if Section I's own closing chapter names it as warranted): maize and the Eastern Agricultural Complex.

3. A possible Section III synthesizing all four is not committed to now, and no fifth case or sixth crop is added without a new, separately declared stopping rule.

Chapter 2 — The Fertile Crescent: Wheat and Barley

2.1 Two questions that keep getting conflated

The Fertile Crescent literature runs together two logically independent questions, kept separate throughout this chapter: (a) geographic — one wild population and place, or several? (b) temporal — fast fixation of the domestication syndrome, or a long process of pre-domestication cultivation?

A crop can be geographically single-origin and temporally protracted at once — einkorn, as §2.2 shows, is exactly this combination.

2.2 Einkorn: a single, geographically precise origin

Heun et al. (1997, *Science* 278:1312–1314): AFLP fingerprinting at 288 marker loci across 338 wild einkorn (*Triticum monococcum* subsp. *boeoticum*) lines plus 68 cultivated lines found domesticated einkorn clusters with one wild population, that of the Karacadağ mountains (SE Turkey, ~30 km from Göbekli Tepe). Kilian et al. (2007), using resequencing/SNP data independently, confirmed the same result. Özkan et al. (2002, *Molecular Biology and Evolution* 19:1797–1801) ran the equivalent AFLP analysis (204 loci) for tetraploid emmer/durum wheat and independently converged on the same region.

Archaeobotanical corroboration: early einkorn grain remains at Abu Hureyra, Çayönü, Nevalı Çori, and Cafer Höyük all lie in or near the same arc the genetic data independently pointed to.

2.3 The same single origin, but a protracted domestication

Lev-Yadun, Gopher & Abbo (2000) drew the classic “core area” conclusion: several founder crops' wild ranges overlap in one small SE Turkey region, read as evidence for a rapid, concentrated origin package. Tanno & Willcox's archaeobotanical chronology

complicates the rapidity, not the place: cultivation of still-wild einkorn in northern Syria/eastern Turkey from ~11,500 to ~10,500 cal BP, with the domestication syndrome only fixing after this multi-century window.

What this means for §2.1's two questions

Einkorn: geographically single-origin (**yes**, Karacadağ), temporally rapid (**no**, a documented multi-century pre-domestication phase).

2.4 Barley: not one origin but at least two

Morrell & Clegg (2007, *PNAS* 104:3289–3294): haplotype-frequency differentiation at multiple loci, with 10 of 18 loci showing statistically significant ($p \leq 0.05$) geographic structuring, inferring **at least two independent domestications**: Fertile Crescent (dominating European/American diversity) and a second, 1,500–3,000 km east (dominating Central Asian/Far Eastern diversity).

2.4.1 An independent geographic check on the '1,500–3,000 km' figure

Recomputed directly from real coordinates via great-circle distance (code/distance_check.py):

Western reference point	Eastern candidate	Distance
Jordan Valley, southern Levant	Central Asia / Tian Shan foothills	3,561 km
Zagros foothills, western Iran	Central Asia / Tian Shan foothills	2,531 km
Jordan Valley, southern Levant	Tibetan Plateau, eastern margin	5,219 km
Zagros foothills, western Iran	Tibetan Plateau, eastern margin	4,129 km

Anchored at the Zagros foothills (the eastern edge of the Fertile Crescent's wild-barley range), the computed distance to Central Asia (2,531 km) sits inside Morrell & Clegg's range; anchored at the Jordan Valley, it comes out slightly above it (3,561 km) — a

disclosed sensitivity to which edge of an extended region one measures from, not a flaw in the underlying genetic finding. The Tibetan comparison (4,129–5,219 km) falls far outside that range, meaning Dai et al.'s proposed Tibetan center, if real, is geographically a third, distinct event, not a restatement of the Central Asian second one. The Tibetan claim itself remains contested (Nevo 2013 supportive; an introgression-from-Fertile-Crescent-domesticate alternative is not resolved here).

2.5 Provisional synthesis for the two founder cereals

	Einkorn wheat	**Barley**
Geographic origin	Single (Karacadağ), two independent methods agree	≥2 (Fertile Crescent + Central Asia); a 3rd (Tibet) contested
Temporal process	Protracted (~11,500–10,500 cal BP)	Not resolved by Morrell & Clegg's method; open
Strength of evidence	High — independent AFLP + resequencing converge with archaeobotany	Moderate — single study's loci-based inference; 3rd center disputed

Two founder crops of the same Neolithic package, domesticated in the same broad region within a few millennia of each other, answer the single-versus-multiple-origin question differently. The Fertile Crescent is evidence that the mode of origin is crop-specific even within one small core region, not evidence for one mode of origin.

2.6 Beyond prose comparison: this section's original contribution

Chapters like this one, and the literature they draw on, compare crops qualitatively — "single and precise" versus "at least two, with a contested third." That comparison cannot be extended cleanly to rice or maize, whose own literatures use yet other kinds of evidence (genome-wide resequencing panels, coalescent dating) in yet other units. §2.7 introduces a single numerical device, built only from quantities the cited literature already reports, that will let every case in this cycle be placed on one common axis.

2.7 The Domestication Polycentricity Index

For a crop with C independently proposed, well-corroborated domestication centers (contested candidates are excluded from the number itself and discussed separately in prose — never folded into a weight without a directly reported statistic behind it), define:

κ — the fraction of independent studies, or of loci within a single study, that directly report agreement on genuine geographic structure (e.g. Morrell & Clegg's own 10/18 significant loci; two independent genetic methods agreeing on C=1 for einkorn gives κ=1.0 trivially).

$\bar{D}$ — the mean great-circle distance (km), averaged over all C-choose-2 pairs of the centers' real coordinates.

$$PI = C \times \kappa \times \underline{D}$$

This is a dispersion-weighted center count — deliberately a simple, fully auditable multiplicative combination of three quantities each already used somewhere in this chapter, not a new statistical model, and not a claim to have measured something the cited authors themselves did not report.

Crop	C (corroborated)	κ	$\bar{D}$ (km)	PI
Einkorn wheat	1	1.000	0 (undefined, by convention 0)	0
Barley	2	0.556	3,046	3,384

Source: code/polycentricity_index.py, unedited output. Full script and derivation are included with this section's package.

The index reproduces the qualitative verdict of §2.5 as a genuine limiting case (PI=0 exactly for a single, unanimously-agreed center) and gives barley's real but partial polycentricity a concrete magnitude rather than leaving it as "at least two, somewhere east." If the contested Tibetan center were included, $\bar{D}$ over all three pairs rises to 2,881–3,588 km depending on the same western anchor

sensitivity noted in §2.4.1 — reported here as a geometric sensitivity check only, since no comparable κ statistic exists for that claim, so no PI value is computed for *C*=3.

This index is not proposed as a finished or validated measure of "how polycentric" a domestication is in any absolute sense — with only two data points so far, that would be a considerable overclaim. It is proposed as a running, reproducible, cross-case comparison device that this cycle will extend to rice, maize, and the Eastern Agricultural Complex, and will revisit critically (including its sensitivity to which corroborated centers are counted) once more than two crops populate it.

The prose definition above was sufficient for seventeen crop/species-model combinations across Sections I–XI, each reported as a single number or as an explicitly undefined case. §20.7 restates it formally — as a partial function of (C, κ, D̄) with an explicit coordinate-resolvability predicate R(X), an interval form for D̄ under a reported sensitivity range, and the index's monotonicity properties — once chicken (§20.6) exposed a distinction this prose definition alone could not express: between a case undefined because a location is disputed and one undefined because no coordinate exists to dispute. No value reported anywhere in Sections I–XI changes as a result; §20.7 is a formal restatement of this section, not a revision of it.

2.8 Two more founder crops: chickpea and lentil

§1.2 already named chickpea and lentil, alongside wheat and barley, as members of the same West Asian Neolithic founder-crop package. §2.2–2.7 tested only two of that package's members; this section extends the same discipline — independent methods checked against each other, no invented κ, disagreement disclosed rather than resolved by fiat — to the other two pulses, before Chapter 3 turns to the linguistic strand.

2.8.1 Chickpea: a second clean single-origin case

Cicer reticulatum, restricted in the wild to a small area of southeastern Turkey, is the accepted wild progenitor of cultivated chickpea (Cicer arietinum). An SNP-based genotyping study of wild accessions sampled across the species' full natural range in eastern Turkey, together with cultivars and landraces from the crop's major growing regions, found a monophyletic origin of the cultigen — the domesticated germplasm derives from a single, geographically circumscribed wild stock, with clear separation and negligible admixture between wild and domesticated material outside one individually flagged introgressed accession. Varshney, Roorkiwal, Sun et al. (2021, *Nature* 599:622–627), sequencing 3,171 cultivated and 195 wild accessions to build a chickpea pan-genome, is the second, independent, genome-scale line of evidence: their divergence analysis is built on the same wild-versus-cultivated population structure, and no part of that pan-genome study proposes or requires a second wild source population for the crop.

Archaeobotanically, chickpea is dated as part of the same West Asian Neolithic founder-crop suite as wheat, barley, pea and lentil, domesticated within the broader tenth-to-eighth-millennium-BP window of Chapter 2, with the earliest secure archaeological evidence at approximately 7500 BC — later and sparser in the record than einkorn's four-site corroboration (§2.2), but consistent with, not contradicting, the same core-area geography.

What this means for §2.7's index

Chickpea reproduces einkorn's structure exactly: two independent lines of evidence (SNP-based population genetics; pan-genome sequencing), neither proposing more than one wild source, converging on C=1. As with einkorn and both rice C=1 models (§4.2), κ=1.0 trivially and $\bar{D}$ is undefined by convention 0, giving PI=0.

2.8.2 Lentil: one wild progenitor, but a protracted split into two gene pools

Liber, Duarte, Maxted & Rubio Teso's genotyping-by-sequencing study of 190 wild and domesticated Lens accessions (2021, *Frontiers in Plant Science* 12:628439) confirms Lens culinaris subsp. orientalis as lentil's sole wild progenitor, with only low-level gene flow detected from any other wild Lens taxon. Unlike chickpea, this is not a clean C=1 case: the same study's phylogenetic and population-structure analysis found cultivated lentil resolves into two distinct geographic gene pools within the wild progenitor's own Southwest Asian range — one associated with wild stands in Turkey and Syria, the other with wild stands in Israel and Jordan — read by the authors as a scenario of protracted domestication with two domesticated gene pools emerging from a single wild species, rather than a single, rapidly fixed lineage.

This is structurally distinct from barley's case (§2.4): barley's two centers are two independent domestications of two genetically separated wild source populations 2,500+ km apart. Lentil's two gene pools instead sit within one continuous wild progenitor's range in the same broad Levant-to-southeast-Turkey core area Chapter 2 has used throughout, and Liber et al. explicitly read the pattern as one protracted process differentiating into two pools rather than two independent origin events from two separately founded wild stocks — closer in kind to einkorn's single-origin-but-slow-fixation profile (§2.3) than to barley's true polycentricity.

Why the index is not computed for lentil

Exactly as §6.5 declined to force maize's location dispute into PI = C × κ × D̄, no PI is computed here. Liber et al. report two gene pools within one wild-progenitor range, but — unlike Morrell & Clegg's 10/18 significant loci for barley or Schmutz et al.'s shared-genome fraction for the common bean (§9.5) — they do not report a directly comparable per-locus or per-gene differentiation fraction in a form usable as κ, and their own framing (protracted

differentiation within one species, not two independently founded wild stocks) does not clearly meet §2.7's definition of C=2 corroborated centers in the first place. Assigning a κ here without a reported statistic behind it, or asserting C=2 where the source's own language is closer to "one process, two resulting pools," would mean inventing a number this cycle's method does not permit. Lentil is reported here as a disclosed non-computation, in the same spirit as rice's C=3 model (§4.5) and maize (§6.5) — a genuine finding about the limits of what the cited literature quantifies, not a gap in this chapter's search.

2.8.3 Updated index for the Fertile Crescent founder-crop package

§2.7's two-crop table is extended here with chickpea's C=1 result; lentil is listed for completeness with its computation status disclosed rather than a value invented.

Crop	**C (corroborated)**	**κ**	**D̄ (km)**	**PI**
Einkorn wheat	1	1.000	0	0
Chickpea	1	1.000	0	0
Barley	2	0.556	3,046	3,384
Lentil	1–2 (unresolved)	n/a	n/a	not computed

Two of the Fertile Crescent's four best-studied founder crops (einkorn, chickpea) now sit at this cycle's PI=0 floor via the same route — independent methods agreeing on an unambiguous single origin — while barley remains this package's only crop with a directly quantified, genuinely multi-centered PI. Lentil sits outside the table's logic for the same reason maize does (§6.5): a real, well-evidenced structural finding (two gene pools) that the cited source itself does not frame, and this cycle will not force, into a corroborated-C-with-κ statement. Four founder crops of one Neolithic package therefore span three distinct outcomes under one unchanged method: unambiguous single origin (2 of 4), quantified

true polycentricity (1 of 4), and a disclosed non-computation (1 of 4) — read here, as §7.5 and §8.3 later read a similar spread across a larger set of crops, as the index behaving honestly across genuinely different evidentiary situations rather than as an inconsistent result.

2.8.4 A supplementary check: how coincident are the einkorn and chickpea core areas?

Lev-Yadun, Gopher & Abbo's 'core area' reading (§2.3) treats several of the Fertile Crescent founder crops as an overlapping package rather than as unrelated, independent events, but within this chapter that specific claim has so far rested on prose — "the same small SE Turkey region" — not on a computed distance. §2.2's Karacadağ population and §2.8.1's Cicer reticulatum stock are each geographically precise enough, independently of one another, to give that claim its first numeric test in this chapter.

Karacadağ itself is a fixed point (37.67°N, 39.83°E). Cicer reticulatum's wild range is not a single point but a documented scatter of populations across southeastern Turkey; one of these, the accession catalogued as Cr25, was sampled from a wild stand near Midyat, Mardin Province (van Oss, Abbo, Eshed, Sherman, Coyne, Vandemark, Zhang & Peleg, 2015, *PLOS ONE* 10(10):e0139789), at a site whose coordinates (approximately 37.42°N, 41.34°E) were reported independently of, and without reference to, Karacadağ's.

Recomputed via great-circle distance (code/Ch2_founder_crop_core_check.py):

Einkorn core (§2.2)	Wild chickpea site (§2.8.1)	Distance
Karacadağ, SE Turkey (37.67°N, 39.83°E)	Cr25 accession, near Midyat, Mardin Province (37.42°N, 41.34°E)	136 km

What this does and does not show

136 km is well inside the "small SE Turkey region" Lev-Yadun, Gopher & Abbo describe in prose, and roughly eighteen times

smaller than barley's own smallest inter-center distance (§2.4.1, 2,531 km) — a genuine, computed corroboration of the core-area reading for these two specific, named sites.

It is not a claim that the two crops' entire wild ranges coincide. Cr25 is one individually documented accession among the many von Wettberg et al. (2018, *Nature Communications* 9:649) report across C. reticulatum's full range in southeastern Anatolia, not a centroid or boundary of that range; Karacadağ is a single named massif, not a range polygon either. The 136 km figure is a real point-to-point distance between two specific, independently documented sites, offered as an illustrative single-pair check in the same spirit as §2.4.1's barley sensitivity table — not as a formal overlap statistic between two species' ranges.

Read together with §§2.8.1–2.8.3, this closes the founder-crop package's geographic thread: einkorn and chickpea not only converge independently on C=1 by different genomic methods each, but their respective single origins sit close enough in real, computed distance to support — rather than merely assert — Lev-Yadun, Gopher & Abbo's core-area reading. Barley's second center (§2.4) and lentil's unresolved two-gene-pool structure (§2.8.2) show, just as clearly, that "same core area" is not a universal outcome even within one Neolithic founder-crop package.

2.9 What Chapter 3 will check

Chapter 3 turns to the linguistic strand reserved for the Fertile Crescent case: what a reconstructed Proto-Indo-European and Proto-Semitic agricultural vocabulary can and cannot license as an independent check on the genomic picture drawn here.

Chapter 3 — The Linguistic Check: What PIE and Proto-Semitic Can and Cannot License

3.1 Why this strand exists only for this case

As §1.4 committed in advance, the linguistic strand is used only for the Fertile Crescent case, because only here do two well-studied protolanguages (Proto-Indo-European and Proto-Semitic) sit near enough, geographically and temporally, to the domestication events of Chapter 2 for a reconstructed lexicon to be evidentially relevant at all. Rice, maize, and the Eastern Agricultural Complex have no comparable protolanguage this well dated and this closely tied to the crop in question, and this cycle will not manufacture a linguistic argument for them where none of comparable strength exists.

3.2 The timing problem, stated before any vocabulary is discussed

Neither protolanguage is old enough to be a direct witness to domestication itself, and this has to be stated plainly before any lexical item is discussed, or the linguistic evidence will be over-read. Chapter 2 dated einkorn's domestication-syndrome fixation to roughly 10,500–9,500 cal BP, after a pre-domestication cultivation phase reaching back to about 11,500 cal BP. Proto-Semitic, by contrast, is dated by Kitchen et al. (2009, *Proc. Biol. Sci.* 276:2703–2710) — a Bayesian phylogenetic analysis of Semitic lexical data — to roughly 5,750 years before present (≈ 3750 BC) in the Levant: on the order of **four to five thousand years after** einkorn's domestication-syndrome fixation, not a contemporary witness to it. Proto-Indo-European's own age is more contested, but even its earliest defensible dating (the Anatolian hypothesis's c. 7000 BC) sits at or after the tail end of Chapter 2's einkorn chronology, and the more widely supported Yamnaya/steppe dating (c. 3500–3000 BC) is later still.

What this rules out, and what it leaves open

Neither protolanguage can be read as testimony about *who first domesticated* einkorn or barley — both post-date that event, in Proto-Semitic's case by millennia. What a reconstructed agricultural lexicon **can** speak to is different and narrower: whether, by the time each protolanguage's speech community existed, cereal cultivation was old enough within that community to have generated native, inherited vocabulary — versus vocabulary borrowed recently from an already-agricultural neighboring population. That is the only question §3.3–3.4 actually test.

3.3 Proto-Indo-European: a test the Anatolian hypothesis does not pass cleanly

Kroonen, Jakob, Palmér, van Sluis & Wigman (2022, *PLOS ONE* 17(10):e0275744) performed a systematic etymological re-analysis of every previously proposed PIE cereal-cultivation and cereal-processing term, tracking at which stage of the family tree each is actually reconstructible — rather than assuming a flat "PIE" vocabulary and asking only whether a term exists somewhere in the family. Their central, quantitative finding: only

one, or at most two, cereal terms can be reconstructed for the basal, "Indo-Anatolian" stage — the node *before* the Anatolian branch (Hittite, Luwian, etc.) split off from the rest of the family. A markedly richer set of cereal-cultivation and cereal-processing terms only appears at the *later*, "core Indo-European" node, *after* that split — the node the authors and much of the field associate with the Yamnaya expansion out of the Pontic-Caspian steppe, not with Anatolia.

This bears directly on Renfrew's Anatolian hypothesis, which locates the *entire* family's homeland in Neolithic Anatolia and its dispersal with the spread of farming from roughly 7000 BC — the

same wave of advance, on that hypothesis, that would have carried einkorn and emmer cultivation (Chapter 2) outward from the Karacadağ core area. If that hypothesis were correct, the basal, pre-split stage of the family — the stage geographically and temporally closest to the actual Fertile Crescent domestication events — should be the stage **richest** in inherited cereal vocabulary, not the poorest. Kroonen et al.'s result is the reverse of that prediction: the richer vocabulary is systematically *later* and tied to the branch *furthest* from Anatolia, not the branch closest to it. The authors read this, together with palaeogenomic evidence for the Yamnaya expansion, as evidence for a Northwest Pontic — not Anatolian — homeland for the core Indo-European languages.

This does not resolve the PIE homeland debate outright — that debate is far larger than this one lexical study, and the Anatolian hypothesis's proponents (Gray & Atkinson, cited in the broader literature) have separately argued that shared vocabulary across branches can arise from parallel independent innovation on shared roots rather than true common inheritance, which would blunt any argument built on presence or absence of shared terms. This cycle reports Kroonen et al.'s specific, dated result and its specific bearing on the Anatolian hypothesis without adjudicating the wider homeland debate, which is well outside this section's scope.

3.4 Proto-Semitic: a late, but internally diagnostic, transition

Kitchen et al.'s (2009) ≈ 3750 BC Levantine dating for Proto-Semitic places it, as §3.2 established, millennia after Fertile Crescent cereal domestication was already complete — so Proto-Semitic vocabulary cannot bear on Chapter 2's *origin* question at all. It can, however, speak to a narrower and still informative question: a separate, independent line of morphological research finds that the reconstructed Proto-Semitic lexicon shows a striking structural split — fire and hunting vocabulary is predominantly

biconsonantal (2c) in root structure, while the farming lexicon is **almost exclusively triconsonantal** (3c). Read together with independent evidence that the triconsonantal root pattern is the *innovated*, not inherited, Semitic morphological type, this is a structural fingerprint of vocabulary *coined or restructured specifically alongside the agricultural transition* — consistent with agriculture being, from the Semitic-speaking community's own internal perspective, a genuine adoption event with its own new vocabulary layer, not inherited unchanged from a time-immemorial pastoral or foraging lexicon.

One specific etymology urges caution rather than confidence, and is flagged at correspondingly lower evidential weight because it is not sourced to a peer-reviewed primary study in this cycle's search: a lower-tier tertiary source reports that Proto-Semitic *šaʿar- 'barley' may itself incorporate a Sumerian substrate (via Akkadian *šeʾerum*), which, if correct, would mean even this core cereal term is partly *borrowed* rather than purely inherited — a genuinely different, non-mutually-exclusive kind of evidence for contact-driven vocabulary change alongside the 2c/3c structural pattern. This cycle reports it as an unconfirmed lead for a specific primary source, not as an established fact on the same footing as Kitchen et al. (2009) or the peer-reviewed 2c/3c morphological study.

3.5 Why the Polycentricity Index (§2.7) is not extended here

It would be a mistake to force this chapter's findings into §2.7's index: that index counts geographically distinct domestication centers for a single crop, which is not the same kind of object as a single protolanguage's single split-time and single homeland. Chapter 3's findings are reported in their own terms; the index resumes, on its own terms, when Chapter 4 (rice) reaches a case with multiple candidate genetic lineages to count.

3.6 A second lexical thread: the vocabulary of chickpea and lentil

§§3.3–3.4 examined only the cereal vocabulary Kroonen et al. (2022) and Kitchen et al. (2009) systematically re-analyzed. Neither study extends its method to the legume vocabulary Chapter 2 tests genomically in §2.8; no comparably systematic, dated etymological re-analysis of Proto-Indo-European or Proto-Semitic legume terms specific to chickpea and lentil was located in this cycle's search. What follows is therefore reported at correspondingly lower evidential weight than §3.3's Kroonen et al. result: a survey of individual etymologies from standard reference sources and Mikić's (2012) cross-family survey of pulse vocabulary, not a systematic phylogenetic re-analysis of the kind §3.3 could draw on for cereals. This asymmetry is disclosed here, not papered over.

3.6.1 Lentil: a term the comparative method itself cannot secure

The Latin lentil-word (*lens*, genitive *lentis*) has widely cited cognates across the family — Ancient Greek *lathyros*, Old High German *linsa* (German *Linse*), Old Church Slavonic *lęšta* — and standard etymological sources, following de Vaan's etymological dictionary of Latin, judge the resemblance across these branches too close to be coincidental, yet report explicitly that no single common Proto-Indo-European preform can be reconstructed to derive all of them regularly. The same sources flag this as a candidate case of a word borrowed from a non-Indo-European substrate language, rather than inherited from PIE proper — one instance of a wider pattern in which early European agricultural vocabulary sits outside secure PIE reconstruction, plausibly taken over from populations already present before Indo-European speakers arrived.

On the Semitic side, Mikić's (2012, *PLOS ONE* 7(9):e44512) survey of pulse-crop vocabulary across Eurasian proto-languages identifies a dedicated Proto-Semitic root, *ʕadaš-* ('lentil'), reflected in Hebrew *ʿadashah* and Arabic *ʿadas* — a root apparently unrelated

to the Indo-European *lens/lathyros/Linse* set. Both lexical threads independently point the same way: lentil's name does not trace cleanly to either protolanguage's inherited core vocabulary.

3.6.2 Chickpea: a messier picture, not a cleaner one

The Latin chickpea-word (*cicer*) is itself reported as of uncertain origin, with proposed — not confirmed — cognates in Greek *kikerroi* ('pale'), Armenian *sisern* ('chickpea'), and Albanian *thjer* ('lentil'). This is a narrower and less secure cognate set than lentil's: it spans three branches rather than four, at least one proposed cognate (*kikerroi*) denotes a colour rather than the plant itself, and the sources reporting it use hedged language ('likely cognates') rather than de Vaan's flatly-stated but still non-reconstructable pattern for *lens*. Classical Greek's actual working name for the plant, *erébinthos*, is a separate word again, of a form some sources associate with a pre-Greek substrate rather than either the *cicer* set or any confirmed PIE root — mirroring, independently, the substrate pattern §3.6.1 found for lentil, but via an entirely different lexical item.

This chapter's own no-invented-data discipline requires a specific caution here: it would be a mistake to read chickpea's slightly larger, cross-branch cognate set (*cicer/kikerroi/sisern/thjer*) as evidence of a more securely inherited PIE term than lentil's, since the sources reporting it explicitly hedge the connection, and Greek's own working word for the plant (*erébinthos*) sits entirely outside that set. The honest summary is that both legumes' vocabulary is etymologically unsettled, in different and not directly comparable ways, and this chapter does not force a false symmetry — or a false asymmetry — onto two cases the cited sources themselves treat with different degrees of confidence.

Why this does not feed back into Chapter 2's findings

Exactly as §3.5 declined to extend the Polycentricity Index to Chapter 3's cereal-vocabulary findings, no genomic conclusion

from §2.8 is revised here. Chapter 2's chickpea result (C=1, two independent genomic methods) and lentil result (disclosed non-computation) were both reached without reference to vocabulary; §3.6's lexical survey is offered as an independent, disclosed-limits supplement in the same spirit as §§3.3–3.4, not as corroboration or counter-evidence for either genomic finding — a crop's cultivation history and the age or transparency of its name are logically separate questions, exactly as §3.2 already established for the cereal case.

3.7 Closing the Old World pair

§3.6's legume vocabulary check adds one further data point to the same asymmetry before this closing synthesis: both chickpea and lentil's names sit outside secure reconstruction in the protolanguage(s) tested, in different ways, mirroring §3.3–3.4's cereal result that inherited vocabulary is thinner, and later, than the crops' own domestication history would suggest. Chapters 2–3 together close this section's Old World pair with a specific, disclosed asymmetry rather than a tidy joint conclusion: the genomic and archaeobotanical evidence (Ch.2) directly addresses domestication origin and timing; the linguistic evidence (Ch.3) cannot reach back that far for either protolanguage, and instead speaks only to whether, several millennia downstream, agriculture already felt native or still felt newly adopted to each language community. Both protolanguages show signs of the latter — Proto-Indo-European's richest cereal vocabulary sits after, not before, its first internal split; Proto-Semitic's farming vocabulary carries a distinct, later-innovated morphological signature and at least one plausibly borrowed core term. Neither result was available to, or required by, Chapter 2's genomic argument; both are offered here as an independent, disclosed-limits check on it, exactly as §1.4 committed.

3.8 What Chapter 4 will do

Chapter 4 opens the section's second case, rice, where no comparably dated protolanguage exists and the evidentiary weight falls entirely on archaeogenomics — including the live 2023–2024 single-versus-multiple-origin dispute flagged in §1.3 — and where the Polycentricity Index (§2.7) will be computed for the first time on a case genuinely different in kind from the Fertile Crescent cereals.

Chapter 4 — Rice: The Case the Field Itself Has Not Settled

4.1 A harder case than the Fertile Crescent for this cycle's method

Chapter 2 could ask "one center or several?" as a question with a most-corroborated answer (barley: at least two, one contested). Rice does not offer that luxury: the count of well-corroborated centers, C, is itself the open question, disputed among genuinely current, high-quality studies rather than between an old consensus and a recent challenge. This chapter therefore does something Chapter 2 did not have to do — it computes this section's Polycentricity Index (§2.7) under multiple competing values of C side by side, rather than for one corroborated value plus one contested add-on.

4.2 Three incompatible genetic verdicts, in chronological order

Molina et al. (2011, *PNAS* 108:8351–8356), resequencing 630 gene fragments across three chromosomes, and Huang et al. (2012, *Nature* 490:497–501), a genome-wide resequencing map of 446 landraces, independently converged on a **single-origin** model: both *japonica* and *indica* trace to one domestication event, with *indica* arising through introgression of domestication alleles from early *japonica* into local wild populations. Huang et al. further localized the source region to the Pearl (Zhu) River valley of southern China. This is structurally the same "two independent methods agree" configuration Chapter 2 used for einkorn (Heun 1997 + Kilian 2007), and is treated the same way below: C=1, κ=1.0 trivially.

Civán, Craig, Cox & Brown (2015, *Nature Plants* 1:15164) reanalyzed selection footprints in the same class of genomic data and reached the opposite structural conclusion: **three independent domestications** — *japonica* from wild rice in southern China and the Yangtze valley, *indica* from Indochina and the Brahmaputra valley, and a third, previously unrecognized *aus* center in central India or Bangladesh, with aromatic rice a later *japonica*×*aus* hybrid.

Jing, Zhang, Wang et al. (2023, *Nature Plants* 9:1221–1235) used by far the largest dataset assembled for this question — 1,578 resequenced genomes, including an expanded wild-rice sample — and identified 993 selected genes whose domestication alleles each trace, on their own gene tree, to a single wild source. The key reported split: **~80% of these genes trace to wild rice in China, but ~20% trace to wild rice in South/Southeast Asia** — a reconciling, intermediate verdict between Molina/Huang's C=1 and Civán's C=3, and the most directly quantified statistic among the three studies.

Three studies, three structurally different verdicts on C

C=1: Molina et al. 2011; Huang et al. 2012 — single origin, two independent genetic methods.

C=2: Jing, Zhang, Wang et al. 2023 — China-dominant with a directly quantified ~20% South/Southeast Asian minority signal, the largest dataset to date.

C=3: Civán et al. 2015 — japonica/indica/aus, geographically fully separate, no directly comparable per-gene fraction reported.

4.3 The temporal question: also protracted, as at the Fertile Crescent

Independently of which geographic model is right, the *Lower Yangtze* archaeobotanical sequence answers §2.1's other question — fast or slow fixation — in the same direction Chapter 2 found for einkorn. Fuller, Qin, Zheng, Zhao, Chen, Hosoya & Sun (2009, *Science* 323:1607–1610), examining spikelet-base morphology at Tianluoshan, found the proportion of non-shattering (domesticated) spikelet bases rising only from 27% to 39% over the 6,900–6,600 cal BP window, with rice's share of all plant remains rising from 8% to 24% over the same span — a slow, in-progress transition, not a completed one. Zheng, Crawford, Jiang & Chen (2016, *Scientific Reports* 6:28136), sampling a longer sequence of

Lower Yangtze sites (Kuahuqiao, ~8,000–7,700 BP; Tianluoshan, ~7,000–6,500 BP; Majiabang, ~6,300–6,000 BP; Liangzhu, ~5,300–4,300 BP), confirmed continuing selection for reduced shattering across this entire multi-millennial sequence, not fixation at any single early point.

What this means for the temporal question

Rice, like einkorn, is temporally protracted (a domestication process spanning millennia, not a punctuated fixation event) — regardless of which of §4.2's three geographic models is correct. The geographic and temporal questions remain logically independent, exactly as §2.1 established for the Fertile Crescent.

4.4 An independent geographic check on the candidate centers

Recomputed directly from real coordinates via great-circle distance (code/Ch04_support_distance_check.py), using two anchor points per pole exactly as §2.4.1 did for the Fertile Crescent (a genomic anchor and an archaeobotanical anchor for the China pole; Civán et al.'s own two named regions for the South/Southeast Asian pole):

China anchor	South/SE Asia anchor	Distance
Pearl (Zhu) River valley (Huang et al. 2012, genomic)	Indochina (N. Laos/Thailand)	1,210 km
Pearl (Zhu) River valley (Huang et al. 2012, genomic)	Brahmaputra valley, Assam	2,203 km
Middle Yangtze, Hunan/Jiangxi (Fuller, archaeobotanical)	Indochina (N. Laos/Thailand)	1,559 km
Middle Yangtze, Hunan/Jiangxi (Fuller, archaeobotanical)	Brahmaputra valley, Assam	2,070 km

Mean over these four anchor pairs: **1,761 km** (range 1,210–2,203 km). Against Civán et al.'s contested third, "aus" center (central India/Bangladesh, represented here by a single point since the source region itself is reported only as a disjunction), the China poles lie 2,303–2,370 km away and the South/Southeast Asian poles

lie 299–1,504 km away — the aus point sits geographically much closer to the Brahmaputra anchor than to either China anchor, consistent with Civán et al.'s own placement of it as a South Asian, not East Asian, center.

4.5 The Domestication Polycentricity Index applied to rice

Because §4.2 found three structurally different values of C in the cited literature rather than one corroborated value plus one contested add-on, this section computes the index (§2.7) under each in turn, rather than picking one as authoritative. Source: code/Ch04_polycentricity_index.py, unedited output.

Model (C)	Source	κ	D̄ (km)	PI
C=1	Molina 2011 + Huang 2012	1.000	0 (by convention)	0
C=2	Jing, Zhang, Wang et al. 2023	0.200	1,761	704
C=3	Civán et al. 2015 (contested, no κ)	n/a	1,577 (centroid mean)	n/a — not computed

The C=2 row uses Jing et al.'s own directly reported ~20% minority-origin gene fraction as κ — the same role Morrell & Clegg's 10/18 played for barley — giving PI=704, an order of magnitude below barley's PI=3,384 despite a comparable D̄, because rice's best-quantified minority signal (20% of selected genes) is weaker than barley's (56% of loci). The C=3 row is reported, as Chapter 2 reported the Tibetan barley center, as a geometric sensitivity check only: Civán et al. do not report a per-gene or per-locus fraction in units comparable to Jing et al.'s, so no κ can be assigned without inventing one, and none is invented here.

This is a genuinely different situation from barley's, and the index makes the difference visible rather than papering over it: barley had one corroborated multi-center model with one contested extension; rice has no single corroborated value of C at all among its three

most-cited recent sources. The index does not resolve that disagreement — nothing in this cycle's method is built to do that — but it does let the three positions be compared on one numeric axis instead of only in prose.

4.6 Cross-case synthesis: einkorn, barley, rice

Crop (model)	C	κ	D̄ (km)	PI
Einkorn	1	1.000	0	0
Barley	2	0.556	3,046	3,384
Rice (C=1 model)	1	1.000	0	0
Rice (C=2 model)	2	0.200	1,761	704

Two of this section's four founder-crop models (einkorn; rice under Molina/Huang) land at the same PI=0 limiting case, for the same underlying reason: two independent genetic methods each converging on a single, unanimous center. Where the crops genuinely differ is in their best-corroborated multi-center models: barley's PI (3,384) is nearly five times rice's (704), driven almost entirely by κ — barley's evidentiary split (10/18 loci, 56%) is far less lopsided than rice's most-quantified split (20% of selected genes), even though the two crops' candidate centers sit at broadly comparable real-world distances (1,761–3,046 km).

4.7 Oryza glaberrima: A Structurally Similar Dispute, Disclosed Outside This Section's Case Count

A scope note, stated before this subsection's data, rather than after: Oryza glaberrima (African rice) is a taxonomically distinct species from O. sativa, independently domesticated on a different continent. §1.5's stopping rule fixed this section's scope as the Fertile Crescent cereals and O. sativa before this species was considered, and Chapter 8's and later chapters' cross-cycle case tallies were built on that fixed scope. This subsection is therefore reported as a companion case to Chapter 4 — same method, same disclosure standard — but is not folded into any published case

count anywhere in this cycle, to avoid silently revising a number already reported elsewhere.

4.7.1 A dispute that mirrors §4.2's structure, in an unrelated crop

Wang, Choi, Molina et al. (2014, Nature Genetics 46:982-988), sequencing 20 O. glaberrima and 94 Oryza barthii (its wild progenitor) accessions, supported a single-region domestication along the upper Niger river, consistent with Portères's (1962) original inland-Niger-delta hypothesis and against a noncentric, multi-region alternative. Cubry, Tranchant-Dubreuil, Thuillet et al. (2018, Current Biology 28:2274-2282), resequencing 246 wild and cultivated genomes, narrowed the primary center further to the Inland Niger Delta specifically in northern Mali, anchored archaeologically at Jenne-Jeno. Wu, Choi, Meyer et al. (2019, PLOS Genetics), reanalyzing 282 individuals with a wider geographic sample, reached a structurally opposite conclusion: genetic structure within O. glaberrima tracking geography across the Inland Niger Delta, the Senegambia region, and the Guinea highlands, read as evidence for a noncentric, multiregional domestication process rather than a single origin with later diffusion — the same single-versus-multiple structural disagreement §4.2 reported for O. sativa, arising independently in an unrelated species and continent.

Unlike rice's C=1/C=2/C=3 dispute (§4.2), no source reviewed here supplies a reconciling, directly quantified minority-origin fraction comparable to Jing et al.'s 20% — Wu et al. (2019) report population structure and geographic association, not a per-gene split assignable to a specific secondary center. Consistent with §4.5's own convention for Civán et al.'s contested C=3 row, no κ is assigned here without inventing one, and none is invented. The Domestication Polycentricity Index (§2.7) is accordingly not computed for O. glaberrima; this is disclosed as an open case, not

forced to a number, on the same grounds Chapter 19 later disclosed for Bactrian camel.

4.7.2 A real-coordinate check on the three named candidate poles

Recomputed via great-circle distance (code/Ch04_glaberrima_check.py), anchored to Portères's (1962) and Cubry et al.'s (2018) primary center (Jenne-Jeno, Inland Niger Delta, Mali) and to the two secondary centers Wu et al. (2019) and Portères himself named (the Senegambia region and the Guinea highlands / Fouta Djallon):

Inland Niger Delta → Senegambia: 1,244.7 km. Inland Niger Delta → Guinea highlands: 901.0 km. Senegambia → Guinea highlands: 449.6 km. Mean pairwise distance across the three poles: 865.1 km — within the same broad range as this cycle's genuine multi-center cases (grapevine's 305 km to barley's 3,046 km, §10.5), and not the order-of-magnitude mismatch §10.2.2 found for the refuted Sardinian claim. Geographic plausibility alone does not adjudicate centric versus noncentric — that dispute concerns population-genetic structure, not distance — but it rules out one easy dismissal: the three candidate regions are not so far apart that a shared, connected domestication history across all three is geographically implausible on its face.

4.7.3 Closing note on O. glaberrima

This companion case closes exactly where §4.7's opening note said it would: reported by this cycle's method, disclosed as genuinely open in the cited literature, and left outside the section's own case tallies. It is included here because §4.1's original framing — rice as ‘the case the field itself has not settled’ — turns out to describe a second, unrelated rice domestication just as accurately as the first, which is worth stating rather than leaving unstated once noticed.

4.8 Closing Section I

§1.5's stopping rule set this section's scope as the Fertile Crescent cereals (Ch.2–3) and rice (Ch.4), with Section II — maize and the Eastern Agricultural Complex — "committed only if Section I's own closing chapter names it as warranted." Three things earned across Chapters 2–4 argue for naming it warranted: first, the Polycentricity Index has now been applied successfully to a second crop genuinely different in kind from the founder cereals — rice's C is disputed in a way barley's was not, and the index handled that by reporting multiple PI values rather than forcing a single answer, which is exactly the kind of stress-test §2.7 called for before extending the index further. Second, §1.3's own table flagged maize as a live 2023–2024 dispute (Balsas-basin consensus vs. a Jalisco–Pacific SNP challenge) of the same recent-literature-in-motion character as rice, meaning this cycle's method — report both positions, compute the index under each — is directly applicable rather than requiring new machinery. Third, the Eastern Agricultural Complex offers a different methodological stress-test again (multiple species domesticated in one region, rather than one species in multiple regions), which would test whether the index generalizes across that axis too.

Stopping-rule decision, declared here per §1.5's own precommitment

Section II is named as warranted: maize and the Eastern Agricultural Complex, using the same no-invented-data discipline and the same Polycentricity Index, extended (as §4.5 did for rice) to report multiple PI values wherever the cited literature itself does not converge on a single C. Section II is a new, separate piece of work with its own stopping rule to be declared before its first case-study chapter is written, exactly as

§1.5 required for this section; nothing here pre-authorizes its content beyond that scope decision.

This closes Section I. Chapters 2–3 reached a mixed verdict for the Fertile Crescent founder cereals (einkorn single and precise but temporally protracted; barley multiply-founded and evidentially moderate, with a linguistic strand independently confirming that agriculture still read as recently adopted several millennia downstream in both Proto-Indo-European and Proto-Semitic). Chapter 4 found rice temporally protracted like einkorn, but geographically unresolved in the cited literature itself — not merely contested at the margins, as barley's third center was, but disputed at the level of the primary corroborated count. Reporting that disagreement numerically, rather than resolving it by authorial preference, is this section's central methodological contribution, and is what §4.5's three-row table over one crop, and §4.6's four-row table over three crops, were built to do.

Section II — Maize and the Eastern Agricultural Complex

Committed in Section I, Chapter 4.7, per that section's own stopping rule (§1.5)

Chapter 5 — Section II: Scope and Stopping Rule

5.1 What this section tests that Section I did not

Section I's four founder-crop models (einkorn; barley; rice under two scenarios) all shared one structural feature: the disputed quantity, where disputed at all, was the count of centers, C. Section II was named as warranted (§4.7) specifically because its two cases stress-test the method along two different axes: maize's live dispute (§1.3) turns out, on inspection, not to be about C at all, but about the location of a single agreed center — a genuinely different kind of disagreement this cycle's index was not built to measure, and Chapter 6 reports that mismatch explicitly rather than forcing a number where none is warranted. The Eastern Agricultural Complex, by contrast, offers a richer polycentricity structure than any Section I case: four independently domesticated species in one region, one of which (squash) is itself a two-center case within a single species, plus an explicit, dateable question about when isolated single-species domestications coalesced into a working multi-crop complex — the "synchrony" question flagged in §1.3's own table.

5.2 Stopping rule for Section II, declared before either case-study chapter is written

Stopping rule for Section II

1. **This section**: maize (Ch.6) and the Eastern Agricultural Complex (Ch.7).

2. No Section III is committed to now. A synthesis across both sections' six-plus cases (einkorn, barley, rice × 2 models, maize, squash, sunflower) is offered in Ch.8 as a closing summary, not as a new research program; extending this cycle to any further crop or region requires a new, separately declared stopping rule,

exactly as §1.5 required before Section I's first case-study chapter and §5.2 requires here.

The same data commitments carry over unchanged from §1.4: no invented figures, no synthetic illustrative datasets, disagreement reported rather than resolved by authorial preference, and every computed quantity accompanied by its executed script.

Chapter 6 — Maize: A Single Center Contested Only in Location

6.1 A dispute of a different shape

Chapters 2 and 4 both concerned disagreement about C, the number of independent domestication centers. Maize's most current dispute, on inspection, is not of that shape at all: essentially every party to it agrees C=1 — maize was domesticated once, from teosinte ssp. parviglumis. What is contested is where within Mexico that single event occurred. This chapter reports that dispute honestly rather than dressing it up as a polycentricity question it is not, and separately reports a second, genuinely different kind of question — not about the count or location of the founding event, but about a second wild taxon's contribution to the crop afterward.

6.2 The Balsas consensus

Matsuoka et al. (2002, *PNAS* 99:6080–6084), phylogenetic analysis of 264 maize and teosinte plants at 99 microsatellite loci, found all maize in a single monophyletic lineage nested within ssp. *parviglumis*, dating the divergence to roughly 9,000 years ago and pointing to the Balsas River basin of southwestern Mexico. Ranere, Piperno, Holst, Dickau & Iriarte (2009, *PNAS* 106:5014–5018) and the companion Piperno et al. paper in the same issue reported archaeological confirmation: the Xihuatoxtla Shelter, near the Iguala Valley in Guerrero, contains a stratified early-Holocene occupation with associated stone tools radiocarbon-dated to at least 8,700 cal BP, with starch-grain and phytolith residues on those tools providing direct evidence of maize and domesticated squash in context. Archaeology and genetics here point to the same region independently, the same "two lines of evidence converge" structure this cycle has used throughout.

6.3 The Jalisco–Pacific challenge

Van Heerwaarden et al. (2011, *PNAS* 108:1088–1092) first reported that some ancestral teosinte alleles appeared concentrated in western, not Balsas, populations. A 2018 preprint reanalysis (bioRxiv 10.1101/239707), using 32,739 SNPs across a substantially expanded sample of 29 teosinte populations including previously undersampled Jalisco material, found that Jalisco-Pacific *parviglumis* populations (Telpitita, Villa Purificación) are genetically early-divergent and basal relative to Balsas populations in their reconstructed population graph, and share more ancestral polymorphism with maize and the outgroup *Tripsacum* than Balsas populations do — the opposite pattern from what a Balsas-origin model predicts. **This specific result has not been confirmed here as having passed peer review in a journal**; it is reported as a preprint-stage challenge, exactly as this cycle's discipline requires when a source's publication status is uncertain (cf. §3.4's treatment of an unconfirmed etymological lead).

6.4 A real-coordinate check on how far apart the two candidates actually are

Recomputed via great-circle distance (code/Ch06_07_support_distance_check.py): the Iguala Valley, Guerrero (Balsas consensus) and the Villa Purificación area of Jalisco (Pacific-coast alternative) are **531 km** apart — a genuinely different location within the same broad Mesoamerican dry-tropical-forest zone, not a fine-grained disagreement about which valley within one small region, but well short of the 1,200–3,000+ km separations found between Section I's genuinely distinct centers (barley, rice).

6.5 Why the Polycentricity Index is not computed for maize

Discipline stated explicitly, as §3.5 did for Chapter 3

The index (§2.7) is built to quantify dispersion *among* independently corroborated centers, weighted by how strongly the evidence supports more than one. Here, C=1 on every side of the dispute — the disagreement is about the identity and coordinates of the single center, not its count. Forcing this into PI = C × κ × D would require treating the two candidate locations as if they were two independently corroborated domestication events, which no cited source claims. No PI is computed here; §6.4's 531 km is reported as a location-uncertainty distance only.

A live loose end, reported rather than adjudicated. A 2025 PubMed listing under the title 'Rio Balsas most likely region for maize domestication' looked, on first sight during this revision, like new confirming evidence for §6.2's Balsas consensus. It is not: the listing re-indexes Hastorf's 2009 commentary on the original Balsas excavations, not a new 2025 study. Separately, an unreviewed bioRxiv preprint ('Was maize domesticated in the Balsas Basin?') argues from teosinte population genetics that western Mexican refugia — Jalisco, Michoacán, Colima — deserve renewed attention, which would sit closer to §6.3's Jalisco–Pacific challenge than to the Balsas consensus. Neither changes §6.5's ⊥: one is not new evidence at all, and the other has not been peer-reviewed. Both are named here rather than silently discarded, on the same discipline that keeps this cycle from quietly narrowing an inconvenient search result.

In the formal terms §20.7.1 later defines, both candidate centers here — the Iguala Valley and the Villa Purificación area — are individually reported points (r=1 for each), so maize's ⊥ is not a case of missing coordinates. It arises because the two points compete for the *same* single center rather than each representing a distinct corroborated one: no source treats them as C=2. §20.7.1 anticipates exactly this configuration in its own text: "R(X) can be 0 even for a single proposed center whose own location, not existence, is

contested." No number changes here (§20.7.4); this note only attaches the later formal label to a judgment already made at §6.5.

6.6 A second, different question: does maize have two wild parents, not two wild birthplaces?

Yang, Wang, Liu, Jin, Vallebueno-Estrada, Calfee et al. (2023, *Science* 382:eadg8940), using the largest sample of traditional maize varieties sequenced to date, found that essentially **all modern maize traces to an ancient admixture event** between early domesticated maize and the *highland* teosinte, *Zea mays* ssp. *mexicana*, occurring in the Mexican highlands roughly 6,200–4,000 cal BP — well after the initial Balsas-lowland domestication event itself. The authors detected *mexicana* ancestry in every maize sample they examined, ancient and modern, including archaeological cobs from the Tehuacán Valley (~5,300 cal BP) and South American material.

Why this is not folded into C

This is structurally different from barley's or rice's multi-center patterns. It is not a second, independent *domestication* event in a second place; it is introgression *from* a second wild taxon *into* the one already-domesticated lineage, after that lineage had already left the Balsas lowlands. The nearest Section I parallel is not barley's second center but Huang et al.'s (2012) rice model, where domestication alleles moved *from* japonica *into* local wild rice to produce indica — introgression enriching or extending a lineage, not a second independently-corroborated center of origin as §2.7 defines C. No PI change follows from this finding; it is reported here because it is well-evidenced, current (2023), and genuinely informative about how modern maize came to be, without being the kind of quantity this section's index was built to count.

6.7 Ancient DNA from the domestication corridor: catching the process in motion

§§6.2–6.6 established maize's geographic and post-domestication introgression picture from modern and near-modern genomes. A separate, methodologically distinct line of evidence — ancient DNA recovered directly from archaeological maize itself — speaks to a different question this chapter has not yet addressed: not where domestication began, but how far along the domestication process had progressed by a fixed, independently dated point partway through it.

Vallebueno-Estrada, Rodríguez-Arévalo, Rougon-Cardoso, Martínez González, García Cook, Montiel & Vielle-Calzada (2016, *PNAS* 113:14151–14156) sequenced three newly recovered maize genomes from San Marcos cave, Tehuacán Valley, Puebla — independent of, and roughly 4,000 years later than, the Balsas-basin domestication event itself (§6.2's ~9,000 BP), radiocarbon-dated to a convergent age of approximately 5,000 years BP. Rather than finding a genome already indistinguishable from modern maize at this age, the authors report a genuinely mixed picture locus by locus: two classic domestication genes, *teosinte branched1* (*tb1*) and *brittle endosperm2* (*bt2*), had already lost most of the nucleotide variability present in wild Balsas teosinte — consistent with strong, largely completed selection — while two others, *teosinte glume architecture1* (*tga1*) and *sugary1* (*su1*), still retained partial ancestral (teosinte-like) nucleotide variation at 5,000 BP. The same three genomes were found to be homozygous and identical by descent across their full length — direct genomic evidence of inbreeding, read by the authors as consistent with a still-small founding population at this stage of the crop's history, deep into the post-domestication period rather than at its origin.

Ramos-Madrigal, Smith, Moreno-Mayar, Gopalakrishnan, Ross-Ibarra, Gilbert & Wales (2016, *Current Biology* 26:3195–3201)

sequenced a separate, independently recovered maize cob genome from the same Tehuacán sequence, directly dated to 5,310 years BP, and reached a compatible conclusion using a different sample and an independent laboratory pipeline: this early cob already carried many alleles associated with modern maize at key domestication loci, yet retained a level of genome-wide diversity higher than that of present-day landraces — a second, independent line of ancient genomic evidence for the same graded, not-yet-complete domestication state Vallebueno-Estrada et al. document.

Why this belongs to the temporal question, not the geographic one

Exactly as §2.1 separated the Fertile Crescent's geographic and temporal questions, and §4.3 kept rice's protracted-fixation finding logically independent of its disputed center count, this ancient-DNA evidence bears only on *how gradually* the domestication syndrome fixed after the single Balsas-lowland event, not on §§6.2–6.4's separate dispute over *where* that event occurred. Maize therefore joins einkorn (§2.3) and rice (§4.3) as a third, independently documented case of a geographically single-origin crop whose domestication syndrome nonetheless took millennia to complete — direct ancient-genome evidence at 5,000–5,310 BP still shows a locus-by-locus mix of fixed and unfixed domestication alleles, roughly four millennia after the Balsas event itself.

6.8 A still-incomplete lineage was already on the move: dispersal chronology

Golson, J. (1989). The origins and development of New Guinea agriculture. In: Harris, D.R. & Hillman, G.C. (eds.), Foraging and Farming: The Evolution of Plant Exploitation. London: Unwin Hyman.

Golson, J., Denham, T., Hughes, P., Swadling, P. & Muke, J. (eds.) (2017). Ten Thousand Years of Cultivation at Kuk Swamp in the Highlands of Papua New Guinea. Canberra: ANU Press.

Kamal, N., Tsardakas Renhuldt, N., Bentzer, J., Gundlach, H., Haberer, G., Juhász, A., Lux, T., Bose, U., Tye-Din, J.A., Lang, D., van Gessel, N., Reski, R., Fu, Y.-B., Spégel, P., Ceplitis, A., Himmelbach, A., Waters, A.J., Bekele, W.A., Colgrave, M.L., Hansson, M., Stein, N., Mayer, K.F.X., Jellen, E.N., Maughan, P.J., Tinker, N.A., Mascher, M., Olsson, O., Spannagl, M. & Sirijovski, N. (2022). The mosaic oat genome gives insights into a uniquely healthy cereal crop. Nature 606(7912), 113–119.

Kistler, Thakar, VanDerwarker, Domic, Bergström, George et al. (2018, *Science* 362:1309–1313) applied genomic analysis to ancient and modern South American maize lineages and dated maize's spread out of Mexico: domestication beginning roughly 9,000 years BP (§6.2), the crop traversing Central America by roughly 7,500 years BP, and reaching South America by roughly 6,500 years BP. Directly relevant to §6.7's finding, the authors' central result is that the lineage carried out of Mexico and into South America was itself only **semi-domesticated** at the point of dispersal — later improvement toward the fully domesticated phenotype occurred independently and in parallel among multiple South American populations, including in southwestern Amazonia, rather than being completed once in Mexico and simply carried outward unchanged.

Why this does not change §7.5's or §8.2's index tables

Kistler et al.'s finding describes the *completion*, in parallel, of one already-initiated domestication process across several downstream populations — not a second, independently corroborated origin of the crop from wild teosinte, which is what §2.7's C counts. It is closer in kind to rice's protracted Lower

Yangtze sequence (§4.3) than to any of this cycle's genuine multi-center cases, and, like §6.6's *mexicana* introgression finding, is reported here because it is well-evidenced and directly relevant to how maize came to be, without being the kind of quantity this section's index was built to count. No PI value is computed or revised as a result.

6.9 What Chapter 7 will check

Chapter 7 turns to the Eastern Agricultural Complex, where — unlike maize — this cycle's index does find real, multiply-corroborated polycentricity: not between candidate locations for one species, but between four independently domesticated species in one region, one of which (squash) is itself genuinely two-centered in the way maize turned out not to be.

Chapter 7 — The Eastern Agricultural Complex: Real Polycentricity, Real Synchrony

7.1 Four species, one contested region

Smith (2006, *PNAS* 103:12223–12228) synthesized archaeological and genetic evidence for four plant species proposed as independent eastern North American (ENA) domesticates — marshelder (*Iva annua*), chenopod (*Chenopodium berlandieri*), squash (*Cucurbita pepo*), and sunflower (*Helianthus annuus*) — against a competing hypothesis then current that ENA was not an independent center at all, but had simply received already-domesticated crops introduced from Mexico. Smith's synthesis found genetic and archaeological evidence supporting independent ENA domestication for all four species, reconfirming the region as one of the world's independent centers of agricultural origin — the status §1.3's own table asserted and this chapter now documents rather than assumes.

7.1.1 A fifth domesticate, described since Smith (2006): erect knotweed

Smith's 2006 synthesis could only report on species already recognized as domesticates at the time of writing. Mueller (2017a, *Novon* 25(2):166–179), using population morphometrics on archaeobotanical assemblages, formally described a fifth, previously unrecognized ENA domesticate: erect knotweed (*Polygonum erectum*), naming a distinct domesticated subspecies, *P. erectum* subsp. *watsoniae*, distinguished from its wild progenitor by larger achenes and a shift from tubercled to smooth achene morphs. Mueller (2017b, *Journal of Anthropological Archaeology* 49:39–50) reported the earliest known occurrence of the domesticated subspecies at the Walker-Noe site (15Gd56), an Adena/Hopewell context in central Kentucky, dated to approximately 1 AD, and documented that contemporaneous Middle Woodland knotweed assemblages from habitation sites in western Illinois remained

undomesticated — a within-region asymmetry in domestication status broadly consistent with §7.4's later finding that ENA's domesticates did not all mature into a uniform, region-wide crop complex at once.

Mueller (2017c, *Human Ecology* 45(2):189–203) dated the full cultivation-to-domestication trajectory: erect knotweed was cultivated in ENA from roughly 3,000 to 600 BP, with the domesticated subspecies' hallmark trait — greatly reduced germination heteromorphism, an evolutionary bet-hedging strategy — only fully established by roughly 900 BP. Unlike Chapter 2's or Chapter 4's founder cereals, this domesticate did not persist as a crop into the historical period: cultivation ceased and the domesticated subspecies is now extinct, known only from the archaeobotanical record.

Why this does not change §7.5's index table

Erect knotweed is a single-region, single-origin domesticate (C=1, no second corroborated center proposed anywhere in the cited literature), so it adds no new row to §7.5's PI table under §2.7's definition — the same status as sunflower prior to the Mexican second-center claim (§7.3), reached here without any competing claim ever having been raised. Its value to this chapter is evidentiary rather than index-numerical: it raises Smith's (2006) four-species ENA count to five, strengthens §7.1's reconfirmation of ENA as a genuine independent center by adding a domesticate identified through post-2006 morphometric work rather than presupposed by it, and gives §7.4's synchrony question one further, precisely dated data point — a domestication process not completed until roughly 900 BP, later than marshelder, chenopod, squash or sunflower's own Late Archaic fixation windows, and later still than Smith & Yarnell's 3,800 BP horizon for a working multi-crop complex at Riverton.

7.1.2 Two cultivated non-domesticates: maygrass and little barley

Not every plant named in the wider "Eastern Agricultural Complex" literature crossed the threshold into domestication that this chapter's five confirmed cases (§7.1, §7.1.1, §7.2, §7.3) pass. Two further taxa — maygrass (*Phalaris caroliniana*) and little barley (*Hordeum pusillum*) — were cultivated for centuries alongside chenopod, marshelder, squash and sunflower, and both are already named in §7.4's own account of the Riverton assemblage as "possible cultivated squash and little barley" alongside that section's five *domesticated* plants — a distinction §7.4 already draws in passing and this section now examines directly.

Maygrass is the better-documented of the two non-domesticates. Fritz (2014), in the standard monographic treatment of the species, states that maygrass was widely cultivated but does not appear to have been domesticated. The archaeobotanical record is specific about why: collections of maygrass fruits recovered from ENA sites do not exhibit obvious morphological change through time (Asch & Asch 1985; Cowan 1978), with only one reported exception — Johannessen (1981) documented a single instance of increased caryopsis size — against an otherwise morphologically static record spanning millennia of use. Cowan's (1978) case for intentional human propagation of maygrass therefore rests on a different kind of evidence entirely: a documented disjunction between the plant's archaeological range (as far north as Illinois and Indiana) and its present-day natural range (the southern United States), read as evidence of deliberate transport and cultivation outside its native distribution, not on any change to the seed itself.

Little barley presents a comparable, independently reached verdict. Hunter (1992), examining archaeological little-barley assemblages from ENA sites, found only equivocal evidence for morphological change — non-significant increases in grain size alongside other qualitative shifts — and Mueller (2017c), citing both Fritz (2014) and

Hunter (1992), describes the domestication status of *H. pusillum* in ENA as a matter of live debate rather than settled fact. A separate southwestern United States population of the same species offers a partial contrast: Adams (2014), summarized in the same literature, argues that the predominance of hull-less (naked) charred caryopses in that region's archaeological record constitutes evidence of a true naked-grain trait — the same trait that became predominant in Old World *Hordeum vulgare*, this cycle's own domesticated barley (§2.4). No comparably clear morphological signal has been reported for ENA's own little-barley population specifically, so this parallel to Chapter 2's founder cereal is suggestive rather than established, and is reported here as such.

Why this is a different kind of exclusion from erect knotweed's

§7.1.1 excluded erect knotweed from §7.5's index table for a reason internal to §2.7's formula: it *is* a corroborated domesticate, just a single-region one (C=1), so it contributes no dispersion for the index to weight. Maygrass and little barley are excluded one step further back: under the cited literature's own morphological criteria, neither has been shown to be a domesticate at all, corroborated or otherwise — the prior question the index presupposes an answer to. This is disclosed here in the same spirit as §2.8.2's non-computation for lentil and §6.5's non-computation for maize, but is a distinct case from both: lentil and maize each have an agreed domestication event whose count or location is unsettled; maygrass and little barley have sustained cultivation with, on the cited morphological evidence, no settled domestication event to count in the first place. §7.4's "at least five domesticated seed-bearing plants" at Riverton should be read against this distinction: little barley's appearance in that assemblage is cultivation evidence, not one of the five domesticated taxa the sentence counts.

7.2 Squash: a genuine two-center case within one species

Unlike maize (Ch.6), *Cucurbita pepo* is a case where two independent domestications are well corroborated by two different kinds of evidence agreeing with each other. *C. pepo* ssp. **pepo** was domesticated in Mexico: the oldest archaeological remains, from Guilá Naquitz cave in Oaxaca, date to roughly 10,000 cal BP, and reconstructed vocabulary for squash in New World ancestral languages independently suggests a comparably early, roughly 6,500 BP linguistic terminus. *C. pepo* ssp. **ovifera** was domesticated separately in eastern North America: isozyme allele data (Decker-Walters et al., synthesized in Smith 2006) show that cultivated ssp. *ovifera*'s alleles are a subset specifically of its wild eastern relative *var. ozarkana*'s (Ozark Plateau/Mississippi Valley), not of the Mexican wild relatives (*var. texana* or ssp. *fraterna*), which lack the domesticate's alleles entirely — genetic evidence pointing to a different wild source population than the Mexican one, independently corroborated by the ENA archaeological sequence (§7.4).

Recomputed via great-circle distance (code/Ch06_07_support_distance_check.py): Guilá Naquitz, Oaxaca, and the Ozark Plateau/Mississippi Valley source region are 2,282 km apart.

C	κ	D̄ (km)	PI
2	1.000	2,282	4,565

κ=1.0 here reflects a different, and in one sense stronger, kind of corroboration than barley's 0.556 or rice's 0.20: it is not a fraction of loci or genes split between two signals, but two *independent kinds* of evidence — molecular (isozyme allele-subset structure) and archaeological/linguistic (independent early dates and vocabulary in each region) — in full agreement on C=2, the same "independent methods agree" structure Ch.2 used for einkorn's C=1, applied here to a multi-center rather than single-center case. The resulting

PI=4,565 is the highest computed anywhere in this cycle, driven by both a large real-world separation and maximal evidential agreement.

7.3 Sunflower: a second-center claim that was raised and specifically refuted

Sunflower offers a useful contrast to squash: a second, Mexican domestication center was proposed, investigated, and did not hold up. Lentz et al. (2001) reported a possible sunflower achene from San Andrés, Tabasco, Mexico, dated to 4,130 BP; Heiser (2008) re-examined the specimen and identified it not as a sunflower achene at all but as a bottle gourd (*Lagenaria siceraria*) seed, a finding Smith (2006) supported. Lentz et al. (2008) subsequently reported three further candidate Mexican achenes from Cueva del Gallo, Morelos, ~2,600 BP, but these specimens were destroyed during the dating process, preventing independent confirmation of their identification. Blackman, Scascitelli, Kane, Luton, Rasmussen, Bye, Lentz & Rieseberg (2011, *PNAS* 108:14360–14365) then tested the question directly with haplotype analysis of three genes independently known to have undergone selective sweeps during early sunflower domestication, and found the results consistent only with **a single domestication center in eastern North America** — the same conclusion the region's molecular and archaeological record had long supported before the Mexican hypothesis was raised.

Why sunflower gets C=1, not a contested C=2

This is not the same situation as barley's contested Tibetan center (Ch.2) or rice's C=3 model (Ch.4), where a real, still-open second signal exists alongside the primary one. Here, the specific empirical basis for a second center (the Tabasco specimen) was directly reexamined and reclassified as a different species entirely, and the strongest available genetic test (Blackman et

al. 2011) came back negative for a second origin. Sunflower is reported here as C=1, PI=0, with the refuted claim documented for completeness rather than carried forward as a live alternative.

7.4 The synchrony question: when did four domesticates become one complex?

Individual ENA species were domesticated on staggered timelines: AMS dating placed squash, marshelder, chenopod and sunflower domestication across a broad Late Archaic window, roughly 5,000–3,800 BP, with no two species firmly shown to have been under cultivation together before roughly 4,000 BP. Smith & Yarnell (2009, *PNAS* 106:6561–6566), reanalyzing archaeobotanical assemblages from a short, well-dated occupation at the Riverton site in Illinois, documented **contemporaneous cultivation** at **3,800 BP** of at least five domesticated seed-bearing plants together — bottle gourd, marshelder (*I. annua* var. *macrocarpa*), sunflower, and two distinct cultivated varieties of chenopod (*C. berlandieri*), alongside possible cultivated squash and little barley. Their explicit finding: *"Before 4000 B.P. there is no indication of a crop complex in ENA, only isolated evidence for single indigenous domesticate species."*

What this answers, and what it leaves open

This directly answers §1.3's "relative sequence and synchrony across 4 species" question: the four-plus ENA domesticates were **not** domesticated as a coordinated package. Each was independently brought under cultivation on its own timeline over roughly a millennium, and only coalesced into a working multi-crop complex by 3,800 BP at sites like Riverton. Smith & Yarnell explicitly read this as evidence against a population-pressure-driven, rapid-package model and for a gradual integration into existing hunting-and-gathering economies in

resource-rich river valleys — a conclusion about process, not just chronology, that this cycle reports without independently testing.

7.5 Cross-cycle synthesis: every case computed in this cycle

Crop (model)	C	κ	D̄ (km)	PI
Einkorn	1	1.000	0	0
Barley	2	0.556	3,046	3,384
Rice (C=1 model)	1	1.000	0	0
Rice (C=2 model)	2	0.200	1,761	704
Maize	1 (location disputed, not C)	n/a	531 (location only)	not computed
Squash (C. pepo)	2	1.000	2,282	4,565
Sunflower	1 (2nd center proposed, refuted)	1.000	0	0

Across both sections, the index's highest values belong to the two cases with the strongest, most unanimous multi-center evidence (squash, PI=4,565; barley, PI=3,384) rather than the two cases with the largest real-world distances alone — rice's C=2 candidates, at 1,761 km, sit closer together than barley's or squash's, but rice's PI is lowest among the genuine multi-center cases because its best-quantified κ (0.20) is the weakest. Three of seven rows are genuine PI=0 single-center cases (einkorn, rice under Molina/Huang, sunflower after Blackman et al.'s test), each reached by a different route: unanimous agreement from the start (einkorn, rice), and a specific contrary claim raised and then empirically refuted (sunflower). Maize sits outside the table's logic entirely, which is itself the chapter's point: not every live dispute in this literature is a polycentricity dispute, and the index is honest about the difference.

7.6 Closing Section II

§5.2's stopping rule set this section's scope as maize and the Eastern Agricultural Complex, and both are now complete. Maize turned out to test the index's boundary condition rather than its main case:

a live, current (2018 preprint) dispute that, on inspection, concerns location rather than count, correctly reported as PI-not-computed rather than forced into a number. The Eastern Agricultural Complex tested the opposite boundary — a region with real, multiply-corroborated polycentricity at two different scales (four independent species; one of those species, squash, independently two-centered) plus a genuine, dateable synchrony question the cited literature answers directly (no working complex before 4,000 BP; a coherent one by 3,800 BP).

Stopping-rule decision for Section II

No Section III is committed to here. This two-section cycle has now applied the Domestication Polycentricity Index to seven crop/model combinations across four independent world regions (the Fertile Crescent, China/South-Southeast Asia, Mesoamerica, and eastern North America), including cases where the index correctly returns zero, cases where it is correctly not computed at all, and one case (squash) returning this cycle's highest value. That range of outcomes is what §2.6 originally asked of it, and this section treats that as a natural close for the current programme rather than a launching point for an unbounded seventh case. Any future extension of this method requires its own new, separately declared stopping rule, exactly as §1.5 and §5.2 required before each of this cycle's two sections.

Chapter 8 — Closing Synthesis: Two Sections, Seven Cases, One Index

8.1 What §5.2 promised, and what this chapter delivers

§5.2 offered a synthesis across both sections' six-plus cases "as a closing summary, not as a new research program." Nothing new is computed here: every C, κ, $\bar{D}$, and PI value in this chapter is carried forward unchanged from the chapter that first derived it (§2.7, §4.5–6, §7.5), each traceable to the executed script that produced it. This chapter's contribution is organizational and interpretive — asking what the completed run, taken as a whole, does and does not show — not a new round of data collection.

8.2 The seven cases, ranked

The same seven rows tabulated in §7.5, here ordered by PI rather than by chapter sequence, to make the index's own ranking legible on its own terms:

Rank	Crop (model)	C	κ	$\bar{D}$ (km)	PI
1	Squash (C. pepo)	2	1.000	2,282	4,565
2	Barley	2	0.556	3,046	3,384
3	Rice (C=2 model)	2	0.200	1,761	704
4 (tie)	Einkorn	1	1.000	0	0
4 (tie)	Rice (C=1 model)	1	1.000	0	0
4 (tie)	Sunflower	1 (2nd center refuted)	1.000	0	0
—	Maize	1 (location disputed, not C)	n/a	531 (location only)	not computed

Reordering changes nothing about the underlying figures, but it sharpens §7.5's observation: the ranking is not driven by geographic distance alone. Rice's C=2 candidates (1,761 km) sit closer together than either squash's (2,282 km) or barley's (3,046 km), yet PI tracks

κ at least as strongly as it tracks D̄ — squash and barley both carry κ at or above 0.556, while rice's best-quantified split (0.200) is the weakest of the three genuine multi-center cases, and that alone accounts for most of the gap between rank 3 and ranks 1–2.

8.3 Three different routes to PI = 0

Four of the seven rows land at the index's floor, and no two arrive there the same way, which is itself a finding about what "zero" can mean under this method:

Three routes to PI = 0, not one

Unanimous from the outset (einkorn, §2.2; rice under Molina/Huang, §4.2–4.3). Two independent genetic methods agree on C=1 before any contrary claim is raised. κ=1.0 is trivial, not evidentially thin.

Proposed, tested, and refuted (sunflower, §7.3). A second-center claim (Lentz et al. 2001) was live long enough to be investigated, was reclassified to a different species on reexamination, and a direct haplotype test (Blackman et al. 2011) returned a negative result for a second origin. C=1 here reflects a claim that was checked and failed, not a claim that was never made.

Outside the index's domain entirely (maize, §6.5). This is not a PI=0 row at all — it is the one case in the cycle where C=1 on every side of a live dispute, because the disagreement concerns the single center's location, not its count. §6.5 declined to compute PI rather than force a location-uncertainty distance (531 km) into a formula built to weight dispersion among independently corroborated centers.

8.4 What the index was, and was not, built to measure

Across both sections the Domestication Polycentricity Index (§2.7) did exactly what §2.6 asked of it: it took quantities the cited

literature already reported — center counts, per-locus or per-gene differentiation fractions, real coordinates — and returned one comparable number per model, without smoothing over disagreement. Where the literature itself did not converge on a single C (rice, §4.5), the index was extended to report multiple PI values side by side rather than adjudicate between them. Where a dispute turned out not to be about C at all (maize, §6.5), the index correctly returned nothing rather than a misleading number. Both extensions were disclosed at the point they were needed, not built in from the start, which is itself consistent with §1.4's original commitment to report scope limitations explicitly rather than design them away in advance.

The index has real limits, stated here rather than left implicit. It is only as good as the κ figure available: einkorn's and squash's κ=1.0 rest on qualitatively different kinds of agreement (two convergent genetic methods; molecular and archaeological/linguistic agreement) than barley's or rice's fractional κ, and the index treats them identically because it multiplies rather than weighting by evidence type. It also has no mechanism for introgression—the case Ch.6.6 flagged for maize (post-domestication *mexicana* admixture) and Huang et al.'s indica-formation model (§4.3) both involve gene flow *into* an already-domesticated lineage, which is a different phenomenon from a second independent domestication and is deliberately left outside C rather than folded into it.

8.5 Four regions, one method

The seven models span four independent world regions — the Fertile Crescent (einkorn, barley), China and South/Southeast Asia (rice), Mesoamerica (maize, squash's ssp. pepo), and eastern North America (squash's ssp. ovifera, sunflower, and by extension the other ENA domesticates surveyed in §7.1) — using one consistent method and one consistent no-invented-data discipline

throughout. That the same formula produces a PI=0 floor case, a mid-range case (rice), a near-ceiling case (barley), and this cycle's maximum (squash), plus one case where it is correctly not computed at all (maize), is read here as evidence that the index behaves sensibly across genuinely different evidentiary situations rather than as evidence that polycentricity itself is common or rare in absolute terms — the seven cases were selected in §1.3 and §5.1 precisely because they disagree with each other, not sampled to be representative of plant domestication as a whole.

8.6 Final stopping-rule declaration

> **No Section III, per §5.2's own precommitment**
>
> §5.2 committed to no Section III at the point Section II's scope was set, and nothing in the completed run of either section changes that. This chapter closes the cycle as planned: two sections, four case-study chapters (Ch.2, 4, 6, 7), one linguistic check (Ch.3), one index (§2.7) applied across all seven models, and this synthesis. Extending the method to any further crop, region, or index refinement — including the evidence-type weighting or introgression handling flagged in §8.4 as open limitations — requires a new, separately declared stopping rule, exactly as §1.5 and §5.2 each required before their own first case-study chapter.

This closes the cycle.

Section III — The Common Bean: A New Stopping Rule

Opened here per Chapter 8, §8.6's own requirement: any extension needs a new, separately declared stopping rule

Chapter 9 — The Common Bean: A Fifth Region, a Sixth Species, and a Third Kind of Question

9.1 A new stopping rule, declared before this chapter's data is presented

Stopping rule for Section III

1. **This section**: one case only — the common bean (*Phaseolus vulgaris*), chosen because it stress-tests the method along a third axis distinct from both prior sections' cases. Section I's cases disputed C itself (rice) or a contested add-on center (barley). Section II's cases disputed a center's location, not its count (maize), or offered uncontested multi-species polycentricity (ENA). The common bean offers a fourth pattern: C=2 is *not* contested by any cited source, but the literature separately disputes something this cycle has not yet had a case to test — whether the *wild species itself* had one geographic origin before either domestication event. §9.2 keeps this question strictly separate from C, exactly as §2.1 separated geography from tempo for the Fertile Crescent cereals.

2. No Section IV is committed to now. This is a single-case section by design; extending this cycle to any further crop or region again requires a new, separately declared stopping rule, exactly as §1.5, §5.2, and §8.6 each required before their own scope was set.

The same data commitments carry over unchanged from §1.4 and §5.2: no invented figures, no synthetic illustrative datasets, disagreement reported rather than resolved by authorial preference, and every computed quantity accompanied by its executed script.

9.2 Two questions, kept separate, as §2.1 first required

The common bean literature runs together two logically independent questions, exactly as §2.1 found for the Fertile Crescent cereals: (a) how many times was the crop independently

domesticated, and where? (b) where did the wild progenitor species itself originate, before either domestication event? §9.3–9.6 address (a); §9.7 addresses (b) on its own terms, as a genuinely different question this cycle has not yet had occasion to separate out this cleanly.

9.3 Two independent domestications, corroborated by two independent methods

Chacón, Pickersgill & Debouck (2005, *Theor. Appl. Genet.* 110:432–444): chloroplast DNA haplotyping (PCR sequencing and PCR-RFLP) across 165 domesticated landraces, 23 weedy accessions, and 134 wild accessions spanning the entire geographic range of wild *P. vulgaris* found 14 chloroplast haplotypes in wild beans, only 5 of which recur in domesticated material, and concluded independent domestications in Mesoamerica and the Andes, each with its own founder effect.

Schmutz, McClean, Mamidi et al. (2014, *Nature Genetics* 46:707–713): the common bean reference genome paper, resequencing 60 wild individuals and 100 landraces from the two gene pools, **"confirmed 2 independent domestications from genetic pools that diverged before human colonization."** This is the same "two different methods, one older and phylogenetic, one newer and genome-wide, converging independently" structure §6.2 documented for maize's Balsas consensus and §7.2 documented for squash — applied here to a third case.

9.4 A real-coordinate check on the two centers

Recomputed via great-circle distance (code/Ch09_support_distance_check.py), using two Mesoamerican archaeobotanical anchors (Tehuacán Valley and Guilá Naquitz Cave, Oaxaca — both dated by Kaplan & Lynch 1999) against the single most-cited and earliest secure Andean anchor (Guitarrero Cave, Ancash, Peru):

Mesoamerican anchor	Andean anchor	Distance
Tehuacán Valley, Puebla	Guitarrero Cave, Ancash	3,759 km
Guilá Naquitz Cave, Oaxaca	Guitarrero Cave, Ancash	3,558 km

Mean over these two pairs: **3,658 km** (range 3,558–3,759 km) — the largest $\bar{D}$ computed anywhere in this cycle, exceeding barley's 3,046 km and squash's 2,282 km, consistent with Mesoamerica and the Andes being the two most geographically distant center-pairs this cycle has examined.

9.5 The Domestication Polycentricity Index applied to the common bean

Schmutz et al. (2014) directly report that of 74 Mb of genome sequence identified as putatively involved in domestication, only 7.234 Mb was shared between the Mesoamerican and Andean domestication events — independent selection on independent genomic regions in each. The fraction *not* shared — 1 − 7.234/74 — is used here as κ, the same "directly reported fraction" role Morrell & Clegg's 10/18 and Jing et al.'s ~20% played earlier. Source: code/Ch09_polycentricity_index.py, unedited output.

C	κ	$\bar{D}$ (km)	PI
2	0.902	3,658	6,601

PI=6,601 is this cycle's highest value to date, surpassing squash's 4,565. Both cases share the same structure that drives PI upward: two independent lines of evidence in near-total agreement (κ=0.902 here, 1.000 for squash) combined with a large real-world separation (3,658 km here, 2,282 km for squash) — the common bean's $\bar{D}$ is larger, which more than offsets its slightly lower κ. As §8.2 already observed for the first seven cases, the ranking continues to track κ at least as strongly as $\bar{D}$: rice's C=2 model, with the smallest $\bar{D}$ among the four genuine multi-center cases now computed, is not also the lowest-PI case only because its κ (0.200) is so much weaker than either barley's, squash's, or the bean's.

9.6 Updated cross-cycle synthesis: eight cases

Crop (model)	C	κ	D̄ (km)	PI
Common bean	2	0.902	3,658	6,601
Squash (C. pepo)	2	1.000	2,282	4,565
Barley	2	0.556	3,046	3,384
Rice (C=2 model)	2	0.200	1,761	704
Einkorn	1	1.000	0	0
Rice (C=1 model)	1	1.000	0	0
Sunflower	1 (2nd center refuted)	1.000	0	0
Maize	1 (location disputed, not C)	n/a	531 (location only)	not computed

The common bean now occupies both extremes at once relative to the rest of the cycle: the largest D̄ of any case (3,658 km) and, among the four genuine multi-center cases, the second-highest κ (0.902, behind only squash's 1.000). §8.2's observation about PI tracking κ at least as strongly as D̄ holds with an eighth case added rather than being an artifact of the original seven.

9.7 A separate question: did the wild species itself have one origin?

Independently of §9.3–9.6's domestication-count question, Bitocchi, Bellucci, Giardini et al. (2012, *PNAS* 109:E788–E796) sequenced nucleotide diversity across the wild *P. vulgaris* range and argued for a **single Mesoamerican origin of the wild species**, with the Andean wild gene pool descending from a founder population that dispersed south from Mesoamerica and then passed through a pre-domestication genetic bottleneck — a bottleneck independently detected by Bitocchi et al. (2013, *New Phytol.* 197:300–313) as three-fold greater reduction in genetic diversity during the Mesoamerican domestication bottleneck than the Andean one, read by that paper as consistent with the Andean wild population having already been depleted *before* its own domestication bottleneck began.

Why this is not folded into C

This is structurally the same kind of separation §6.6 drew for maize's *mexicana* introgression: a question about the *species'* history before domestication, not about how many times domestication itself independently occurred. Schmutz et al. (2014) make the compatibility explicit: their genome data "conform to the Mesoamerican origin model of the common bean, with an Andean bottleneck that predated domestication," while still reporting asymmetric wild-to-wild gene flow (Mesoamerica→Andes migration rate 0.135, Andes→Mesoamerica 0.087) and still confirming two independent domestication events afterward. A single-origin wild species that later diverged into two isolated gene pools, each independently domesticated, is C=2 by §2.7's definition regardless of whether the wild species itself had one geographic origin or several — exactly as barley's contested Tibetan center (Ch.2) and rice's C=3 model (Ch.4) were kept as prose-only discussion rather than folded into an invented κ, this cycle keeps the bean's species-origin question in prose here rather than treating it as a rival value of C.

9.8 Lima bean: a sister case with a directly conflicting statistical verdict

Phaseolus lunatus, lima bean, is the second most economically important Phaseolus crop after the common bean and shares its two-region (Mesoamerica/Andes) domestication geography, but its Mesoamerican side carries a genuinely unresolved sub-question the common bean's own literature (§9.1–9.6) does not have: whether Mesoamerica itself was one domestication center or two.

Wild lima bean is structured into at least three geographically distinct gene pools: Mesoamerican I (MI, central-western Mexico), Mesoamerican II (MII, southeastern Mexico through Guatemala and Costa Rica, with a broader range extending into northern South

America), and Andean I (AI, a narrow range in the Andes of Ecuador and northern Peru) — confirmed with genome-wide SNP data by Chacón-Sánchez & Martínez-Castillo (2017, *Frontiers in Plant Science* 8:1551), who also found suggestive evidence of a fourth, Colombian gene pool (AII). Cultivated lima beans fall into two landrace groups matching this wild structure by seed size and geography: small-seeded Mesoamerican "Sieva" and "Potato" types, and large-seeded Andean "Big Lima" types — directly paralleling the common bean's own Mesoamerican/Andean split (§9.3).

Where lima bean diverges from the common bean's cleaner two-method agreement (§9.3) is inside Mesoamerica itself. Motta-Aldana et al. (2010) had proposed two competing scenarios for the Mesoamerican landraces: (1) two independent domestications, one from wild gene pool MI and a separate one from wild gene pool MII, or (2) a single domestication from MI followed by post-domestication admixture with wild MII populations, producing the apparent MII-associated landraces without a second true domestication event. Chacón-Sánchez & Martínez-Castillo (2017) tested these two scenarios directly with an Approximate Bayesian Computation (ABC) approach on 2,527 genome-wide SNPs (30 wild MI, 30 wild MII, 30 domesticated MI, and all 17 available domesticated MII accessions), using two different estimation methods on the same simulated dataset.

Scenario	**Direct-approach posterior**	**Logistic-approach posterior**
1. Independent domestications within MI and MII	0.720	0.000
2. Single domestication (MI) with admixture from wild MII	0.280	1.000

The two estimation methods, applied by the same authors to the same underlying simulated and observed data, return opposite verdicts: the direct approach favors two independent Mesoamerican domestications (posterior 0.720), while the weighted

polychotomous logistic regression approach favors a single Mesoamerican domestication with admixture (posterior 1.000, with scenario 1 receiving no support at all under that method). Chacón-Sánchez & Martínez-Castillo state this plainly rather than picking a preferred method: both scenarios may be supported by the genetic data, and the two ABC estimators disagree with each other on which is better supported.

Why no single PI is computed for lima bean's Mesoamerican sub-structure

This is a genuinely new situation for this cycle's index: not a case where the literature is split between different studies (rice, §4.2), nor one where a single study's two estimation methods agree but a contested extra claim exists (barley's Tibetan center, §2.4), but one where the same authors, the same dataset, and the same statistical framework return opposite best-supported models depending on which of two standard ABC estimators is used. Reporting a single κ for "Mesoamerican C=1 vs. C=2" here would require choosing one estimator's verdict over the other's without a principled reason to do so — exactly the kind of authorial resolution of disagreement §1.4 committed this cycle never to perform. No PI is computed for the Mesoamerican sub-structure; both posteriors are reported in full in the table above instead.

The Mesoamerica/Andes split itself, unlike the MI/MII question, is not in dispute: every cited source agrees the Andean gene pool (AI) is genetically distinct from both Mesoamerican pools and was domesticated separately, consistent with the common bean's own well-corroborated C=2 Mesoamerica/Andes structure (§9.3). Representative points within each cited wild-gene-pool region (central-western Mexico for MI; the Guatemala–Costa Rica sector of MII's range; the Ecuador/northern-Peru sector of AI's range) give, via great-circle distance (code/Ch09_lima_bean_distance_check.py): MI–MII 1,516 km; MI–

AI 3,802 km; MII–AI 2,417 km — a mean AI-to-Mesoamerica distance of 3,109 km, comparable to the common bean's own 3,658 km Mesoamerica–Andes separation (§9.4), and consistent with the same two continental-scale regions being involved in both Phaseolus species.

The two species' domestication chronologies are strikingly asynchronous. Andean lima bean domestication is placed at approximately 2000 BC — within the same broad millennium as the common bean's own Andean domestication (§9.4's Guitarrero Cave evidence) — while Mesoamerican lima bean domestication (whichever of §9.8's two scenarios is correct) is placed at approximately 800 AD, roughly 2,800 years later. This is the largest within-crop domestication-timing gap reported anywhere in this cycle, and is offered here as a disclosed, unexplained asymmetry rather than a resolved one: no cited source in this chapter's search directly addresses why lima bean's Mesoamerican domestication lagged so far behind both its own Andean sister-event and the common bean's broadly contemporaneous Mesoamerican and Andean events (§9.3–9.4).

9.9 Closing Section III

This single-case section did what §9.1 set out to test: a domestication-count question with no live dispute (C=2, agreed by chloroplast and genome-wide evidence alike) sitting alongside a genuinely separate, still-substantive question — the wild species' own geographic origin — that this cycle's index is correctly not built to answer and does not attempt to. The result is this cycle's highest PI value (6,601), reached not because the underlying dispute is deeper than barley's or rice's but because both κ and $\bar{D}$ happen to be large together in this one case, which §9.5 reports as an observation about this case, not a claim that common bean's origin

is somehow more thoroughly established than the cycle's other C=2 cases.

Final stopping-rule declaration for Section III

No Section IV is committed to here. Three sections, nine chapters, eight crop/model combinations across five independent world regions (Fertile Crescent; China/South-Southeast Asia; Mesoamerica; eastern North America; the Andes) have now been carried through this cycle's single index under one unchanged no-invented-data discipline. A further case — sorghum, cotton, or any other crop this chapter does not name — would need its own stopping rule declared first, in keeping with how every section here has opened.

This closes Section III.

Section IV — Grapevine: The Smallest Distance Between Two Real Centers

Opened here per Chapter 9, §9.9's own requirement: any extension needs a new, separately declared stopping rule

Chapter 10 — Grapevine: Two Centers, Barely Apart

10.1 Why grapevine, and what this chapter tests

This chapter is again a single case — grapevine (Vitis vinifera) — chosen because it can test something none of this cycle's other C=2 cases can. Every prior multi-center case (barley, rice, squash, common bean) paired a directly reported κ with a large real-world $\bar{D}$ (1,761–3,658 km). Dong et al.'s (2023, Science 379:892–901) grapevine genome study reports two independently corroborated centers only a few hundred kilometers apart — the first case here where a strong κ might sit alongside a small $\bar{D}$, directly testing whether §8.2's and §9.6's finding, that PI tracks κ at least as strongly as $\bar{D}$, still holds when the two pull apart. As with bean, no further case is committed to beyond this one.

The same data commitments carry over unchanged: no invented figures, no synthetic illustrative datasets, disagreement reported rather than resolved by authorial preference, and every computed quantity accompanied by its executed script.

10.2 Two concurrent, independent domestications

Dong, Duan, Xia et al. (2023, *Science* 379:892–901): whole-genome analysis of 3,525 cultivated and wild *Vitis* accessions (2,503 *V. vinifera*, 1,022 *V. vinifera* subsp. *sylvestris*) found that cultivated group CG1 (Western Asian table grapevines) and CG2 (Caucasian wine grapevines) each descend from a distinct wild *sylvestris* population (Syl-E1 and Syl-E2 respectively) that had already genetically separated during the Pleistocene, long before either domestication event. Outgroup f3 statistics, an AIC-based phylogenetic model comparison, and MSMC2 split-time estimation all independently favored a **dual-origin model over a single primary domestication center**, with population-split times for both the CG1/Syl-E1 and CG2/Syl-E2 pairs converging on **≈11,000 years**

ago (95% CI ≈10,500–12,500 years ago) — statistically indistinguishable between the two pairs, meaning the two domestications were concurrent rather than sequential.

10.2.1 A competing model: single origin plus post-domestication introgression

Dong et al.'s (2023) two centers, CG1 and CG2, are both located within the same Western Asia/Caucasus corridor (§10.3 computes only 305 km between their archaeological anchors). A separate, earlier dispute concerns a geographically more distant third claim: whether Western European wine grapes — over 70% of Iberian Peninsula cultivars carry DNA compatible with a western, European sylvestris source — represent an independent western Mediterranean domestication, or introgression from local wild populations into vines already domesticated in Western Asia. Magris, Jurman, Fornasiero, Paparelli, Schwope, Marroni, Di Gaspero & Morgante (2021, *Nature Communications* 12:7240), whole-genome sequencing 204 V. vinifera accessions (122 newly resequenced, plus 48 wild and 33 feral sylvestris), report that all their analyses support a single domestication event in Western Asia, with the distinctive Western European cultivar diversity arising from numerous, pervasive introgressions from European wild sylvestris populations after that single domestication — not from a second, independent domestication event in the west.

Why this does not revise §10.4's PI computation

This is the same distinction §6.6 drew for maize's post-domestication mexicana admixture: introgression from a wild source population into an already-domesticated lineage is not, under §2.7's definition, a second independently corroborated domestication center. Magris et al.'s single-origin-plus-introgression model addresses a different geographic axis (Western Asia vs. western Mediterranean/Iberia) than Dong et al.'s CG1/CG2 distinction (Western Asia vs. Caucasus, both

within the same 305 km corridor computed in §10.3), so the two studies are not in direct, head-to-head conflict over the same claim — but Magris et al.'s result does mean that a third candidate center sometimes proposed in the wider literature (an independent western Mediterranean domestication) is, on this genome-scale evidence, better explained as introgression into an already-domesticated lineage than as a genuine third origin. No PI is revised or extended to C=3 here: exactly as §6.5 declined to compute a location-uncertainty distance for maize, this cycle does not fold a refuted or reclassified third-center claim into the index (cf. sunflower, §7.3, for the same treatment of a claim that did not survive testing).

10.2.2 A real-coordinate check on a proposed, and since reinterpreted, third center

A separate and older claim, distinct from §10.2.1's Western European introgression debate, proposed Sardinia itself as an independent secondary domestication center. Grassi, Labra, Imazio, Spada, Sgorbati, Scienza & Sala (2003, Theoretical and Applied Genetics) reported two Sardinian cultivars (Bovale murru and Bovale muristellu) sharing roughly half their alleles at six nuclear SSR loci with three individuals from a local wild sylvestris population, and read this as evidence of a secondary domestication event distinct from Dong et al.'s two corroborated centers (§10.2). No source reviewed here treats Sardinia as a third pole within Dong et al.'s own CG1/CG2 framework; it is examined here on its own terms, as a claim the later literature has since revisited rather than confirmed.

Recomputed via great-circle distance (code/Ch10_sardinia_check.py), anchored to the same two Western Asia/Caucasus sites already used in §10.3 (Hajji Firuz Tepe and Areni-1 Cave) and to a geographic centroid of Sardinia — a regional-grain anchor rather than a single named site, since the

sampling in Grassi et al. (2003, 2006) is reported at island scale, on the same convention already applied to sheep's broad zone (§16.4):

Hajji Firuz Tepe → Sardinia centroid: 3,180.5 km. Areni-1 Cave → Sardinia centroid: 3,062.6 km. Both figures are roughly ten times §10.3's own two-center baseline of 305 km — Sardinia sits an order of magnitude farther from either established center than the two established centers sit from each other, the opposite geographic signature from a genuine third pole of a tight regional cluster.

The distance alone does not settle the claim — geographic remoteness is consistent with either a true independent domestication or a false one — but the later genetic literature independently converges on the latter reading. Zecca, De Mattia, Lovicu, Labra, Sala & Grassi (2010, Plant Biology), resampling the same Sardinian wild populations with 13 SSR loci, found that the putative hybrid individuals underlying the 2003 claim are better explained as cultivar introgression into wild stands — domesticated vines escaping into, and interbreeding with, local wild populations — rather than as evidence of a domestication event native to the island. This is the same evidentiary pattern this cycle labeled a raised-and-refuted claim for sunflower's second center (§7.3): an initial signal, read at the time as a second center, that did not survive reexamination with better-targeted sampling. Grapevine's C=2 result (§10.2–§10.4) is unaffected; this subsection reports why a plausible-sounding third candidate does not revise it, rather than leaving that candidate undiscussed.

10.3 A real-coordinate check on the two centers

Recomputed via great-circle distance (code/Ch10_support_distance_check.py), anchored to the earliest directly cited archaeological wine evidence within each of Dong et al.'s named domestication regions: Hajji Firuz Tepe, West Azerbaijan, Iran (northern Zagros, within the “Western Asia”

center; McGovern et al. 1996, *PNAS*, tartaric-acid residue dated to c. 5400–5000 BC) and Areni-1 Cave, Vayots Dzor, Armenia (southern Caucasus, within the "Caucasus" center; Barnard et al. 2011, *PNAS*, integrated winemaking installation dated to c. 4000 cal BC):

Western Asia anchor	Caucasus anchor	Distance
Hajji Firuz Tepe, Iran	Areni-1 Cave, Armenia	305 km

305 km is by far the smallest $\bar{D}$ of any multi-center case in this cycle — barley's smallest anchor pair alone (Zagros–Central Asia, 2,531 km) is more than eight times larger. Both centers sit within the same broad Zagros–Caucasus mountain corridor rather than on different continents or subcontinents, unlike every other C=2 case this cycle has examined.

10.4 The Domestication Polycentricity Index applied to grapevine

Dong et al. directly report domestication-associated selective-sweep gene counts for each group: 1,140 genes (132 genomic regions) for CG1 and 887 genes (137 regions) for CG2, of which only 189 genes (31 regions) are shared between both. The fraction of the combined gene set *not* shared — arising independently in each domestication — is used here as κ, the same role Schmutz et al.'s 7.234/74 Mb played for the common bean (§9.5). Source: code/Ch10_polycentricity_index.py, unedited output.

C	κ	$\bar{D}$ (km)	PI
2	0.897	305	547

PI=547 is the **lowest value among every genuine multi-center case computed in this cycle** — lower than rice's C=2 model (704), despite grapevine's κ (0.897) being closer to squash's and the common bean's than to rice's (0.200). §10.1's question is answered directly: a strong, well-corroborated κ does *not* guarantee a high PI when $\bar{D}$ is small enough. §8.2 and §9.6 observed that PI tracked κ at least as strongly as $\bar{D}$ across seven and eight cases respectively; grapevine is this cycle's clearest case where $\bar{D}$, not κ, is the binding constraint

— a correction to that earlier pattern rather than a confirmation of it, and exactly the kind of result §10.1 opened this section to find.

10.5 Updated cross-cycle synthesis: nine cases

Crop (model)	C	κ	D̄ (km)	PI
Common bean	2	0.902	3,658	6,601
Squash (C. pepo)	2	1.000	2,282	4,565
Barley	2	0.556	3,046	3,384
Rice (C=2 model)	2	0.200	1,761	704
Grapevine	2	0.897	305	547
Einkorn	1	1.000	0	0
Rice (C=1 model)	1	1.000	0	0
Sunflower	1 (2nd center refuted)	1.000	0	0
Maize	1 (location disputed, not C)	n/a	531 (location only)	not computed

With grapevine added, the cycle now spans PI values from 0 to 6,601 across five genuine multi-center cases, and the ranking no longer reduces to either quantity alone: barley (κ=0.556, D̄=3,046) and grapevine (κ=0.897, D̄=305) sit at opposite ends of the κ spectrum among the five, yet land in the middle and the bottom of the PI ranking respectively, because PI is a product of both terms and neither dominates uniformly across cases this cycle has now examined. This is read here as the index behaving as §2.7 designed it to — a transparent multiplicative combination with no single term privileged — rather than as a defect in any one case's figures.

10.6 Closing Section IV

This single-case section did what §10.1 set out to test: whether a strong, recent, high-profile κ could be paired with a small D̄, and whether the cycle's earlier observation about PI tracking κ would survive that combination. It did not — grapevine's PI is this cycle's lowest genuine multi-center value despite its κ being its third-highest, which sharpens rather than undermines §2.7's original

design: the index reports what the cited evidence gives it, including combinations that complicate a pattern this cycle had provisionally noticed in three earlier sections.

Final stopping-rule declaration for Section IV

No Section V is committed to here. Four sections, ten chapters, nine crop/model combinations across six independent world regions (Fertile Crescent; China/South-Southeast Asia; Mesoamerica; eastern North America; the Andes; Western Asia/Caucasus) have now been carried through this cycle's single index under one unchanged no-invented-data discipline. Taking up a further case would again mean declaring its stopping rule first, exactly as this cycle has done at the outset of every section so far.

This closes Section IV.

Chapter 11 — Pig Domestication: Testing the Method Beyond Plants

11.1 A new stopping rule, declared before this chapter's data is presented

Stopping rule for Section V

1. This section: one case only — pig domestication (*Sus scrofa*), chosen because it stress-tests this cycle's method along an axis none of the prior ten chapters could: every case so far has been a plant, evidenced by population genetics of living cultivars, archaeobotanical seed/rind morphology, and occasionally reconstructed vocabulary. Pig domestication is evidenced instead by zooarchaeology (tooth wear, kill-off age profiles, body-size reduction) and ancient/modern mitochondrial DNA phylogeography of an animal — a genuinely different evidence base. The question this section asks is not "is pig domestication polycentric" (it plainly is, and more so than any plant case in this cycle) but whether the Domestication Polycentricity Index, built and tuned entirely on plant evidence across Sections I–IV, still produces a meaningful, honestly-caveated number when the underlying data type changes this much.

2. No Section VI is committed to now. This is a single-case section by design, exactly as Sections III and IV were; extending this cycle again requires a new, separately declared stopping rule, exactly as §1.5, §5.2, §8.6 (Ch.8's closing), §9.9, and §10.1 each required before their own scope was set.

The same data commitments carry over unchanged from every prior section: no invented figures, no synthetic illustrative datasets, disagreement reported rather than resolved by authorial preference, and every computed quantity accompanied by its executed script (code/Ch11_support_distance_check.py).

11.2 Why an animal case is a genuine methodological test, not a change of subject

Every case in Sections I–IV shares a structural feature the Polycentricity Index quietly depends on: for a plant, the wild progenitor's present-day range is a reasonably direct proxy for where domestication could have happened, because wild cereals, rice, cucurbits and grapevine are photosynthetic, climate-bound, and effectively immobile across a human lifetime. *Sus scrofa*, the wild boar, is none of these things. Larson, Dobney, Albarella, Fang, Matisoo-Smith, Robins, Lowden, Finlayson, Brand, Willerslev, Rowley-Conwy, Andersson & Cooper (2005, *Science* 307:1618–1621) sequenced mitochondrial DNA from 686 wild and domestic pig specimens and found that wild boar itself originated in island Southeast Asia and dispersed across essentially the whole of Eurasia well before any domestication event — meaning a candidate "center" for pigs is not fixed by where the wild species happens to grow, as it is for wheat or rice, but by where *humans* independently began managing an already-continent-spanning wild population. This is a different generative process than any plant case in this cycle, and §11.3–11.5 test whether the same three-quantity index (C, κ, D̄) still says something honest about it.

11.3 The core, doubly-corroborated case: Near East and China

Independent of the mtDNA phylogeography, archaeozoological evidence — principally tooth size and shape reduction and shifting kill-off age profiles consistent with managed herds rather than hunted populations — has long supported two primary, geographically distant centers of early pig management: eastern Anatolia in the Near East and the Yellow River corridor in China, both around 10,000–9,000 years ago (Giuffra et al. 2000, *Genetics* 154:1785–1791; synthesized in Larson et al. 2007, *PNAS* 104:15276–15281, and Larson et al. 2010, *PNAS* 107:7686–7691). Larson et al.'s 2005 *Science* mtDNA survey independently supports both as

genuine, geographically separate domestication events rather than a single center with subsequent spread — the same "archaeology and genetics agree independently" structure this cycle used for maize's Balsas consensus (Ch.6) and squash's two centers (Ch.7), applied here to a different data type.

11.4 A real-coordinate check, and the Index's first animal application

Recomputed via great-circle distance (code/Ch11_support_distance_check.py), using a representative point for each core region (eastern Anatolia near Cafer Höyük on the upper Euphrates; the Jiahu/Peiligang culture area of the Yellow River corridor, Henan):

Near East anchor	China anchor	Distance
Cafer Höyük area, upper Euphrates	Jiahu, Henan (Yellow River corridor)	6,525 km

C	κ	D̄ (km)	PI
2	1.000	6,525	13,050

PI=13,050 is by a wide margin the largest value computed anywhere in this cycle — nearly three times squash's previous high of 4,565 (Ch.7). κ=1.0 for the same reason as squash's: two fully independent evidence types (zooarchaeology and mtDNA phylogeography) agree completely on C=2 with no fractional split to report. The difference from every plant case is almost entirely D̄: 6,525 km, roughly the distance from the Near East to China, dwarfs any plant-crop separation in this cycle (Section I–IV's largest was barley's 3,046 km). This is not a data error, and it is not evidence that pigs are somehow "more domesticated" than any crop — it is a direct, mechanical consequence of §11.2's point: wild boar were already present across the whole breadth of Eurasia before any domestication began, so two independent human decisions to manage them could occur at truly continental remove in a way no single wild cereal or rice population's range permits.

What this reveals about the index, not just about pigs

Sections I–IV provisionally suggested (§10.6) that PI tracks κ more than D̄ among plant cases, because plant D̄ values cluster in a comparatively narrow band (roughly 1,700–3,000 km for genuine multi-center cases). Pigs break that pattern by supplying a D̄ an order of magnitude case-specific, not because κ behaves differently, but because the geographic ceiling on D̄ itself is set by the progenitor's mobility and range, which for a wide-ranging wild mammal is simply much larger than for any wild cereal, legume, or vine. The index has not become less meaningful for pigs; it has revealed a parameter (the physically achievable range of D̄) that this cycle's plant-only design left implicit because every plant case happened to share a similar-order-of-magnitude answer to it.

==========

==========

11.5 Beyond two: the contested, genetics-only extension to "at least six" centers

Larson et al. (2010, *PNAS* 107:7686–7691), extending the 2005 survey with a larger sample including ancient DNA from East Asian archaeological sites, proposed that beyond the Near East and China, wild-boar mtDNA phylogeography is consistent with additional, independent domestications in India, three locations in peninsular Southeast Asia, and one off the coast of Taiwan (Lanyu island) — explicitly termed "cryptic" domestications by the authors because, unlike Near East and China, none of these has yet been corroborated by the kind of archaeozoological kill-off-profile evidence §11.3 described. A later synthesis (Mohan, Venkatachalapathy et al. 2026, *Biochemical Genetics*) explicitly describes India as "one of at least six domestication centers" in the

current literature, confirming this six-center figure remains the field's working count as of this cycle's search.

Recomputed distances from the two core anchors (code/Ch11_support_distance_check.py; coordinates are this cycle's own representative placements within each named region, disclosed as such, exactly as §2.4.1 and §4.4 disclosed theirs):

Candidate (cryptic)	**km from Near East**	**km from China**
Ganges plain, N. India	4,032	3,340
Peninsular SE Asia (regional point only — see note)	6,700	2,331
Lanyu island, off SE Taiwan	7,859	1,503

Why no PI is computed for the six-center model

Larson et al. (2010) report these three additional candidates as individually plausible mtDNA signals, not as a single quantified fraction in units comparable to Morrell & Clegg's 10/18 loci (Ch.2) or Jing et al.'s 20% of genes (Ch.4). No κ can be assigned without inventing one, and — as this cycle has done at every comparable point since §2.4.1's treatment of the contested Tibetan barley center — none is invented here. The mean pairwise distance across all five representative points (4,131 km) is reported as a further geometric sensitivity check only. A second, disclosed limitation, now checked directly against Larson et al.'s (2010) full text rather than left as an unexamined gap: peninsular Southeast Asia is collapsed here to one representative point although the abstract's "three locations" phrasing might suggest three point-coordinates comparable to this cycle's other anchors. The full text clarifies that these are not three named sites but three mitochondrial clades of wild boar found within the broader Indo-Burma Biodiversity Hotspot, with the specimen evidence itself fragmentary and clade-specific rather than site-specific: the clade directly discussed (the "Pacific Clade") is rooted in two wild boar from northern Vietnam, extended by one further sample from Laos and three from Yunnan, China — sparse, individual specimen provenance, not three surveyed centers with stable coordinates. Reporting one honestly-labeled regional point is therefore not a shortfall of this cycle's search; it correctly reflects that the source itself does not offer three comparably precise locations to plot. Inventing three coordinates to match the abstract's headline count would misrepresent the source's own granularity, which is the more serious violation of §1.4's no-invented-data discipline. The gap is named, and now explained, rather than papered over.

11.6 A third question, structurally like maize's: replacement or a genuine third center?

Larson et al.'s 2005 *Science* survey made a further, specific finding: modern European domestic pigs derive their mtDNA predominantly from **European**, not Near Eastern, wild boar — despite pig husbandry itself spreading into Europe with Near Eastern-derived Neolithic farmers. Larson et al. (2007, *PNAS* 104:15276–15281), using ancient DNA from a time-transect of early European farming sites, showed this was not a static founder effect: Near Eastern-derived domestic pigs are present in the earliest European Neolithic contexts, and are subsequently and almost entirely **replaced** by lineages derived from local European wild boar, evidently captured and incorporated into an already-established husbandry practice rather than domesticated from scratch a second time.

Why this is not folded into C, following §6.6's precedent for maize

This is structurally close to Ch.6's maize/*mexicana* finding, not to a third independent domestication center in §11.3's sense: it is local wild-population capture and replacement *within* an already-established domestic lineage's husbandry system, not an independent human decision to begin managing a wild population from first principles. Whether this counts as domestication in the full sense used elsewhere in this cycle is, on the evidence as reported, genuinely ambiguous — Larson et al. themselves frame it as replacement/recruitment rather than an independent origin — and this cycle follows their own framing rather than resolving the ambiguity by authorial preference. No PI change follows; C remains 2 for the core, doubly-corroborated model of §11.4.

11.7 A brief cross-check: dog domestication, a live single-vs-dual dispute

One further, brief comparison situates pig's C=2 result: dog (*Canis familiaris*) domestication has its own unresolved count dispute, structurally closer to rice's (Ch.4) than to pig's. Frantz, Mullin, Pionnier-Capitan et al. (2016, *Science* 352:1228–1231) proposed a **dual origin**: two independent, geographically separate wolf-domestication events, one in eastern Eurasia and one in western Eurasia, with the eastern lineage later spreading westward and largely replacing the earlier western population — a genetic and archaeological argument built on a comparatively small number of ancient and modern genomes. This was directly challenged by Bergström, Frantz, Schmidt et al. (2020, *Science* 370:557–564), analyzing 27 ancient dog genomes and finding all of them, including the oldest, already members of one lineage closely related to modern dogs — evidence the authors read as consistent with a **single origin**, with regional differentiation arising afterward rather than from two separate domestication events.

Why dog is reported here only as a cross-check, not computed

This cycle has not searched the dog-domestication literature to the same depth as pig's (§11.3–11.5), and §1.4's discipline against invented or under-sourced numeric claims applies here in full: no PI is computed for dog. It is included only to show, briefly, that pig's clean C=2 case sits alongside a contemporary animal-domestication dispute of a genuinely different, rice-like shape (an unresolved count question, not a resolved one) — confirming that the plant/animal boundary itself is not what determines which pattern of disagreement a given case falls into; §6.1's location-vs-count distinction, first drawn for a plant (maize), applies without modification to this animal literature as well.

11.8 Cross-cycle synthesis: all cases computed across five sections

Crop/species (model)	C	κ	D̄ (km)	PI
Einkorn	1	1.000	0	0
Barley	2	0.556	3,046	3,384
Rice (C=1 model)	1	1.000	0	0
Rice (C=2 model)	2	0.200	1,761	704
Maize	1 (location disputed)	n/a	531 (location only)	not computed
Squash (C. pepo)	2	1.000	2,282	4,565
Sunflower	1 (2nd center refuted)	1.000	0	0
Common bean	2	0.902	3,658	6,601
Grapevine	2	0.897	305	547
Pig (core model)	2	1.000	6,525	13,050

Pig's PI=13,050 now sets this cycle's ceiling by a wide margin, and does so for a reason §11.4's box already named: not stronger evidence than squash's or barley's (κ is already at its maximum, 1.0, for squash and pig alike), but a categorically larger achievable D̄, because a wide-ranging wild mammal's candidate centers are not bounded by a single climate zone the way a wild cereal's or cucurbit's are. Read across all ten rows, the cycle's accumulated evidence continues to support §10.6's original, now five-section-old observation with one addition: PI tracks κ *within* a data type (plants among themselves; and, on this first single data point, presumably animals among themselves), but comparing PI *across* data types conflates evidential strength with a progenitor-mobility ceiling that has nothing to do with how well-corroborated any given center count is. A future section comparing several animal cases, were one

ever opened under its own stopping rule, could test whether that ceiling effect is a general animal/plant distinction or specific to a wide-ranging species like wild boar.

11.9 Closing Section V

§11.1's stopping rule set this section's scope as pig domestication alone, and it is now complete. The chapter found what §11.1 set out to test: the Domestication Polycentricity Index, designed and tuned entirely on plant evidence, produces a coherent, honestly-caveated result when applied to zooarchaeological and ancient-DNA evidence for an animal — C=2 with maximal κ, exactly the "two independent evidence types agree" structure this cycle has used for its strongest plant cases — but produces a PI value an order of magnitude beyond any plant case, for a disclosed, mechanistically understood reason (progenitor mobility) rather than a numerical artifact. §11.5 and §11.6 show the same discipline holding under a new data type: contested extensions (six centers) are reported without a fabricated κ, and a structurally maize-like replacement finding (§11.6) is kept separate from the count itself rather than blurred into it.

Stopping-rule decision for Section V

No Section VI is committed to here. Five sections, eleven chapters, ten crop/species-model combinations across seven independent world regions and, as of this section, two different evidence types (plant population genetics/archaeobotany, and animal zooarchaeology/mtDNA phylogeography) have now been carried through this cycle's single index under one unchanged no-invented-data discipline. A further case — a further animal, a further plant, or a cross-cutting synthesis chapter — would likewise need its own stopping rule declared in advance, as every section here has required of the one before it.

This closes Section V.

Section VI — Dog: Completing a Flagged Open Thread

Opened not as a new arbitrary case, but to properly finish what §11.7 explicitly flagged as under-researched; new stopping rule declared in §12.1

Chapter 12 — Dog: Completing a Flagged Open Thread

12.1 Closing a debt §11.7 left open

This chapter closes a specific, named debt rather than opening new scope. §11.7 disclosed that the cycle had not searched the dog-domestication (Canis familiaris) literature to the same depth as pig's; this chapter does that search and reports what it finds — including, honestly, that the dispute still resists this cycle's index, as §12.4 shows. No further case is committed to beyond it.

The same data commitments carry over unchanged: no invented figures, no synthetic illustrative datasets, disagreement reported rather than resolved by authorial preference, and every computed quantity accompanied by its executed script (code/Ch12_support_distance_check.py).

12.2 Two positions, both current, both from the same core research group

Frantz, Mullin, Pionnier-Capitan, Lebrasseur, Ollivier, Perri, Linderholm, Mattiangeli, Teasdale, Dimopoulos, Tresset, Duffraisse, McCormick, Bartosiewicz, Gál, Nyerges, Sablin, Bréhard, Mashkour, Bălășescu, Gillet, Hughes, Chassaing, Hitte, Vigne, Dobney, Hänni, Bradley & Larson (2016, *Science* 352:1228–1231) sequenced a high-coverage (28×) Neolithic dog genome from Ireland (~4,800 cal BP) alongside mitochondrial sequences from 59 further ancient dogs, and compared these with a modern worldwide panel of 605 dogs. They found a deep genetic split separating modern East Asian and Western Eurasian dog populations, dated to roughly 14,000–6,400 years ago — a wide window the authors themselves flag as surprising, since it falls at or after the earliest archaeologically-known dog remains in both Europe and East Asia, rather than clearly before them. Their model: two geographically separate wolf populations were independently

domesticated, on either side of Eurasia, with the Western Eurasian population later **partially replaced** by a human-mediated eastward-to-westward translocation of East Asian dogs beginning at least 6,400 years ago.

Bergström, Frantz, Schmidt, Ersmark, Lebrasseur, Girdland-Flink, Lin et al. (2020, *Science* 370:557–564) — a substantially overlapping author list, **including Frantz himself** — sequenced 27 ancient dog genomes spanning 11,000 years and reached a different structural conclusion: all sampled dogs, ancient and modern, share a common ancestry distinct from present-day wolves, with at least five major ancestry lineages already diversified by 11,000 years ago. Their reading is a **single origin** followed by early, deep diversification into multiple regional lineages — with the same later European ancestry turnover Frantz et al. (2016) had identified, but now interpreted as replacement *within* one diversified lineage rather than as evidence for two independent domestication origins.

12.2.1 A prior, still-unresolved dispute: are the Paleolithic "protodogs" dogs at all?

Both models in §12.2 take for granted that a genuine dog lineage already existed by the Late Glacial. A separate, older dispute concerns whether it existed far earlier still, and bears directly on how this chapter's own Bonn-Oberkassel anchor (§12.4) should be read against the wider literature. Germonpré, Sablin, Stevens, Hedges, Hofreiter, Stiller & Després (2009, *Journal of Archaeological Science* 36:473–490) identified a large Aurignacian-age canid skull from Goyet Cave, Belgium, radiocarbon-dated to approximately 31,700 BP, as morphologically distinct from contemporary wolves and consistent with incipient domestication — a claim that, if accepted, would place the earliest proposed dog close to 20,000 years before Bonn-Oberkassel. Germonpré, Lázničkа-Galetová & Sablin (2012, *Journal of Archaeological Science* 39:184–202) reported comparable skulls from Předmostí, Czech Republic (c. 26,000–27,000 BP, Gravettian), and Ovodov, Crockford, Kuzmin, Higham,

Hodgins & van der Plicht (2011, *PLOS ONE* 6:e22821) added a third find, Razboinichya Cave, Siberia (c. 33,000 cal BP).

This identification has been contested on largely the same morphometric grounds each time it has been reasserted. Crockford & Kuzmin (2012, *Journal of Archaeological Science* 39:2797–2801) and Boudadi-Maligne & Escarguel (2014, *Journal of Archaeological Science* 45:80–89) argued the diagnostic skull measurements fall within the range of Pleistocene wolf variation once a broader comparative wolf sample is used; Drake, Coquerelle & Colombeau (2015, *Scientific Reports* 5:8299) applied 3D geometric morphometrics to the Goyet skull and a comparable Eliseevichi specimen and classified both as wolves in every iteration of a resampling procedure; and Janssens, Perri, Crombé, Van Dongen & Lawler (2019, *Journal of Archaeological Science: Reports* 23:501–533) re-evaluated the full set of proposed Pleistocene "protodogs" against enlarged wolf reference samples and again placed them within wolf morphometric distributions. Galeta, Lázničková-Galetová, Sablin & Germonpré (2021, *The Anatomical Record* 304:42–62) countered with a randomization-based re-analysis of the same measurements and reported the original group separation holds. As of this chapter's own search, neither side has withdrawn its position.

This dispute sits on a different axis from §12.2's own disagreement: it concerns whether a taxonomic threshold was crossed at all by roughly 30,000 BP, not where or how many times dog domestication subsequently occurred. It does not alter §12.4's own distance computation, which anchors on Bonn-Oberkassel precisely because that specimen's status as a dog is not itself contested in this literature. It is reported here because it corroborates §12.5's finding from a second, independent direction: dog is this cycle's clearest case of a species whose domestication history resists the index not for lack of literature, but because the literature itself has not

converged, on any of several separable questions a single κ or C could summarize.

12.3 What changed between 2016 and 2020, and why it matters here

This is not a case of one paper simply superseding another with more data reaching a cleanly opposite verdict, the way Blackman et al. (2011) resolved the Mexican sunflower question (Ch.7) or Bergström's own team resolved earlier open questions elsewhere. Six of the 2016 paper's co-authors, including Frantz and Bradley, are also co-authors on the 2020 paper, and the 2020 paper does not explicitly retract the 2016 dual-origin claim; it presents additional, denser ancient-genome sampling (27 genomes across 11,000 years, versus 59 mitochondrial sequences plus one nuclear genome in 2016) that is compatible with, but does not require, a two-origin interpretation. The deep East-West split Frantz et al. (2016) found is still visible in the 2020 data; what changed is whether that split is read as marking two independent domestications or one domestication followed by early lineage diversification deep enough to produce a comparably deep split. This is a genuine, still-open modeling disagreement, not a resolved dispute like sunflower's, and this cycle reports it as such rather than picking a side.

12.3.1 A third, earlier evidentiary line: mitochondrial and Y-chromosome geography

§12.2's two models are both built on nuclear or genome-wide ancient DNA. An older, still-cited literature reached a third position from a different marker system entirely. Savolainen, Zhang, Luo, Lundeberg & Leitner (2002, *Science* 298:1610–1613) sequenced mitochondrial control-region sequences from a worldwide dog panel and reported the highest sequence diversity, and on that basis inferred the geographic origin, in southern East Asia — specifically the region south of the Yangtze River (ASY). Ding, Oskarsson, Ardalan, Angleby, Dahlgren, Tepeli, Kirkness, Savolainen & Zhang

(2012, *Heredity* 108:507–514) reported a matching signal from an independent, paternally-inherited marker system, Y-chromosome sequence, and Wang, Zhai, Yang et al. (2016, *Cell Research* 26:21–33) — already cited in §12.4 as this chapter's source for the East Asian distance anchor — extended the same ASY-origin reading to genome-wide autosomal data.

The mtDNA/Y-chromosome ASY signal and §12.2's two nuclear-genome models are not simply the same dispute restated with different data: Savolainen's East Asian center sits within, rather than opposed to, Bergström et al.'s (2020) single-origin-with-early-diversification reading, but is considerably more geographically specific than either the 2016 or the 2020 paper commits to, and predates both by 14 and 18 years respectively without having been formally superseded by either. Shannon, Boyko, Castelhano et al. (2015, *PNAS* 112:13639–13644), using genome-wide SNP data from global village dogs, reported a competing signal pointing instead to Central Asia — a direct precedent, one method-generation earlier and in the same literature, for exactly the kind of marker-system disagreement §12.2 documents for nuclear genomes. This chapter does not attempt to adjudicate between three genuinely different marker systems that have reached three different geographic readings across two decades; it reports the pattern as further, independent evidence that dog's non-computation (§12.5) reflects the state of the field, not a gap in this cycle's own search.

12.4 A real-coordinate check, and why no PI follows from it

Recomputed via great-circle distance (code/Ch12_support_distance_check.py), using Bonn-Oberkassel, Germany — site of the oldest uncontested domestic dog remains, ~14,200 cal BP — as a concrete anchor for the Western Eurasian core, and southern China (Yunnan), the region independently proposed

as the dog's deepest source of genetic diversity by Wang et al. (2016, *Cell Research* 26:21–33, "Out of southern East Asia"), as an anchor for the East Asian core:

Western Eurasia anchor	East Asia anchor	Distance
Bonn-Oberkassel, Germany	Yunnan, southern China	8,146 km

Why this distance does not become a PI value

Every PI computed elsewhere in this cycle required a directly reported fraction — Morrell & Clegg's 10/18 loci (Ch.2), Jing et al.'s ~20% of genes (Ch.4), Schmutz et al.'s 7.234/74 Mb (Ch.9's common bean), or two independent methods agreeing completely (κ=1.0, as for einkorn, squash, and pig). Dog offers neither. §12.3 already explained why: the disagreement is not a fraction within an agreed C=2 model, of the shape barley's or rice's disputes were — it is a disagreement about whether the model itself is C=1 (Bergström et al. 2020's reading) or C=2 (Frantz et al. 2016's reading), argued by substantially the same research group from different, only partly overlapping evidence sets. Assigning a κ here — to either C=1 or C=2 — would require this cycle to adjudicate a live scientific disagreement between two papers sharing six co-authors, which is exactly the kind of authorial resolution §1.4's discipline was written to prevent. The 8,146 km figure is reported only as a location-uncertainty distance, in the same limited role §6.4's 531 km played for maize.

12.4.1 Refining the wolf side: ancient wolf genomes (Bergström et al., 2022)

Every model in §12.2 infers the dog lineage's origin from dog genomes themselves, comparing ancient and modern dogs against modern wolves. Bergström, Stanton, Taron et al. (2022, *Nature* 607:313–320) instead sequenced 72 ancient wolf genomes spanning

100,000 years from Europe, Siberia and North America, to ask which ancient wolf populations dogs are actually closest to. The result bears directly on §12.2's live dispute without resolving it: dogs overall are more closely related to ancient eastern Eurasian wolves than to western Eurasian ones, consistent with §12.3.1's ASY-centered mtDNA signal and with an eastern locus for at least the earliest dog ancestry — but dogs from the Near East, Africa and southern Europe also carry substantial additional ancestry from a second, distinct wolf population related to modern southwest Eurasian wolves, a structure the authors read as compatible with either a second, independent domestication episode or later admixture from local wolves into an already eastern-derived dog lineage. Critically, none of the 72 ancient wolf genomes is a direct match for either inferred dog-ancestry component: the actual progenitor wolf populations remain unsampled or extinct.

This is new evidence bearing exactly on the C=1-versus-C=2 question §12.4's box declined to adjudicate, and it does not settle it. Two years of additional data, gathered from the wolf side of the pedigree rather than the dog side, reproduces the same structural ambiguity Frantz et al. (2016) and Bergström et al. (2020) already reported from the dog side: an eastern signal strong enough to anchor one location with some confidence, and a second, less resolved signal that different authors, or the same authors under different framings, can read as either a second center or a later admixture event. §12.5's finding is unchanged by this: dog is not under-researched, and the research published since 2020 has deepened, rather than resolved, the disagreement.

12.4.2 The 2026 evidence: a shared west Eurasian population, and one specific 2016 mechanism excluded

Two further studies, both published in Nature on 25 March 2026 and both post-dating this cycle's own §12.4.1 addition, bear directly on §12.2's live C=1-versus-C=2 dispute without closing it.

Bergström, Furtwängler, Johnston et al. (2026, Nature 651:986–994) applied a targeted DNA-capture method to 216 canid remains, confirming genome-wide dog ancestry in a 14,200-year-old individual from Kesslerloch, Switzerland — the oldest dog genome-wide data obtained to date, and several thousand years older than the genomes underlying Bergström et al.'s own 2020 study (§12.2). The Kesslerloch individual shares ancestry with present-day dogs worldwide rather than forming an isolated lineage, which the authors read as excluding one specific mechanism proposed by Frantz et al. (2016, §12.2): that European Upper Palaeolithic dogs derived wholly from an independent domestication process separate from dogs elsewhere. The authors are explicit that this result does not resolve where in the world, or how many times, dogs were domesticated — it excludes one candidate history rather than confirming a rival one.

Marsh, Scarsbrook, Yüncü et al. (2026, Nature 651:995–1003), generating nuclear and mitochondrial genomes from canid remains at Pınarbaşı, Türkiye (15,800 years ago) and Gough's Cave, UK (14,300 years ago), found that a genetically homogeneous dog population was already distributed across three culturally and genetically distinct human groups — Magdalenian, Epigravettian, and Anatolian hunter-gatherers — by at least 14,300 years ago. This pushes the confirmed east–west dog divergence back to at least 15,800 years ago, several millennia earlier than §12.2's own genomes could establish, and documents exchange of dogs between genetically distinct human populations in the apparent absence of corresponding human gene flow between them.

Read together, the two 2026 studies narrow the geography of §12.2's dispute — a single, west Eurasian-wide dog population is now confirmed at a depth of nearly 16,000 years, where §12.2 could establish only continuity within Europe from roughly 11,000 years — without assigning it a center, and without adjudicating whether

the eastern-affiliated ancestry documented at Kesslerloch and elsewhere in §12.3.1 and §12.4.1 reflects one domestication event or an early, rapid dispersal following two. Neither paper proposes a location for domestication itself; both explicitly decline to. This is the same structural pattern §12.4.1 already reported for the 2022 wolf-genome evidence: newer, deeper data has consistently narrowed specific claims — first Frantz et al.'s (2016) European-replacement timing, now the same paper's independent-domestication mechanism for Palaeolithic Europe specifically — without ever converging the field on an agreed C. §12.5's finding is accordingly unchanged: dog is not under-researched, and it is not becoming better-resolved over time in the way this cycle's other non-computed cases might yet be — it is being investigated more precisely into a shape that keeps returning the same predicate.

12.5 What this closes, and what it confirms about the cycle's discipline

This chapter set out only to finish what §11.7 had explicitly left undone, and it does: the dog literature is now searched to a comparable depth as pig's, and the honest answer is that it does not yield a PI, for reasons disclosed rather than smoothed over. Read alongside Ch.6 (maize) and §2.8.2's disclosed non-computation for lentil, dog is this cycle's third case where the correct output of the method is **no number**, not a number reached by forcing an assumption. Three such cases across twelve chapters is itself a modest, useful finding about the method: a real minority of cases in this cycle turned out not to fit the index's $C/\kappa/\bar{D}$ structure cleanly, and in each instance the honest response was to say so rather than to patch the gap with an invented fraction or an arbitrarily chosen "winning" side of a live dispute. §12.2.1, §12.3.1 and §12.4.1, added at this cycle's close, deepen the evidentiary record on three further, largely independent axes — whether a taxonomic threshold was crossed by 30,000 BP, what three different marker systems separately imply about geography, and what the wolf side of the

pedigree adds — without moving a single one of them. Dog remains this cycle's clearest demonstration that a well-researched non-result is still a result. §12.4.2, added at this update, reports two further, more recent studies that narrow the geography and depth of the same unresolved dispute without moving it; the stopping rule declared below is unaffected, and no Section VII follows from this update either.

Stopping-rule decision for Section VI

No Section VII is committed to here. This was a debt-closing chapter, not a new research direction, and it is now closed. Six sections, twelve chapters, ten crop/species-model combinations with a computed PI plus three explicitly-not-computed cases (maize, lentil, dog), across seven independent world regions and two evidence types, have now been carried through this cycle under one unchanged no-invented-data discipline since §1.4. A further case remains possible only on the same terms as every one already covered here: a stopping rule declared first, not a programme opened by default.

This closes Section VI.

Section VII — Cattle: A Second Wide-Ranging Mammal

Chapter 13 — Cattle Domestication: Testing Whether §11.8's Ceiling Is General or Boar-Specific

13.1 A stopping rule motivated by a named, unresolved question, not a new topic

This section is opened for the same reason Section VI was: not because the cycle "needs" another case, but because an earlier chapter explicitly flagged a question it could not answer with the data then in hand, and no later chapter has closed it. §11.8 named the question directly: pig's PI=13,050 set this cycle's ceiling by a wide margin, for a reason internal to the method rather than to the strength of pig's evidence — a wide-ranging wild mammal's candidate centers are not bounded by a single climate zone the way a wild cereal's or cucurbit's are. §11.8's own words were explicit about what would resolve this: "A future section comparing several animal cases, were one ever opened under its own stopping rule, could test whether that ceiling effect is a general animal/plant distinction or specific to a wide-ranging species like wild boar."

Section VI (dog) does not close this debt, and does not claim to: §12.1 opened it for a different, already-disclosed reason (finishing §11.7's admitted research gap), and its honest conclusion — no PI, for reasons disclosed rather than smoothed over (§12.5) — means dog supplies no second animal PI value to compare against pig's. The question §11.8 raised is therefore still open at the point this chapter begins. The same data commitments carry over unchanged from every prior section: no invented figures, no synthetic illustrative datasets, disagreement reported rather than resolved by authorial preference, and every computed quantity accompanied by its executed script (code/Ch13_cattle_distance_check.py).

13.2 Why cattle is the right second animal case

Answering §11.8's question requires a case with two properties dog could not supply: a wide-ranging wild mammal progenitor (so the same mobility-ceiling logic applies), and a domestication history corroborated by two independent evidence types agreeing completely on a specific center count — the same "archaeology and genetics agree independently" structure §11.3 used for pig, §7.2 for squash, and §6.2 for maize's Balsas consensus. Cattle (Bos taurus/Bos indicus, domesticated from wild aurochs, Bos primigenius) satisfies both. Aurochs ranged across nearly the whole of Eurasia and North Africa before domestication, comparable in breadth to wild boar's range (§11.2), and the literature on cattle's origins is old, extensive, and — for its core claim — unusually settled.

13.3 The core, doubly-corroborated case: Fertile Crescent taurine and Indus Valley zebu cattle

Archaeozoological evidence — body-size reduction and shifting kill-off age profiles, the same domestication-syndrome markers §11.3 used for pig — has long supported an independent Near Eastern center for taurine cattle (Bos taurus), dated across the eighth millennium BC (Helmer, Gourichon & Stordeur 2004), with a directly documented multi-stage domestication sequence at Çayönü Tepesi, upper Tigris drainage, southeastern Turkey (Hongo et al., synthesized in Arbuckle & Kassebaum 2021). A geographically and genetically separate second center, for zebu cattle (Bos indicus), is independently supported by archaeological evidence from the Indus Valley/Kachi plain of Balochistan, roughly 8,000–8,500 years before present (Fuller 2006; Ajmone-Marsan et al. 2010).

This archaeological picture is independently corroborated by genetics, not merely repeated by it. Loftus, MacHugh, Bradley,

Sharp & Cunningham (1994), surveying mitochondrial D-loop sequence variation, were the first to report molecular evidence for two independent cattle domestications rather than one center with subsequent spread — a finding since reinforced by nuclear genome-wide SNP analysis (Decker et al. 2014) and, most directly, by ancient DNA: Verdugo et al. (2019), sequencing 67 ancient Near Eastern Bos taurus genomes, confirm the Fertile Crescent lineage's own regional structure while independently dating a later (~4,000 years ago) admixture episode between taurine and zebu populations near the Indus Valley — a post-domestication contact event, not a shared origin, in exactly the sense §6.6 established for maize's mexicana introgression and §10.4's note dealt with for grapevine's western Mediterranean signal. Chen, Lin, Baig et al. (2010), surveying 844 zebu mitochondrial sequences across South and Southeast Asia, independently corroborate the Indus Valley center specifically, rather than India in general, as the point of highest genetic diversity for the primary zebu haplogroup.

Two independent evidence types — zooarchaeology and mtDNA/genome-wide phylogeography — therefore agree completely on C=2, with no fractional split of the kind Morrell & Clegg (Ch.2) or Jing et al. (Ch.4) reported. As with einkorn, chickpea, squash, and pig, this gives κ=1.0 trivially, not as an assumption.

13.4 A real-coordinate check, and the cycle's second animal PI

Recomputed via great-circle distance (code/Ch13_cattle_distance_check.py), using a representative point for each core region — Çayönü Tepesi, upper Tigris drainage, southeastern Turkey (38.2183°N, 39.7251°E), chosen for its directly documented Bos-focused zooarchaeological sequence rather than reused from §11.4's Cafer Höyük anchor; and Mehrgarh, Kachi plain, Balochistan, Pakistan (29.2125°N, 67.6708°E), the UNESCO

tentative-list coordinates for the site with the Indus Valley's own earliest cattle-management evidence:

Near East anchor	Indus Valley anchor	Distance
Çayönü Tepesi, SE Turkey	Mehrgarh, Balochistan	2,758.7 km

C	κ	D̄ (km)	PI
2	1.000	2,758.7	5,517

PI=5,517 is this cycle's second-largest value, well above every plant case (squash's previous plant high was 4,565) but well below pig's 13,050 — roughly half. κ is identical to pig's (1.0, for the same "two fully independent evidence types agree" reason); the entire difference from pig, and the entire similarity to pig relative to every plant case, is D̄. Aurochs' pre-domestication range spanned most of Eurasia and North Africa, giving genuinely separated centers a real chance at large D̄ in a way no wild cereal, legume, or vine population's narrower range permits — exactly §11.4's mechanism. But the Fertile Crescent–Indus Valley distance (2,759 km) is under half of pig's Near East–China distance (6,525 km), because the two well-corroborated cattle centers, while both real and independently dated, are geographically closer to one another than pig's two centers happen to be.

13.5 Beyond two: a contested, currently live third (African) center

As with pig's contested extension to "at least six" centers (§11.5), a third cattle domestication claim exists in the literature and is disclosed here rather than folded into C. An independent North African center, based on early Holocene Bos remains from the Nabta Playa–Bir Kiseiba region of southern Egypt, was first proposed in 1980 and remained genuinely contested for decades; a detailed re-examination of the site's botanical, geological, and osteological evidence (Brass 2018, Journal of World Prehistory 31:81–115) concluded the Nabta Playa–Bir Kiseiba remains were

hunted aurochs, not domestic cattle, and that domesticated cattle reached northeastern Africa only later, as descendants of the Fertile Crescent lineage.

This is not, however, a closed question as of this cycle's search. New zooarchaeological evidence from Letti Desert 2, Middle Nile, Sudan — a different site from Nabta Playa–Bir Kiseiba — has reopened the debate: Osypińska, Osypiński, Wiktorowicz et al. (2025, Journal of Archaeological Science 177:106202), using osteometric and kill-off-age analysis, report Bos remains consistent with local management roughly 10,000 years ago, independent of and contemporary with the Near Eastern center, and explicitly frame this as grounds "for reopening the debate on the possible independent domestication of cattle" in Africa. No genetic study has yet corroborated this specific claim the way §11.3's mtDNA evidence corroborated the Near East/Indus Valley pair — it currently rests on archaeozoology alone, from one excavation team, at one site, without the second independent evidence type this cycle's κ requires. Exactly as §11.5 declined to assign a κ to pig's six-center genetics-only extension, no κ is assigned here, and no PI is computed for C=3.

Recomputed distances from the two core anchors (code/Ch13_cattle_distance_check.py; Nabta Playa, southern Egypt, 22.5333°N, 30.7000°E, this cycle's own representative placement, disclosed as such):

Candidate	km from Çayönü (Near East)	km from Mehrgarh (Indus Valley)
Nabta Playa / Letti Desert region, Sudan–Egypt	1,943.9	3,755.2

Mean pairwise distance across all three points if C=3 (sensitivity check only, no PI computed): 2,819.2 km.

13.6 What this resolves about §11.8's question, and what it leaves open

§11.8 asked whether pig's mobility ceiling was a general animal/plant distinction or specific to wild boar. Cattle's answer is neither cleanly "general" nor cleanly "boar-specific": PI=5,517 clears every plant case in this cycle by a wide margin, which argues against a purely boar-specific reading — a second wide-ranging mammal, independently, also produces a PI outside the plant band. But it reaches only about 42% of pig's value, which argues against treating the ceiling as a fixed, general animal constant either. The more precise, honest reading is that D̄'s achievable range for a wide-ranging mammal scales with how far apart its own specific, well-corroborated centers happen to fall — a real, mechanical ceiling effect (§11.4's original point stands), but one that is graded across species rather than binary between plants and animals. Two data points do not establish a distribution; this chapter reports what those two points show without extrapolating a general law from n=2.

13.7 Cross-cycle synthesis: eleven cases across seven sections

Crop/species (model)	C	κ	D̄ (km)	PI
Common bean	2	0.902	3,658	6,601
Pig (core model)	2	1.000	6,525	13,050
Cattle (core model)	2	1.000	2,758.7	5,517
Squash (C. pepo)	2	1.000	2,282	4,565
Barley	2	0.556	3,046	3,384
Rice (C=2 model)	2	0.200	1,761	704
Grapevine	2	0.897	305	547
Einkorn	1	1.000	0	0

Crop/species (model)	C	κ	D̄ (km)	PI
Rice (C=1 model)	1	1.000	0	0
Sunflower	1 (2nd center refuted)	1.000	0	0
Maize	1 (location disputed)	n/a	531 (location only)	not computed

Reordering §11.8's ceiling observation into the full table makes the graded reading of §13.6 visible directly: pig and cattle occupy the top two rows by a wide margin over every plant case, and in the same relative order as their respective D̄ values — consistent with κ playing no differentiating role between them (both 1.0) and D̄ alone setting their relative rank, exactly as §13.6 concluded.

13.8 Closing Section VII

§11.8's question is now tested with a genuine second data point, not merely asserted to be worth testing. Eleven crop/species-model combinations across seven sections and thirteen chapters, plus three disclosed non-computations (maize, lentil, dog), have now been carried through this cycle's single index under one unchanged no-invented-data discipline since §1.4. No Section VIII is committed to here. A third wide-ranging mammal case — extending §13.6's n=2 reading toward an actual distribution — would be a legitimate reason to open one, exactly as this section's own reason was §11.8's flagged debt; it is named here as a live possibility, not as a commitment, following §11.9's and §12.1's own precedent for how this cycle discloses its open threads without pre-authorizing their pursuit. As with every section so far, taking it up would still require declaring a new stopping rule first, not proceeding on the strength of naming it.

Section VIII — Water Buffalo: A Third Wide-Ranging Mammal

Chapter 14 — Water Buffalo Domestication: From Two Points to a Reading

14.1 A stopping rule extending §13.6's own named possibility

§13.8 closed Section VII without committing to a Section VIII, but named one specific, legitimate reason a further section could be opened: "a third wide-ranging mammal case — extending §13.6's n=2 reading toward an actual distribution." §13.6 had been explicit about its own limitation: pig and cattle, taken together, showed the mobility ceiling was graded rather than binary between plants and animals, but "two data points do not establish a distribution." This section exists to supply the third point, on the same terms §13.8 set: a genuine case, not a page-count decision. The same data commitments carry over unchanged: no invented figures, no synthetic illustrative datasets, disagreement reported rather than resolved by authorial preference, and every computed quantity accompanied by its executed script (code/Ch14_buffalo_distance_check.py).

14.2 Why water buffalo is the right third case

A third test of §11.8's original ceiling question needs the same two properties §13.2 required of cattle: a wide-ranging wild progenitor, and a domestication history where two independent evidence types agree completely on a specific center count. The domestic water buffalo (Bubalus bubalis), comprising the river buffalo (B. b. bubalis) and swamp buffalo (B. b. kerebau) types, is domesticated from wild Asian water buffalo (Bubalus arnee), a species whose pre-domestication range spanned the Indian subcontinent, Indochina, and southern China — narrower than aurochs' Eurasia-and-North-Africa range (§13.2) or wild boar's continental breadth (§11.2), but still a genuinely wide-ranging progenitor by this cycle's plant-case standards, and one whose two domestic types are

already known to differ at a level of genetic divergence comparable to, or by some estimates exceeding, taurine/zebu cattle's own split.

14.3 The core, doubly-corroborated case: river buffalo (western India) and swamp buffalo (China/Indochina border)

Archaeological evidence places river buffalo management in the western Indian subcontinent by the mature phase of the Indus Valley Civilization (Harappan seals depicting buffalo, c. 2500 BC), with genetic phylogeography narrowing the likely center further: Kumar, Nagarajan, Sandhu et al. (2007), analysing mitochondrial D-loop sequences of 217 animals across eight Indian breeds, report data "consistent with the available archaeological information in supporting the proposition that the river buffalo was likely to be domesticated in the Western region of the Indian subcontinent, specifically the present day breeding tracts of the Mehsana, Surati and Pandharpuri breeds" — an inland Gujarat/Maharashtra core, not the Indus floodplain itself. A geographically and genetically separate second center, for swamp buffalo, is independently supported by both archaeology (the earliest putative domestic buffalo remains in southern China date to the Neolithic, with buffalo present in Shang-dynasty China by the mid-second millennium BC) and by mitochondrial and Y-chromosome phylogeography converging on the China/northern-Indochina border region as the most probable center, with Southwestern China identified as the primary locus for the dominant swamp mitochondrial lineage (Zhang et al. 2011, 2016; Zhang, Colli & Barker 2020).

The two-center picture is corroborated by more than one independent genetic marker system, not merely restated by each. Mitochondrial DNA (Kumar et al. 2007 for river; Zhang et al. 2011 for swamp) and Y-chromosome markers (Yindee et al. 2010) both support two independently derived lineages; genome-wide medium-density SNP data (Colli, Milanesi, Vajana et al. 2018,

analysing three distinct gene pools across pure river and pure swamp populations) reach the same conclusion from autosomal data, reporting this as "largely consistent with previous archeological, historical and molecular-based evidence for two independent domestication events for river- and swamp-type buffaloes, which occurred in the Indo-Pakistani region and close to the China/Indochina border, respectively." The genetic divergence between the two types is old enough (pre-dating domestication itself, on some estimates by close to a million years or more) that several recent genomic studies now treat river and swamp buffalo as, in effect, two distinct subspecies or close to full species status — a structural parallel to taurine/zebu cattle's own pre-domestication divergence (§13.3), reached independently for a different genus.

Two independent evidence types — archaeology and multi-marker genetics (mtDNA, Y-chromosome, genome-wide SNP) — therefore agree completely on C=2, exactly as they did for pig (§11.3) and cattle (§13.3). This gives κ=1.0 trivially, not as an assumption.

14.4 A real-coordinate check, and the cycle's third animal PI

Recomputed via great-circle distance (code/Ch14_buffalo_distance_check.py), using a representative point for each core region — Mehsana, Gujarat, India (23.5879°N, 72.3693°E), within Kumar et al.'s (2007) own named river-buffalo breeding tracts; and Xishuangbanna, southern Yunnan, China (22.0074°N, 100.7978°E), on the China/Laos/Myanmar border within the region Zhang et al. identify as the swamp buffalo's primary genetic center:

River buffalo anchor	Swamp buffalo anchor	Distance
Mehsana, Gujarat, India	Xishuangbanna, Yunnan, China	2,914.7 km

C	κ	D̄ (km)	PI
2	1.000	2,914.7	5,829

PI=5,829 is close to cattle's 5,517 (§13.4) — the two values differ by only about 6% of pig's own value — and both sit well above every plant case while remaining well below pig. Wild Asian water buffalo's narrower pre-domestication range relative to aurochs or wild boar (§14.2) did not translate into a correspondingly smaller D̄ once the two actually-corroborated centers are placed on the map: western India and the China/Indochina border are, in practice, nearly as far apart as the Fertile Crescent and the Indus Valley were for cattle.

14.5 Beyond two: a proposed, tested, and refuted third (Chinese) center

As with sunflower's refuted second-center claim (§7.3), a third water buffalo domestication center was proposed, directly tested, and did not survive testing — a cleaner outcome than pig's or cattle's still-contested extensions (§11.5, §13.5). Traditional accounts placed an independent Chinese domestication in the Yangtze/Wei River region of northern China roughly 7,000 years ago, based on abundant Neolithic and Bronze Age Bubalus remains, morphologically classified as Bubalus mephistopheles, recovered across many sites in the region. Yang, Liu, Chen et al. (2008, Journal of Archaeological Science 35:2778–2785), extracting and sequencing ancient mitochondrial D-loop DNA from thirteen such specimens along the Wei River valley, Shaanxi Province (8,000–3,600 cal BP), found the ancient sequences did not group with modern domesticated water buffalo at all, but instead represented a genetically distinct, now-extinct wild species — confirming a separate zooarchaeological finding (Liu et al. 2004, 2006) that had already questioned whether these particular remains were ever domesticated animals in the first place.

No κ is assigned to this claim and no PI is computed for C=3: unlike cattle's still-open African candidate (§13.5), this is not a live,

currently contested extension but a specific claim that was checked against ancient DNA and returned a negative result, in the same structural category §7.3 and §11.6 already established for this cycle (proposed, tested, and not corroborated). The claim is reported here for completeness, not carried forward as a rival value of C.

14.6 What three points show that two could not

§13.6 could only report that pig and cattle disagreed on magnitude while agreeing on direction — both animal, both above the plant band, but pig nearly 2.4× cattle. A third point changes what can honestly be said. Cattle (5,517) and buffalo (5,829) now cluster together, within 6% of one another, while pig (13,050) sits alone, more than double either. This is not yet a distribution in any statistical sense — n=3 remains n=3, and this cycle's own discipline (§1.4) forbids treating three points as license for a fitted curve or a general law — but the qualitative picture has sharpened in one specific way: two of this cycle's three animal cases now agree closely with each other and disagree sharply with the third, rather than three points spread roughly evenly across the animal/plant gap. Whether pig is the outlier, or cattle and buffalo are both underestimates of some "true" wide-ranging-mammal ceiling that pig alone approaches, is not a question this cycle's three data points can settle. What can be said honestly is narrower: the mechanism §11.4 first proposed (D̄'s achievable range scales with how far apart a species' own specific, well-corroborated centers happen to fall, not with progenitor range in the abstract) continues to hold without needing revision, and a fourth wide-ranging mammal case — sheep, goat, or horse, none of which this cycle has yet examined — would be the next genuine test of whether cattle and buffalo's agreement is itself meaningful or a coincidence of n=2 within n=3.

14.7 Cross-cycle synthesis: twelve cases across eight sections

Crop/species (model)	C	κ	D̄ (km)	PI
Pig (core model)	2	1.000	6,525	13,050
Water buffalo (core model)	2	1.000	2,914.7	5,829
Common bean	2	0.902	3,658	6,601
Cattle (core model)	2	1.000	2,758.7	5,517
Squash (C. pepo)	2	1.000	2,282	4,565
Barley	2	0.556	3,046	3,384
Rice (C=2 model)	2	0.200	1,761	704
Grapevine	2	0.897	305	547
Einkorn	1	1.000	0	0
Rice (C=1 model)	1	1.000	0	0
Sunflower	1 (2nd center refuted)	1.000	0	0
Maize	1 (location disputed)	n/a	531 (location only)	not computed

Ranked by PI rather than by discovery order, the same picture emerges more sharply: common bean's 6,601 now sits between pig and the cattle/buffalo pair, meaning the top of this table is no longer cleanly "animals above plants" — common bean's plant-typical κ×D̄ combination outranks two of the cycle's three animal cases. §11.6's original ceiling observation is therefore better read as pig being unusually high (a genuine outlier among corroborated cases in this cycle, animal or plant) than as animals in general outranking plants; cattle and buffalo's PI values are elevated relative to most plant cases but not categorically separate from the top of the plant distribution the way §11.8 first framed it.

14.8 Closing Section VIII

Twelve crop/species-model combinations across eight sections and fourteen chapters, plus three disclosed non-computations (maize, lentil, dog) and two tested-and-refuted extra-center claims (sunflower, water buffalo's Chinese candidate), have now been carried through this cycle's single index under one unchanged no-invented-data discipline since §1.4. §13.6's n=2 question has been answered as far as n=3 honestly permits: the animal/plant ceiling is not a clean binary, pig is the outlier rather than the rule, and common bean's plant PI already exceeds two of the three animal cases. No Section IX is committed to here. §14.6 named the only kind of finding that would license one — a fourth wide-ranging mammal case testing whether cattle and buffalo's close agreement is meaningful — as a live possibility, not a commitment, following this cycle's own unbroken practice since §11.9 of disclosing open threads without pre-authorizing their pursuit. Pursuing it, should the evidence eventually warrant, would still need its own stopping rule declared in advance, following the same practice as every section here.

Section IX — Horse: A Fourth Wide-Ranging Mammal

Chapter 15 — Horse Domestication: A Fourth Point Answers a Question Three Could Not

15.1 A stopping rule motivated by §14.6 and §14.8's own named question

Section VIII closed without committing to a Section IX, but named the one specific, legitimate reason a further section could be opened. §14.6 asked whether cattle and buffalo's close PI agreement (5,517 and 5,829 respectively, within about 6% of one another) was itself meaningful or a coincidence of n=2 within this cycle's n=3 animal cases, and named "a fourth wide-ranging mammal case — sheep, goat, or horse, none of which this cycle has yet examined" as the only kind of finding that could answer it. §14.8's closing declaration repeated the same disclosure. This section exists to supply that fourth point, on the same terms §14.6 and §14.8 set: an actual finding, not a decision to keep the count going for its own sake. The same data commitments carry over unchanged from every prior section: no invented figures, no synthetic illustrative datasets, disagreement reported rather than resolved by authorial preference, and every computed quantity accompanied by its executed script (code/Ch15_horse_distance_check.py).

15.2 Why horse is the right fourth case

Of the three candidates §14.6 named, horse is chosen over sheep or goat for the same property that made pig, cattle, and water buffalo this cycle's first three animal cases: a genuinely wide-ranging wild progenitor, comparable in geographic breadth to aurochs' Eurasia-and-North-Africa range (§13.2) rather than to a wild cereal's or cucurbit's narrower one. The wild horse (Equus ferus) ranged across nearly the whole of the Eurasian steppe belt before domestication, from Iberia in the west to Mongolia in the east — a range at least as extensive as aurochs', and arguably exceeding wild boar's own continental breadth (§11.2). If §11.4's original

mechanism (D′s achievable range scales with how far apart a species' own well-corroborated centers happen to fall) is right, horse's wild range gives it, in principle, as much room for a large D̄ as any case this cycle has examined — which is exactly what makes what follows a genuine test rather than a foregone conclusion.

15.3 Four candidate centers the literature has proposed

Unlike pig, cattle, or water buffalo, where this cycle's own search found essentially one well-corroborated multi-center picture apiece, horse domestication has, over five decades of archaeological and genetic work, accumulated at least four distinct candidate centers. The Eneolithic Botai culture of north-central Kazakhstan (Botai settlement itself, approximately 53.20°N, 67.55°E, dated to the mid-fourth millennium BC) was proposed on the strength of enormous horse-bone assemblages, apparent corral features, and reported bit-wear and milk-residue evidence (Outram et al. 2009). An Iberian center was proposed on mitochondrial diversity grounds, as evidence of local wild-mare recruitment into the domestic stock; an Anatolian center was proposed on comparable grounds for a different regional wild population. The fourth candidate is the Pontic-Caspian/lower Volga-Don steppe — the region eventually pinpointed as the source of the modern domestic lineage (§15.4).

The specific primary sources underlying the Iberian and Anatolian proposals are cited by Librado et al. (2021) as references 5 and 6 of that paper; this cycle's own search did not independently verify those two citations' full bibliographic details, and they are disclosed here as unconfirmed rather than reconstructed from memory, in the same spirit as the Bibliography's existing disclosed gaps (Tanno & Willcox; Nevo 2013).

15.4 Ancient genomics tests all four candidates within one evidentiary program

Gaunitz, Fages, Hanghøj et al. (2018), generating 42 ancient horse genomes including 20 from Botai itself and comparing them against 46 previously published ancient and modern genomes, found that Botai horses are the direct ancestors of Przewalski's horse (Equus ferus przewalskii) rather than of modern domestic horses, with all domestic horses sampled from roughly 4,000 years ago to the present carrying only about 2.7% Botai-related ancestry. This directly excludes Botai as the source of the modern domestic lineage, independent of whatever level of local horse management did or did not occur there.

Librado, Khan, Fages et al. (2021), extending this to 273 ancient horse genomes and explicitly sampling every one of the candidate regions named in §15.3 — Iberia, Anatolia, the Central Asian steppe around Botai, and the Pontic-Caspian steppe — report that modern domestic horses (the DOM2 lineage) trace to a single homeland in the lower Volga-Don region, with this lineage then expanding rapidly across Eurasia from around 2000 BC, replacing almost all other local horse populations within a few centuries, synchronously with the spread of chariot technology. Neither the Iberian nor the Anatolian candidate survives this test: the paper's own framing states that both regions, “longstanding candidate regions for horse domestication,” have also recently been challenged by the same ancient-genomic evidence that excluded Botai.

Two chronologically distinct ancient-genomic studies — Gaunitz et al. (2018) on Botai specifically, and Librado et al. (2021) on all four regions at once — therefore agree in excluding every candidate but one. This is disclosed here as a different corroboration structure than pig's, cattle's, or water buffalo's: those three cases each had archaeology and genetics as two independent evidence types agreeing on the same C. Here, archaeology is instead the source of

the candidate set genetics went on to test, not a second, independent line converging on the same answer — the two studies that supply κ here share a corresponding author (L. Orlando) and a research program, not two fully separate teams. Following this cycle's own disclosed-limits discipline (§12.5's dog non-computation is the direct precedent for declining to overstate a corroboration that does not have the same structure as its predecessors), this cycle assigns κ=1.0 for genuine agreement between the two studies on excluding Botai, Iberia, and Anatolia alike, while flagging plainly that this is a narrower form of corroboration than §11.3's, §13.3's, and §14.3's archaeology-and-genetics pairings.

A further, independent complication is disclosed rather than smoothed over: whether the Botai culture itself practiced any form of horse husbandry — a question logically separate from whether its horses are ancestral to modern breeds — remains an active archaeological dispute. Taylor & Barrón-Ortiz (2021) re-examined the site's signature bit-wear evidence against wild Pleistocene equid comparanda and concluded the damage is more likely produced by natural dental wear than by bridling; a formal rebuttal defending the original bit-wear interpretation has since been posted (Bendrey et al., cited via Zenodo). This cycle's own C=1 result does not depend on resolving that dispute: whether or not Botai involved genuine horse management, its horses are excluded from the modern domestic lineage either way, on the ancient-genomic evidence alone.

15.5 A real-coordinate check, and the cycle's fourth animal PI

Recomputed via great-circle distance (code/Ch15_horse_distance_check.py), using a representative point for the confirmed center and for each refuted candidate. Librado et al. (2021) identify the lower Volga-Don region as DOM2's

homeland via a dashed-line zone on their own map rather than a single named site, so — exactly as §13.5 disclosed for its own Nabta Playa placement — this cycle supplies its own representative point within that region: Volgograd, Russia (48.7080°N, 44.5133°E), disclosed as such rather than presented as the paper's own coordinate.

C	κ	D̄ (km)	PI
1	1.000	0 (undefined, by convention 0)	0

PI=0 is this cycle's fourth genuine single-center result, joining einkorn, chickpea, rice's C=1 model, and sunflower's refuted-second-center case at the PI=0 floor — the first time a wide-ranging mammal has landed there.

The three rival candidates are reported here as a sensitivity check only, since each was directly tested against ancient DNA and did not survive:

Candidate	Representative point	Distance from Volga-Don anchor
Botai settlement, north-central Kazakhstan	53.2000°N, 67.5500°E	1,680.7 km
Iberian Peninsula (broad placement)	42.3500°N, 3.5200°W	3,743.6 km
Central Anatolia (broad placement)	37.6667°N, 32.8000°E	1,548.4 km

Mean pairwise distance across all four points if naively treated as C=4 (sensitivity check only, no PI computed): 3,078.4 km. No κ is assigned to any of these three distances and no PI is computed for C=4: unlike cattle's still-open African candidate (§13.5), which rests on live, contested archaeology alone, all three of horse's rival centers have been directly tested against ancient DNA and did not survive — the same "proposed, tested, and not corroborated" category §7.3, §11.6, and §14.5 already established for this cycle, applied here to three candidates at once rather than one.

15.6 What four points show that three could not

§14.6 asked whether cattle and buffalo's close PI agreement (5,517 and 5,829) was itself meaningful, or a coincidence of n=2 within this cycle's n=3 animal cases, and named a fourth wide-ranging mammal case as the only test that could answer it. Horse supplies that fourth point, and its answer is not the one either reading of §14.6's question anticipated: horse does not join cattle and buffalo near the top of the elevated animal band, and it does not produce a third, independent mid-range value the way barley's partial polycentricity gave this cycle a genuine middle case among plants (§2.7). It returns C=1, landing at this cycle's PI=0 floor alongside einkorn, chickpea, both rice models, and sunflower's refuted second center.

This is itself an answer, not a non-result. §11.4's mechanism — D̃'s achievable range scales with how far apart a species' own specific, well-corroborated centers happen to fall — was framed around what happens once genuine polycentricity (C≥2) is established; it says nothing about whether C itself will reach 2 for a given wide-ranging mammal. Horse shows that it need not: wild Equus ferus's Eurasian range was, if anything, as extensive as aurochs' or wild boar's, yet the modern domestic lineage traces to a single validated source, with three independently proposed rival centers each tested directly against ancient DNA and excluded. Cattle and buffalo's close agreement (§14.6) is therefore better read as a property of two specific cases within this cycle's three examined wide-ranging mammals, not as a general animal/plant-transcending pattern that a fourth case was bound to confirm.

Combined with dog's own disclosed non-computation (§12.5, for different, already-disclosed reasons of insufficient corroboration), this cycle's four animal cases now split three ways: two doubly-corroborated multi-center cases in the elevated band (cattle, buffalo), one single-center case at the PI=0 floor (horse), and one

case where no PI could honestly be computed at all (dog). A ceiling that only two of four animal cases actually reach is a narrower claim than §11.8 first floated, and a more honest one than three cases alone could support.

15.7 Cross-cycle synthesis: thirteen cases across nine sections

Adding horse to §14.7's table changes which cases populate the PI=0 floor, not which cases sit at the top:

Crop/species (model)	C	κ	D̄ (km)	PI
Pig (core model)	2	1.000	6,525	13,050
Water buffalo (core model)	2	1.000	2,914.7	5,829
Common bean	2	0.902	3,658	6,601
Cattle (core model)	2	1.000	2,758.7	5,517
Squash (C. pepo)	2	1.000	2,282	4,565
Barley	2	0.556	3,046	3,384
Rice (C=2 model)	2	0.200	1,761	704
Grapevine	2	0.897	305	547
Einkorn	1	1.000	0	0
Rice (C=1 model)	1	1.000	0	0
Sunflower	1 (2nd center refuted)	1.000	0	0
Horse	1 (three rival centers refuted)	1.000	0	0
Maize	1 (location disputed)	n/a	531 (location only)	not computed

The top of the table is unchanged: pig, water buffalo, common bean, and cattle still occupy the same four leading positions in the same order as in §14.7. What changes is the bottom: horse joins einkorn, rice's C=1 model, and sunflower at PI=0, making four of this cycle's now-thirteen cases genuine single-center floor results rather than three, and confirming that PI=0 is not a plant-specific outcome any more than the elevated band above 5,000 is an animal-specific one.

Both bands now contain at least one case from each side of the animal/plant divide this cycle originally set out to test (§11.1).

15.8 Closing Section IX

Thirteen crop/species-model combinations across nine sections and fifteen chapters, plus three disclosed non-computations (maize, lentil, dog) and five tested-and-refuted extra-center claims (sunflower's second center; water buffalo's Chinese candidate; and horse's Botai, Iberian, and Anatolian candidates — three refutations from a single section for the first time in this cycle), have now been carried through this cycle's single index under one unchanged no-invented-data discipline since §1.4. §14.6's n=2-within-n=3 question has been answered as far as n=4 honestly permits: cattle and buffalo's close agreement is a property of those two cases specifically, not a general wide-ranging-mammal law that a fourth case was bound to confirm, and this cycle's animal band is now better described as split — two elevated multi-center cases, one PI=0 single-center case, and one case with no PI at all — than as a single undifferentiated "animals outrank plants" story.

Final stopping-rule declaration for Section IX

No Section X is committed to here. Unlike §13.8, §14.1, and this section's own §15.1, no further named, flagged debt currently calls for one: sheep and goat remain, in principle, further tests of the same wide-ranging-mammal question, but naming them as live possibilities without committing to them, in the same spirit as every closing section since §11.9. As in each of those sections, taking either up would still call for its own stopping rule, declared before the data, not after.

This closes Section IX.

Section X — Sheep and Goat: The Fifth and Sixth Wide-Ranging Mammals

Opened on the two live possibilities §15.8 named together without committing to either; new stopping rule declared in §16.1

Chapter 16 — Sheep Domestication: A Single Broad Zone, Not a Fifth Multi-Center Case

16.1 A stopping rule for Section X, covering both named live possibilities at once

Stopping rule for Section X

1. This section: two cases, not one — sheep (*Ovis aries*) and goat (*Capra hircus*), the two candidates §15.8 named together as the only live possibilities left after Section IX, without committing to either. Both are wide-ranging Near Eastern caprines, frequently co-excavated at the same Neolithic sites, which makes them a genuine pair rather than two unrelated extensions: this section asks whether two closely related, similarly dated, geographically overlapping domesticates resolve to the same C under this cycle's own discipline, or to two different ones for two different, specific, source-grounded reasons.

2. No Section XI is committed to now. This is a two-case section by design, exactly as Section I's rice-and-cereals scope and Section II's maize-and-ENA scope each covered more than one case under a single declared rule; going beyond it would call for a fresh stopping rule of its own, declared before any further data is taken up.

The same data commitments carry over unchanged from every prior section: no invented figures, no synthetic illustrative datasets, disagreement reported rather than resolved by authorial preference, and every computed quantity accompanied by its executed script (code/Ch16_sheep_distance_check.py, code/Ch17_goat_distance_check.py).

16.2 Why sheep and goat, examined together, are a genuine methodological test

Horse (Ch.15) answered a single, narrow question — whether cattle and water buffalo's close PI agreement was itself meaningful or a coincidence of n=2. Sheep and goat pose a different kind of test. Unlike horse, which this cycle treated as one self-contained case, sheep and goat share almost everything a domestication case can share short of being the same species: the same broad Fertile Crescent arc from southeastern Anatolia to the Zagros, the same tenth-millennium-BP horizon, and, at sites such as Ganj Dareh and Aşıklı Höyük, the same excavated deposits. If this cycle's index only tracked gross geography — continental separation the way pig's Near East/China split did (§11.4's box) — two such closely paired cases might be expected to land on similar C and PI values by default. §16.3–§16.8 and Chapter 17 show this is not what happens: the literature itself, read on its own terms, supports C=1 for sheep and a directly quantified C=2 for goat. That divergence is reported here as a reassurance about the index's sensitivity to real evidentiary differences, not as a new general finding about caprines.

16.3 The archaeological record: a shared arc, and a disclosed asymmetry at the very same sites

Zooarchaeological demographic evidence — changes in kill-off age structure consistent with herd management rather than hunting — places early caprine management across a band running from southeastern Anatolia (~10,500 BP) to central Anatolia (10,400–9,400 BP, most fully documented at Aşıklı Höyük) and into the Zagros. Stiner, Munro, Buitenhuis, Duru & Özbaşaran (2022, *PNAS* 119:e2110930119) describe an “endemic pathway” to both sheep and goat domestication at Aşıklı Höyük specifically, based on corralling evidence and demographic profiles internal to that one Central Anatolian sequence.

A more recent, site-specific finding complicates the Zagros half of this picture for sheep in particular. de Groene, Bendrey, Müldner, Coogan & Matthews (2023, *Journal of Archaeological Science: Reports* 49:103936), re-examining faunal and isotopic evidence from Ganj Dareh, Bestansur and Jarmo, report that there is no zooarchaeological evidence for local domestication of sheep in the Zagros region, and that smaller-bodied domestic sheep may instead have been introduced there from a neighbouring region — while goat, at the same sites, shows the clearer local management signal (§17.2 returns to this contrast directly). This is a genuine revision from Zeder's own earlier, broader framing of the Zagros as "one of the primary independent centers of animal domestication, particularly the domestication of sheep and goats" (Zeder 2008), and this cycle reports the revision rather than the earlier, more convenient reading — the same disclosed-revision discipline §15.4 applied to the Botai bit-wear dispute.

16.4 The genetic record: one broad zone, and an earlier multi-haplogroup hypothesis that did not survive broader sampling

Her, Rezaei, Hughes, Naderi, Duffraisse, Mashkour et al. (2022, *Animal Genetics* 53:452–459) sequenced 213 new cytochrome-b sequences and 54 new control-region sequences from wild Asiatic mouflon (*Ovis gmelini*) across its range, together with contemporary and ancient domestic sheep, and confirmed *O. gmelini* as the sole maternal ancestor of domestic sheep while excluding urial and argali contributions. Their control-region data show haplogroups A, B, C and E shared between domestic sheep and wild *O. gmelini* specifically in eastern Anatolia and central Zagros, and explicitly exclude regions further east, where only wild-type haplogroups were found. Critically, this is reported as one combined zone, not as two geographically separable centers: the same four haplogroups recur on both the Anatolian and Zagros sides, so the current genetic evidence cannot subdivide the zone further.

This supersedes an earlier reading of the same broad haplogroup diversity. Smaller surveys — five phylogenetically distinct mtDNA lineages had been identified across domestic sheep by the mid-2000s (Guo et al. 2005; Pedrosa et al. 2005 and others cited in the review literature) — were read by some as evidence for multiple, independent domestication events, structurally the same inference squash's second center and pig's six-center extension invited from limited haplogroup counts alone. Her et al.'s (2022) much larger, range-wide wild-reference sampling does not support that reading: the haplogroup diversity is present within one broad zone rather than distributed across geographically separate, independently corroborated centers.

Why “mosaic” does not mean “polycentric”

Daly, Mullin, Hare et al. (2025, *Science* 387:492–497) sequenced 118 ancient sheep genomes spanning 12,000 years and found that genomes from central Türkiye ~8000 BCE are genetically proximal to, but do not fully explain, later populations' ancestry — language the authors summarize as a “mosaic of wild ancestries.” This cycle reads that finding carefully rather than as a fifth multi-center case: a mosaic of wild ancestries describes ongoing local introgression from regional wild mouflon populations as domestic sheep dispersed outward from a single zone of origin, not multiple independent human decisions to domesticate. This is the same distinction §11.6 drew for pig's European wild-boar recruitment (local capture and replacement within an already-established husbandry system, not a second independent domestication) — applied here to a different species and a different data type.

16.5 A real-coordinate check: two named sub-areas inside one zone, not two centers

Recomputed via great-circle distance (code/Ch16_sheep_distance_check.py), using a representative point for each of the two named sub-areas of Her et al.'s (2022) single confirmed zone — not treated as a C=2 distance, for the reason given in §16.4: the same haplogroups recur in both sub-areas, so this cycle's own discipline against inventing an unsupported split applies directly.

Central Anatolia anchor	Central Zagros anchor	Distance
Aşıklı Höyük, Aksaray Province	Ganj Dareh, Kermanshah Province	1,269.0 km

This 1,269.0 km figure is reported as an internal-breadth sensitivity check only — a measure of how large Her et al.'s (2022) single zone actually is, not a second center's distance from a first.

C	κ	D̄ (km)	PI
1	1.000	0 (undefined, by convention 0)	0

PI=0 places sheep at this cycle's now-familiar single-center floor, alongside einkorn, rice's C=1 model, sunflower, and horse — but, as §16.6 and §16.7 disclose, for a structurally different reason than any of those four.

16.6 Why sheep gets C=1, not a contested C=2 (a fifth, distinct reason for landing at the floor)

A fifth path to PI=0

This cycle's four prior single-center (or effectively single-center) cases each reached PI=0 by a different route: einkorn was never seriously contested (§2.2); rice's C=1 model is one of several models for a genuinely disputed count (§4.x); sunflower's second center was proposed and then specifically refuted by direct genetic testing (§7.3); horse's three rival centers were each

proposed and then excluded by ancient DNA (§15.4–§15.6). Sheep adds a fifth: no specific second center was ever proposed and tested here in the first place. Her et al.'s (2022) range-wide wild-reference sampling simply did not find the geographic separation a genuine C=2 claim would require — the earlier multi-haplogroup readings were never formalized into a named, located second center the way barley's Tibetan candidate or pig's Indian and Southeast Asian candidates were. This cycle reports the distinction rather than collapsing it into "yet another single-center case," since the evidentiary path matters as much as the destination throughout this cycle's own discipline (§2.1's geography/tempo separation set this precedent from the first chapter).

This cycle's four earlier PI=0 cases each reached the floor by a distinct route, and naming sheep's own route requires distinguishing it from all four rather than restating any one. Einkorn (§2.2) reached C=1 because two fully independent genetic methods converged unanimously on a single center, with no rival ever seriously proposed. Rice's C=1 model (§4.2) reached the same value because two independent methods (Molina et al. 2011; Huang et al. 2012) converged, while a third study (Civán et al. 2015) proposed a rival multi-center reading that this cycle reported rather than adjudicated. Sunflower (§7.3) and horse (§15.5) reached C=1 by a third route: a specific rival center was proposed and then directly tested — against achene morphology and against ancient DNA, respectively — and did not survive.

Sheep fits none of these three patterns. §16.4's genetic record does not unanimously confirm one point in the way einkorn's did, nor does it adjudicate between named rival centers the way horse's did: Her et al. (2022) report one broad zone that the current wild-reference sampling cannot subdivide, not a single resolved point with rivals excluded. And §16.3's archaeological record does not

converge with genetics on a shared answer the way pig's, cattle's, or water buffalo's did (§11.3, §13.3, §14.3); if anything, de Groene et al.'s (2023) re-examination of Ganj Dareh, Bestansur and Jarmo cuts the other way, finding no zooarchaeological evidence for local Zagros domestication of sheep specifically, and proposing introduction from elsewhere within Her et al.'s own broad zone. C=1 for sheep is therefore not a positive finding of a single confirmed origin point, in the sense einkorn's or horse's C=1 was. It is the finest-grained count the current evidence jointly supports: genetics rules out everything east of the Anatolia–Zagros arc but cannot resolve points within it, and the most recent archaeology inside that arc undercuts rather than confirms any one sub-location as the origin.

This is sheep's fifth, distinct reason for landing at PI=0: not unanimous confirmation, not a tested and excluded rival, but an evidentiary resolution limit that happens to coincide with C=1 rather than demonstrate it outright. §16.7 develops the asymmetry between the two evidence types that produces this reading in more detail; §17.1–§17.4 report why goat, examined across the same arc and largely the same sites, does not share it.

16.7 A disclosed corroboration asymmetry between archaeology and genetics

Sheep's C=1 result does not rest on the same "archaeology and genetics independently converge on the same answer" structure this cycle used for pig, cattle, and water buffalo (§11.3, §13.3, §14.3). Instead, the two evidence types play different, complementary roles here: genetics (Her et al. 2022) sets the zone's outer boundary and rules out an eastern extension, but cannot currently subdivide the zone internally; archaeology, in its most recent, site-specific form (de Groene et al. 2023), narrows candidate locations within the zone but positively questions local Zagros origination for sheep specifically, pointing instead to introduction from a neighbouring

part of the same broad zone. This is disclosed here as a third distinct corroboration structure this cycle has now encountered, following §15.4's own disclosure that horse's corroboration (two studies sharing a corresponding author) was narrower than pig's, cattle's, or water buffalo's doubly-independent pairings. Sheep's is narrower still: the two evidence types do not test the same claim twice, they test two different, adjacent parts of one claim.

16.8 Closing note on sheep, and the transition to goat

Chapter 16 closes with sheep at C=1, PI=0, for reasons specific to sheep's own evidentiary record. Chapter 17 turns to goat, domesticated across the same broad arc, on a similar timeline, and in some cases at the very same sites — where, as §17.2–§17.4 show, the literature supports a directly quantified, if highly unequal, C=2.

Chapter 17 — Goat Domestication: A Real, Quantified, Highly Unequal Second Center

17.1 A structurally different case from sheep, despite the shared arc

Goat (*Capra hircus*) shares its wild progenitor's range, its domestication horizon, and several of its key excavated sites with sheep — including Ganj Dareh itself, where both species were managed within the same Aceramic Neolithic sequence. §17.2–§17.5 show that, despite this overlap, goat's own literature supports a claim sheep's does not: a second, geographically distinct, directly quantified domestication signal, small but real, standing apart from the dominant center in a way no cited source claims for sheep.

17.2 Archaeology: Ganj Dareh and the case for local Zagros domestication

Zeder & Hesse (2000, *Science* 287:2254–2257) analyzed kill-off age and sex profiles of goat remains from Ganj Dareh and reported a demographic signature — heavy culling of young males with females retained longer — consistent with deliberate herd management rather than hunting, dated to approximately 10,000 BP. This is the direct archaeological basis for reading Ganj Dareh as a genuine, local Zagros domestication locus for goat specifically. §16.3 already disclosed the pointed contrast the more recent de Groene et al. (2023) re-analysis draws at these same sites: sheep at Ganj Dareh lack this local signal, while goat shows it clearly — a genuine, sourced asymmetry between two co-excavated species at a single site, not an artifact of this cycle's own treatment.

17.3 Genetics: a directly quantified, highly unequal two-center split

Naderi, Rezaei, Taberlet et al. (2007, *PLoS ONE* 2(10):e1012) first identified six mtDNA haplogroups across a large domestic goat sample. Naderi, Rezaei, Pompanon, Blum, Negrini et al. (2008, *PNAS* 105(46):17659–17664) then sampled 473 wild bezoar (*Capra*

aegagrus) individuals across 43 populations spanning the species' full range, divided into eight geographic regions, and ran an AMOVA to localize each haplogroup's likely domestication center.

Their result is a genuine C=2, but sharply unequal. The main signal — haplogroup A, accounting for the large majority of domestic goats worldwide — traces to a broad zone covering eastern Anatolia and extending into northern and central Zagros, the likely origin of almost all domestic goats today. A second, geographically separate signal — associated with the C haplogroup — traces to a population expansion centered on the Central Iranian Plateau (Yazd and Kerman provinces) and the Southern Zagros (Fars province). Naderi et al. report this second center's contribution to the current domestic goat population directly and explicitly: rather low, at 1.4%.

17.4 A real-coordinate check, and this cycle's first directly quantified near-floor PI

Recomputed via great-circle distance (code/Ch17_goat_distance_check.py), using Ganj Dareh, Kermanshah Province, Iran, as this cycle's representative point for the major center (disclosed as such: Naderi et al. name a zone, not a single site, and Ganj Dareh is independently the best-documented location within it, converging with the archaeology of §17.2 and the ancient genomics of §17.5), against Yazd, Iran, as this cycle's representative point for the minor center's named provinces:

Major-center anchor	Minor-center anchor	Distance
Ganj Dareh, Kermanshah Province	Yazd, Iran	693.1 km

Naderi et al.'s (2008) own directly reported 1.4% figure — the fraction of the modern domestic mtDNA pool tracing to the minor center — is used here as κ, the same "directly reported fraction" role Morrell & Clegg's 10/18 loci (barley, §2.4), Jing et al.'s ~20%

(rice, Ch.4), and Schmutz et al.'s shared-genome fraction (common bean, §9.5) played earlier in this cycle.

C	κ	D⁻ (km)	PI
2	0.014	693.1	19.4

What a near-floor, non-zero PI means

Goat's PI=19.4 is a new kind of result for this cycle. It is not PI=0 (sunflower, horse): unlike those cases, the second signal here was not tested and refuted — Naderi et al. (2008) affirmatively report it as a real, if minor, contributor, corroborated further by the ancient genomics of §17.5. Nor does it resemble rice's C=2 model (κ=0.200, PI=704) or barley's (κ=0.556, PI=3,384), where the second center's fractional support, while partial, is an order of magnitude larger. Goat's 1.4% is the smallest directly reported corroboration fraction this cycle has used anywhere, and the resulting PI — 19.4 — sits closer to the C=1 floor than to any of this cycle's other genuine C=2 cases, without actually being zero. This is offered as a further, informative middle case for the index: a real second center can be corroborated and still produce a PI close to the floor, when its own reported contribution is this small.

17.5 A further complication, disclosed rather than folded into the core model: ancient genomics' "mosaic domestication"

Daly, Delser, Mullin, Scheu, Mattiangeli et al. (2018, *Science* 361(6397):85–88) sequenced 83 ancient goat genomes (51 with genome-wide coverage) spanning Paleolithic to Medieval contexts across the Near East. Their central finding is explicitly titled a "mosaic": multiple divergent ancient wild goat sources were domesticated in a dispersed process, with bezoar haplogroups A (Anatolia) and B (North Iran) identified as the main maternal ancestors of Neolithic domestic goat, alongside minor contributions

from central and east Iran, and these early populations contributing unevenly to modern goats in Asia, Africa and Europe.

This sits in a disclosed tension with §17.3's core model rather than simply confirming it. Naderi et al.'s (2008) modern-mtDNA survey reads as one dominant center (98.6%) and one small, clearly secondary one (1.4%); Daly et al.'s (2018) ancient-DNA survey instead names two "main" maternal ancestors — Anatolia and North Iran — without the same lopsided framing, and adds still further minor central/east Iranian contributions distinct from both. The two studies are not measuring quite the same thing (modern population-wide mtDNA frequency versus ancient, site-anchored genomic ancestry across a dispersed time series), and this cycle does not resolve the tension by picking whichever reading is more convenient for a clean number, following the same disclosed-disagreement discipline §15.3–§15.4 applied to horse's rival candidate centers.

Daly, Mattiangeli, Hare et al. (2021, *PNAS* 118(25):e2100901118) add a further, independent line: 14 nuclear and 32 mitochondrial ancient genomes from Ganj Dareh and Tepe Abdul Hosein, both Zagros sites, showing two distinct genetic clusters as early as ~8200 cal BC — a majority group with domestic affinity ("Zagros Main") and a smaller group with stronger wild affinity — combined with long runs of homozygosity, a sex bias in the archaeozoological remains, and demographic profiles across all excavated layers. This independently corroborates §17.2's and §17.3's Zagros-adjacent major center specifically, using a third evidence type (ancient nuclear genomics) alongside the archaeozoology and modern mtDNA already discussed — the same "multiple independent evidence types agree" structure this cycle has valued highly since pig's C=2 case (§11.3), even as §17.5's own North Iran finding complicates the minor center's precise shape.

Why no new PI is computed for the ancient-genomic "mosaic" picture

Daly et al. (2018, 2021) do not report a directly comparable population-fraction number the way Naderi et al.'s (2008) 1.4% figure supplies one. "Main maternal ancestors" (Anatolia and North Iran) versus "minor contributions" (central/east Iran) is a qualitative ranking, not a quantified split into which a κ could honestly be read. Following this cycle's discipline since §11.5's treatment of pig's own contested six-center extension, no κ is invented here to force a second PI. The North Iran distance is reported below as a geometric sensitivity check only.

Major-center anchor	North Iran sensitivity anchor	Distance (sensitivity only)
Ganj Dareh, Kermanshah Province	Gorgan, Golestan Province	691.0 km

This 691.0 km figure — coincidentally close to §17.4's core 693.1 km — is disclosed for completeness and is not used in any PI computation.

17.6 Cross-cycle synthesis: fifteen cases across ten sections

Adding sheep and goat to §15.7's table changes the shape of the low end without disturbing the top:

Crop/species (model)	C	κ	D̄ (km)	PI
Pig (core model)	2	1.000	6,525	13,050
Common bean	2	0.902	3,658	6,601
Water buffalo (core model)	2	1.000	2,914.7	5,829
Cattle (core model)	2	1.000	2,758.7	5,517

Crop/species (model)	C	κ	D̄ (km)	PI
Squash (C. pepo)	2	1.000	2,282	4,565
Barley	2	0.556	3,046	3,384
Rice (C=2 model)	2	0.200	1,761	704
Grapevine	2	0.897	305	547
Goat (core model)	2	0.014	693.1	19.4
Einkorn	1	1.000	0	0
Rice (C=1 model)	1	1.000	0	0
Sunflower	1 (2nd center refuted)	1.000	0	0
Horse	1 (three rival centers refuted)	1.000	0	0
Sheep	1 (single broad zone)	1.000	0	0
Maize	1 (location disputed)	n/a	531 (location only)	not computed

Goat's PI=19.4 becomes the cycle's lowest non-zero, non-refuted PI — well below grapevine's 547, the previous low end for a genuine C=2 case — extending the range the index can now express between a corroborated-but-tiny second center and the C=1 floor. Sheep joins the floor group as its fifth member, and, per §16.6's box, for a fifth distinct reason: never formalized into a tested second center in the first place, rather than never contested, one of several disputed models, proposed-and-refuted, or confirmed-against-multiple-tested-rivals.

17.7 What sheep and goat, examined together, add to the cycle's own self-knowledge

Two co-excavated, closely related, similarly dated caprines from the same broad region resolve to genuinely different C values under this cycle's own disclosed-limits discipline — not because the method treats them differently, but because the underlying literature itself supports different, specific claims for each: a broad, internally unsubdivided zone for sheep; a small, directly quantified, and independently ancient-DNA-corroborated second center for goat. This is reported as a methodological reassurance rather than a new general finding: the index does not flatten two superficially similar cases into the same number when their own cited sources genuinely diverge, and it does not manufacture a difference where the sources agree, either — the same discipline §16.2 set out to test.

17.8 Closing Section X

Fifteen crop/species-model combinations across ten sections and seventeen chapters, plus sheep's own disclosed single-zone result and goat's own disclosed ancient-genomic complication, have now been carried through this cycle's single index under one unchanged no-invented-data discipline since §1.4. §15.8's own named live possibilities — sheep and goat — have both now been examined, on their own terms, to the depth their own literatures currently support.

Final stopping-rule declaration for Section X

No Section XI is committed to here. One further wide-ranging mammal case remains, in principle, untested by this cycle: camel (*Camelus dromedarius* and/or *C. bactrianus*), whose own domestication geography and center count this cycle has not yet searched. Naming it as a live possibility, in the same spirit as every closing section since §11.9, is as far as this cycle's own

discipline goes without committing to it outright; opening it would still need a stopping rule declared beforehand, as every prior section has required.

This closes Section X.

Section XI — Camel: A Real Domesticate on One Side, a Genuinely Unresolved Center on the Other

The seventh wide-ranging mammal named as a live possibility at the close of Section X; new stopping rule declared in §18.1

Chapter 18 — Dromedary Domestication: A Sixth Path to the Single-Center Floor

18.1 A stopping rule for Section XI, covering the one case named at the close of Section X

Stopping rule for Section XI

1. This section: two cases, not one — dromedary (*Camelus dromedarius*) and Bactrian camel (*Camelus bactrianus*), the two extant domestic camel taxa, examined as separate chapters because their own evidentiary records diverge sharply, in the same spirit §16.1 set out for sheep and goat. §17.8's closing box named camel, undifferentiated by species, as the one remaining untested wide-ranging mammal; this section does the search that naming promised.

2. This section discloses in advance, rather than after the fact, that the two chapters are not expected to land the same way. §18's own literature converges cleanly on one location by two independent evidence types; §19's literature is still actively split between two rival hypotheses, with no directly reported fraction available to weight a second center the way goat's 1.4% or barley's 10/18 loci did. Chapter 19 may therefore close without a computed PI, in the same disclosed manner as maize (§17.6's table). This is stated here, before either chapter is written, so that an unresolved Chapter 19 is read as an honest result of this section's own stopping rule, not a shortfall against it.

3. No Section XII is committed to now. Taking one up would call for the same first step every prior section has taken: declaring its own stopping rule before any data is presented.

The same data commitments carry over unchanged from every prior section: no invented figures, no synthetic illustrative datasets, disagreement reported rather than resolved by authorial

preference, and every computed quantity accompanied by its executed script (code/Ch18_dromedary_distance_check.py, code/Ch19_bactrian_distance_check.py).

18.2 The archaeological record: a single, well-excavated corner of Arabia

Uerpmann & Uerpmann (2002, *Journal of Oman Studies* 12:235-260), drawing on osteological, pictorial, and cultural-context evidence, place the appearance of the domestic dromedary in south-eastern Arabia in the late second millennium BCE, with earlier specimens from the same region read as wild. Magee (2015, *Zeitschrift für Orient-Archäologie* 8:253-278), synthesizing artifactual, textual, and archaeological evidence from southern Arabia to Syria, including material from the United Arab Emirates, reaches the same regional conclusion. The most direct site-level evidence comes from Magee's own excavations at Muweilah and Tell Abraq, in the present-day UAE, where Muweilah alone has produced close to ten times as many domesticated-dromedary bones as any other single contemporary site in the Middle East — the same kind of single-site excavation density this cycle has treated as strong corroboration since Aşıklı Höyük's role in §16.3 and §16.5.

18.3 The genetic record: archaeology and genetics converge on the same corner, independently

Almathen, Charruau, Mohandesan, Mwacharo, Orozco-terWengel, Pitt, Abdussamad, Uerpmann, Uerpmann, De Cupere, Magee et al. (2016, *PNAS* 113:6707-6712) combined ancient DNA from wild and early-domesticated dromedaries with nuclear microsatellite and mitochondrial data from 1,083 modern animals across the species' range. Their central finding: wild dromedaries from the south-eastern Arabian Peninsula are identified among the founders of the domestic dromedary population, a result the authors themselves report as being in agreement with the archaeological findings already discussed in §18.2 — the same site-specific region

Magee, and Uerpmann & Uerpmann, had independently proposed from artifactual and osteological evidence alone.

This is a structurally distinct corroboration pattern from anything else in this cycle. Pig, cattle, and water buffalo (§11.3, §13.3, §14.3) used doubly independent archaeology-genetics agreement to corroborate a *second* center inside an already-established C=2 case. Dromedary uses the same doubly independent structure to corroborate the *only* center in a C=1 case — archaeology proposed south-eastern Arabia first, on artifactual grounds alone, and genetics, working from a completely independent data type, arrived at the same corner of the map rather than at a rival one.

18.3.1 A disclosed complication: restocking from the wild, and a later trans-continental overprint

§18.2–§18.3's convergence answers where domestication happened; it does not exhaust what the genetic record has to say about what happened afterward. Almathen et al. (2016) themselves report a second finding, distinct from the corroboration already discussed: approximate Bayesian computation over their combined microsatellite and mitochondrial dataset favored a 'restocking from the wild' model over either a single clean domestication or repeated independent domestications — an initial domestication event followed by further introgression from wild, now-extinct dromedary populations. This complicates the demographic history without reopening §18.2–§18.4's geographic result: restocking describes gene flow into an already-established domestic population from wild individuals in the same region, not a second, geographically distinct center of domestication.

Lado, Elbers, Doskocil et al. (2020, Communications Biology 3:387), applying a genome-wide SNP panel (22,721 markers) to 95 modern dromedaries across three continents, extended this picture in two further ways left undiscussed until now. First, demographic reconstruction detected a population decline through the Late

Pleistocene glacial period, predating domestication by tens of thousands of years, with no additional bottleneck signal at the domestication horizon itself (c. 3,000–4,000 years before present) — consistent with, and independently corroborating, Almathen et al.'s own earlier mitochondrial finding of no domestication-era population decline. Second, the modern population's very low genome-wide differentiation ($F_{xs} = 0.006$ between Africa and Asia) was traced to post-domestication gene flow along historic caravan corridors — the Incense and Silk Roads — rather than to a shared origin alone: effective migration surfaces show elevated gene flow precisely along the Mediterranean coastal corridor linking North Africa to the Arabian Peninsula, with the Horn of Africa standing out as the one region of persistently low migration, isolated by the Ethiopian highlands.

None of this revises §18.6's C=1, PI=0 result — both studies locate the founding population in the same south-eastern Arabian corner §18.2–§18.4 already established. What it adds is a disclosed layer the corroboration-only reading of §18.3 would otherwise leave silent: the modern dromedary's genetic structure is not simply an echo of where domestication happened, but a compound signal of that origin overwritten by three millennia of trade-driven gene flow — the same kind of post-domestication overprint this cycle's cattle (§13.5) and horse (§15.4) chapters treated as a separate question from center count, not a revision of it.

18.4 A real-coordinate check: two excavated sites, one small zone

Recomputed via great-circle distance (code/Ch18_dromedary_distance_check.py), using Magee's own two most fully excavated south-eastern Arabian sites as an internal-breadth sensitivity check — not a C=2 distance, since both sites sit inside the single zone both archaeology and genetics independently support:

Muweilah anchor (Sharjah, UAE)	Tell Abraq anchor (Umm Al Quwain, UAE)	Distance
25.3573°N, 55.4033°E	25.4890°N, 55.5490°E	20.7 km

At 20.7 km, this is the tightest internal-breadth figure this cycle has yet computed — smaller than sheep's 1,269.0 km spread across Anatolia and the Zagros (§16.5), because dromedary's two key sites sit within a single modern emirate rather than across a continental arc. This is disclosed as a further confirmation of how narrowly Uerpmann & Uerpmann's and Magee's own proposed zone is drawn, not as a second center's distance from a first.

C	κ	D̄ (km)	PI
1	1.000	0 (undefined, by convention 0)	0

A sixth path to PI=0

This cycle's five prior single-center (or effectively single-center) cases each reached PI=0 by a different route: einkorn was never seriously contested (§2.2); rice's C=1 model is one of several models for a genuinely disputed count (§4.x); sunflower's second center was proposed and then specifically refuted by direct genetic testing (§7.3); horse's three rival centers were each proposed and then excluded by ancient DNA (§15.4–§15.6); sheep's zone was never formalized into a tested, located second center in the first place (§16.6). Dromedary adds a sixth, and in one respect the cleanest of the six: no second center was ever seriously proposed for dromedary at all, and the one center that was proposed — from archaeology alone, years before the genetic study existed — was independently reaffirmed rather than merely left unchallenged. This is reported as a further data point on how the index's floor gets reached, not as evidence that PI=0

cases are becoming routine: §18.5 and Chapter 19 show the same broader camel question still contains a genuinely unresolved half.

18.5 A disclosed tempo dispute, kept separate from the geography question

Consistent with the geography/tempo separation this cycle declared from its first chapter (§2.1), a live dispute over dromedary domestication's *date* is disclosed here without being allowed to unsettle §18.2–§18.4's geographic result. Uerpmann & Uerpmann's and Magee's own osteological and figurine evidence supports a first-millennium-BCE domestication signal, with clear domesticated dromedary figurines appearing at Muweilah in the eighth century BCE. Other readings of textual and artifactual material — summarized, among others, by Heide and by Macdonald — push a working-camel presence in the archaeological record back into the third millennium BCE across multiple parts of the ancient Near East. This cycle does not adjudicate the date dispute, which concerns tempo, not center count; §18.2–§18.4's C=1 result depends only on *where*, not *when*, and holds under either reading of the timeline.

18.6 Closing note on dromedary, and the transition to Bactrian camel

Chapter 18 closes with dromedary at C=1, PI=0, on the strongest single-location corroboration structure this cycle has found for any C=1 case. Chapter 19 turns to the dromedary's two-humped relative, domesticated in a wholly different arid-zone territory, on a similar general timeline, but — as §19.2–§19.5 show — without anything like Chapter 18's clean convergence.

Chapter 19 — Bactrian Camel Domestication: A Genuinely Open Question, Reported Rather Than Forced

19.1 A structurally different case from dromedary, despite the shared genus

Bactrian camel (*Camelus bactrianus*) shares its genus, its general Old World arid-zone adaptation, and a broadly similar domestication horizon with dromedary, but not its evidentiary clarity. §19.2–§19.5 show that, unlike dromedary, no single center currently commands convergent support from both archaeology and genetics: the literature itself remains split between two named, actively defended hypotheses, and the most recent large-scale genomic study narrows the question without fully closing it. This cycle reports that openness directly, following the same disclosed-limits discipline maize's §17.6 entry already established, rather than picking whichever reading would produce the cleaner number.

19.2 Two rival hypotheses, named and still both defended

Burger (2019, *Animal Genetics* 50:598-604) frames the current state of the field as an open contest between two hypotheses. HI places domestication in north-eastern Iran and the adjacent Kopet Dagh foothills of south-western Turkmenistan — historically "Bactria", the region that gave the domestic two-humped camel its name. HII places a center of domestication further east, in territory such as southern Kazakhstan or north-western Mongolia, where communities are argued to have lived alongside wild camels over an extended period. Both hypotheses have named, published defenders; neither has been retracted.

Peters & von den Driesch (1997, *Journal of Zoology* 243:651-679) argued specifically against HI, concluding that none of the evidence so far brought forward for local domestication in the Kopet Dagh area holds up to closer scrutiny, and that the post-Pleistocene

distribution of the wild camel did not extend into Central Asia in the first place — placing the true center further east. This is a direct, named rejection of one candidate by a specific research group, structurally similar to the refutation moves this cycle used for sunflower (§7.3) and horse's rival centers (§15.4–§15.6), except that here no replacement single center has itself gone on to be independently corroborated the way horse's Volga-Don homeland was.

19.3 The most recent genomic evidence increasingly favors the western side of the split, without closing the question

Mohandesan, Fitak, Corander, Yadamsuren, Chuluunbat, Abdelhadi, Raziq, Nagy, Stalder, Walzer, Faye & Burger (2017, *Scientific Reports* 7:9970) sequenced 24 full camel mitogenomes across the genus and, alongside their primary purifying-selection findings, estimated a divergence between domestic and wild Bactrian camels around 1.1 (0.58-1.8) million years ago — deep enough to place the domestic lineage's own origin well outside the wild Bactrian camel's present-day Mongolian and Chinese range, consistent with a source population further west than HII's Mongolia-centered framing. Ming, Yuan et al. (2020, *Communications Biology* 3:1), performing whole-genome sequencing of 128 wild and domestic camels across Asia, sharpen this further: among domestic Bactrian camels, those from Iran show the largest genetic distance from all other sampled populations and occupy the most basal, earliest-splitting position in the phylogeny, despite documented admixture between domestic Bactrian camels and dromedaries around the Caspian Sea. Ming et al. read this combined pattern as support for a Central Asian origin with later eastward migration into Mongolia, where wild Bactrian camels themselves contributed little to the domestic gene pool despite sharing habitat there.

Read together, Mohandesan et al. (2017) and Ming et al. (2020) — both drawing on the same Vetmeduni Vienna research tradition as Almathen et al.'s (2016) dromedary work (§18.3) — increasingly favor the western side of the HI/HII split specifically: Iranian Bactrian camels' basal phylogenetic position points toward a source population in or near Iran, not toward Kazakhstan or north-western Mongolia. This is a genuine narrowing since Peters & von den Driesch's (1997) rejection of Kopet Dagh, and it favors HI's general region over HII's. It does not, however, confirm the specific Kopet Dagh foothill locations Peters & von den Driesch had examined and rejected: 'Iran' as reported by Ming et al. is a country-level sampling category, not a site-level claim, and no source reviewed for this chapter has gone back to test the specific Kopet Dagh archaeological candidates against this newer genomic signal. This cycle reads the dispute as narrowed — from a roughly even HI/HII contest to a genomically-favored western zone within which the precise center still is not pinned down — rather than as closed.

Why no κ is assigned here

Unlike goat's Naderi et al. (2008) 1.4% figure, or barley's Morrell & Clegg 10/18 loci, no source reviewed for this chapter reports a directly quantified fraction splitting a confirmed major center from a confirmed minor one. Mohandesan et al. (2017) and Ming et al. (2020) favor a western/Iranian source population over a further-east one, but neither names and quantifies two rival, simultaneously real centers the way Naderi et al. did for goat — they support one region over a rival region, not a major-plus-minor split within one confirmed system. Following this cycle's discipline since §11.5's treatment of pig's own six-center extension, and repeated for Bactrian camel's own ancient-genomic mosaic case in §19.4, no κ is invented here to force a PI where the cited sources do not themselves supply one.

19.4 A further complication: wild camel range now documented further west than assumed

Suska-Malawska, Kot, Gręzak, Mętrak, Khudjanazarov & Szymczak (2022, *The Holocene*) report chemical and isotopic evidence consistent with camel keeping and milking at Ayakagytma, a Neolithic open-air site in the south-eastern Kyzylkum Desert of Uzbekistan, dated to the Keltaminar culture horizon (circa 3000-4000 cal BCE). The same paper notes that wild Bactrian camel remains have separately been reported at this site from a sixth-millennium-BCE horizon, which the authors read as extending the documented range of wild camel — and therefore the geographic field a domestication center could plausibly sit within — further west than HII's Kazakhstan/Mongolia framing had assumed. This complicates a clean HI/HII binary rather than resolving it: it does not support Kopet Dagh specifically, but it narrows the geographic gap between the two named hypotheses. No coordinate-level distance is computed for Ayakagytma here, since this cycle's own discipline against inventing precision it does not have applies directly — the site's own reported location is regional, not a single surveyed point the way Aşıklı Höyük's or Ganj Dareh's are.

19.5 A real-coordinate check on the named HI/HII contrast, as a sensitivity measure only

Recomputed via great-circle distance (code/Ch19_bactrian_distance_check.py), using Anau, Turkmenistan, as this cycle's representative point for HI's Kopet Dagh foothill placement (a real excavated site in the region, with camel remains reported there since Duerst 1908), against two representative points for HII's further-east framing:

HI anchor (Anau, Turkmenistan)	HII candidate	Distance (sensitivity only)
37.8667°N, 58.3333°E	Almaty, Kazakhstan (southern Kazakhstan candidate) — 43.2565°N, 76.9285°E	1,676.8 km
37.8667°N, 58.3333°E	Bayan-Ölgii, Mongolia (north-western Mongolia candidate) — 48.9700°N, 89.9639°E	2,810.0 km

Both distances are reported as a geometric sensitivity check on how far apart the two named hypotheses actually sit, not as a C=2 computation: no source reviewed for this chapter treats HI and HII as two independently corroborated, simultaneously real centers the way Naderi et al. (2008) treated goat's major and minor signals. One of the two named hypotheses is understood, across this literature, to be the domestication center — the dispute is over which, not over whether both contributed.

19.6 Reporting an unresolved case: no PI is computed for Bactrian camel

Following the maize precedent

§17.6's synthesis table already carries one entry — maize — reporting a location dispute with a sensitivity-only distance and no computed PI, rather than forcing a number the cited sources do not themselves support. Bactrian camel is this cycle's second such case, for a related but distinct reason: maize's dispute is over the *number and location* of centers within a genus few doubt was domesticated somewhere in the Americas; Bactrian camel's dispute is over *which of two named, specific regions* hosted a single center that is not itself in doubt. Both are reported as 'not computed' rather than resolved by authorial preference, following this cycle's discipline since §1.4.

This cycle's own position, stated plainly: Bactrian camel was domesticated once, from a single wild source population, per the monophyletic-origin finding of Ji, Cui, Ding, Geng & Meng (2009, *Animal Genetics* 40:377-382) — so C=1 is very likely the correct center count. What remains genuinely unresolved, across archaeology and genomics alike, is *where* that one center sits. The weight of the most recent genomic evidence (Mohandesan et al. 2017; Ming et al. 2020) has shifted toward HI's general western zone — Iran and its surroundings — over HII's Kazakhstan/north-western-Mongolia framing, on the strength of Iranian Bactrian camels' basal phylogenetic position. But this is a country-level, not a site-level, result: it does not by itself vindicate the specific Kopet Dagh foothill candidates Peters & von den Driesch (1997) examined and rejected, and no source reviewed here has re-tested those specific sites against the newer genomic signal. Reporting a narrowed-but-still-undetermined location, rather than picking a single coordinate to manufacture a PI, is this cycle's own discipline applied honestly to a case that has moved since Section X's closing box named it, without yet resolving the way dromedary's did.

Bactrian camel's ⊥ fits the same branch as maize's under §20.7.1: a single corroborated center (C=1, per Ji, Cui, Ding, Geng & Meng 2009) whose own location is contested between named regional candidates (HI/HII, §19.2), rather than a case lacking any reported coordinate at all. §19.5's 1,676.8–2,810.0 km range is therefore a location-uncertainty sensitivity figure in exactly §6.4's sense, not a D̄ awaiting a κ value. No number changes here (§20.7.4); this note only attaches the later formal label to a judgment already made at §19.6.

19.7 What camel, examined as two chapters, adds to the cycle's own self-knowledge

Two congeneric domesticates, adapted to similar arid environments and domesticated on roughly comparable timelines,

resolve to opposite evidentiary states under this cycle's own discipline: dromedary reaches this cycle's cleanest single-center corroboration yet (§18.4's box), while Bactrian camel joins maize as this cycle's second case where honest reporting means declining to compute a PI at all. This is not a defect in the index: a method that could not produce 'not computed' as an honest answer would not be trustworthy when it does produce a number. §16.2 and §17.7 asked whether closely related, similarly dated cases resolve differently for real, source-grounded reasons; Chapter 18 and this chapter answer the same question again, this time finding not just a different C, but a different *kind* of answer altogether.

19.8 Cross-cycle synthesis: seventeen crop/species-model combinations across eleven sections

Adding dromedary and Bactrian camel to §17.6's table changes the composition of the PI=0 floor group and adds a second not-computed entry:

Crop/species (model)	C	κ	D̄ (km)	PI
Pig (core model)	2	1.000	6,525	13,050
Common bean	2	0.902	3,658	6,601
Water buffalo (core model)	2	1.000	2,914.7	5,829
Cattle (core model)	2	1.000	2,758.7	5,517
Squash (C. pepo)	2	1.000	2,282	4,565
Barley	2	0.556	3,046	3,384
Rice (C=2 model)	2	0.200	1,761	704
Grapevine	2	0.897	305	547

Crop/species (model)	C	κ	D̄ (km)	PI
Goat (core model)	2	0.014	693.1	19.4
Einkorn	1	1.000	0	0
Rice (C=1 model)	1	1.000	0	0
Sunflower	1 (2nd center refuted)	1.000	0	0
Horse	1 (three rival centers refuted)	1.000	0	0
Sheep	1 (single broad zone)	1.000	0	0
Dromedary	1 (archaeology-genetics convergence)	1.000	0	0
Maize	1 (location disputed)	n/a	531 (location only)	not computed
Bactrian camel	1 (location disputed)	n/a	1,676.8–2,810.0 (sensitivity only)	not computed

The PI=0 floor group now has six members, each reaching it by its own disclosed route (§18.4's box). The 'not computed' group has grown from one case to two — maize and Bactrian camel — sharing a structure (single-center-probable, location-disputed) despite belonging to a plant and an animal respectively, which this cycle reads as a further reassurance that 'not computed' is a genuine, repeatable category in the index's own output space, not a one-off exception carved out for maize alone.

19.9 Closing Section XI

Seventeen crop/species-model combinations across eleven sections and nineteen chapters have now been carried through this cycle's single index under one unchanged no-invented-data discipline since §1.4. Dromedary's own disclosed convergence and Bactrian camel's own disclosed non-resolution have both now been

examined, on their own terms, to the depth their own literatures currently support.

Final stopping-rule declaration for Section XI

No Section XII is committed to here. This cycle does not currently have a further named, flagged wide-ranging-mammal candidate in hand: dog, horse, cattle, water buffalo, pig, sheep, goat, dromedary, and Bactrian camel have now all been examined, and no source reviewed across this cycle's eleven sections has named a further major mammalian domesticate this cycle has not yet touched. Any Section XII would therefore need to either revisit a disclosed open thread from an already-covered case — Bactrian camel's own HI/HII dispute (§19.6) is the most obvious candidate, should new evidence resolve it — or justify, from scratch, why a new case type belongs in this cycle at all. Naming a specific candidate here without one currently in view would be the same unsupported invention this cycle has declined at every floor and ceiling reached so far. Committing to it now, rather than naming it as a live possibility, would break the one pattern this cycle has kept since its first chapter: a stopping rule declared before the case, never after.

This closes Section XI. -e

Section XII — Chicken: A First Case Outside Mammalia

A new case type, justified from scratch as §19.9 required of any Section XII; opened as a single-chapter section by design, following the precedent of Sections III and IV.

Chapter 20 — Chicken Domestication (Gallus gallus domesticus): Convergent Geography Without a Computable Index

20.1 A stopping rule for Section XII, declared before the case is restated

Stopping rule for Section XII

1. This section examines one case: chicken (Gallus gallus domesticus), the first bird — and first non-mammalian — case in this cycle. §19.9 closed Section XI with no further named wide-ranging-mammal candidate in hand and required any Section XII to justify a new case type from scratch rather than merely add a new animal to the mammal list. §20.2 restates that justification before any evidentiary finding is used to support it.

2. This section is informed by, and formalises, a preliminary reconnaissance already carried out on this exact question, under the same no-invented-data discipline, before this chapter's own stopping rule was declared. Reusing that reconnaissance's findings here does not violate the declare-before-analysing sequence §1.4 requires: the reconnaissance was explicitly scoped as non-committal (§R.0 of that note), precisely so that a real stopping rule could still be declared, and possibly declined, afterward. This chapter is that declaration.

3. This section precommits to the possibility of a ⊥ ('not computed') result, and to a specific kind of ⊥ distinct from every prior instance of it. §17.6 (maize) and §19.6 (Bactrian camel) both returned ⊥ because of a live dispute over which of several named locations hosts a single accepted center. Chicken's own literature (§20.3–§20.5) instead converges on a single broad region without either convergent evidentiary line supplying a site-level coordinate. If this chapter reaches that outcome, it is to be read as the honest result of this stopping rule, not a shortfall against it —

the same disclosure Bactrian camel's own §18.1 made for itself in advance.

4. No Section XIII is committed to here. Any further bird, or further non-mammalian, non-plant case, would need both its own stopping rule declared in advance and its own from-scratch justification for extending the cycle's case-type roster a second time — the same bar every section here has had to clear.

The same data commitments carry over unchanged from every prior section: no invented figures, no synthetic illustrative datasets, disagreement reported rather than resolved by authorial preference, and every computed or attempted quantity traceable to a specific cited source.

20.2 Why a bird, and why chicken specifically, belongs in this cycle

Every case this cycle has examined before this chapter — nine mammals and eight plants, across eleven sections and nineteen chapters — shares one of two taxonomic kingdoms and, among animals, one class. Admitting chicken requires the same kind of advance justification §16.1 and §18.1 each gave their own narrower scope decisions, stated here in three parts.

1. Evidentiary richness. Chicken is the world's most numerous domestic animal, and the subject of a very large, still-active genomic and zooarchaeological literature — in section comparable to any mammal this cycle has treated, and considerably larger than dromedary's or Bactrian camel's own.

2. A live, multi-sided dispute, not a settled case chosen to pad the count. Chicken sits at the intersection of three not-fully-reconciled evidentiary lines: a large modern-genome single-origin result, an older but not retracted multiple-maternal-origin mitochondrial literature, and a 2022 zooarchaeological reassessment that

overturned the accepted chronology at more than 600 sites. §20.3–§20.5 examine each in turn.

3. A genuinely new failure mode for the index, not merely a new animal. As §20.6 shows, chicken does not resolve into any of the categories the cycle's synthesis table (§19.8) contained before this chapter — corroborated PI, PI=0, or 'not computed because of a live location dispute'. It adds a fourth: strong geographic convergence between two main evidentiary lines, without either supplying the site-level coordinates the index's own $D\bar{}$ term requires. §20.7 formalises this as a permanent addition to the index's own definition, on the same footing as §2.7's original contribution.

On admitting a new case type at all

The justification is methodological, not taxonomic: chicken is a stress test of whether the Domestication Polycentricity Index generalises past the specific data shape — excavated point-sites, nuclear or mitochondrial center-count statistics — that nine mammal cases and eight plant cases have so far supplied it with. A method that only works for large, slow-breeding terrestrial mammals and Neolithic founder crops would be a narrower tool than this cycle has so far claimed. This is the justification §19.9 required before naming a new case type, supplied here in full before §20.3 opens the case itself.

20.3 The archaeozoological record: from a dispersed consensus to a single confirmed origin

For most of the twentieth century, chicken domestication was placed loosely in South or Southeast Asia on the strength of scattered early site reports across the Indus Valley, northern China, and mainland Southeast Asia, with individual claims rarely cross-checked against direct dating or against misidentification of other galliform or anseriform species.

Peters, Lebrasseur, Irving-Pease, Paxinos, Best, Smallman et al. (2022, *PNAS* 119(24):e2121978119) undertook the most systematic reassessment of this record to date: a critical review of chicken remains reported from more than 600 sites in 89 countries, combining zoogeographic, morphological, osteometric, stratigraphic, contextual, iconographic and textual criteria, supplemented by a direct radiocarbon-dating programme on 23 of the previously proposed earliest specimens from western Eurasia and north-west Africa. Their central finding: the first unambiguous domestic chicken remains, by their own combined criteria, are found at Ban Non Wat in central Thailand, dated to approximately 1650–1250 BCE — several millennia later than many earlier claims for Chinese or South Asian sites had proposed, and centuries later than some earlier Southeast Asian dating had assumed.

The same paper directly disputes several of the specific claims that had previously supported a dispersed, multi-regional archaeological picture: a proposed "earliest chicken" from a New Kingdom Theban tomb is re-identified as a misidentified duck; Egyptian Gallus depictions on a 19th- and 20th-Dynasty ostracon and silver bowl are read as possibly representing wild junglefowl rather than domestic chicken; and the radiocarbon programme itself showed that numerous earlier claims for the first appearance of chickens in Europe were spurious, pushing the confirmed European date to roughly 800 BCE. Unambiguous chicken remains in lower Egypt are pushed forward to the Achaemenid period (c. 550–330 BCE), and directly radiocarbon-dated bones place chickens in Pre-Aksumite northern Ethiopia by roughly 800–600 BCE.

This is a structurally different kind of correction from anything §18–§19 encountered for camel. Peters et al. do not propose a rival center location; they remove much of the evidentiary basis that had previously supported several proposed centers at all, by re-

examining the specimens themselves rather than by proposing a new one. §20.5 returns to why this matters for how C should be counted.

20.4 The genomic record: a large single-origin result against an older, not-retracted multiple-origins literature

Wang, Thakur, Peng, Jiang, Frantz, Li, Zhang, Otecko, Liu, Wu, Guo, Zheng, Esmailizadeh, Hirimuthugoda, Ashari, Suladari, Zein, Kusza, Sohrabi, Kharrati-Koopaee, Shen, Zeng, Yang, Wu, Yang, Ma, Dai, Xiang, Hou, Huang, Rehman, Muzahid, Hoque, Silva, Le, Mwacharo, Hanotte, Shu-Jin, Zhang & Zhang (2020, *Cell Research* 30:693–701) analysed 863 genomes drawn from modern chickens and from representatives of all five red-junglefowl (Gallus gallus) subspecies and the other three Gallus species. Their central conclusion is that domestic chickens derive primarily from the subspecies *Gallus gallus spadiceus*, whose present-day distribution centers on south-western China, northern Thailand and Myanmar, and that chickens were subsequently translocated across South and Southeast Asia, interbreeding locally with other junglefowl subspecies and species along the way. Fumihito et al. (1994, *PNAS* 91:12505–12509), working from a much smaller mitochondrial dataset, had already proposed a single-subspecies matriarchic origin, so the qualitative single-origin conclusion is not new to Wang et al.; what is new is the scale — 863 genomes against a handful of mitochondrial lineages — and the specific subspecies attribution.

Set against this is an older but not formally retracted multiple-origins literature. Liu, Wu, Yao, Li, Luo, Andersson & Zhang (2006, *Molecular Phylogenetics and Evolution* 38:12–19) argued from mitochondrial control-region sequences for multiple maternal origins across the Asian range. Kanginakudru, Metta, Jakati & Nagaraju (2008, *BMC Evolutionary Biology* 8:174), analysing 76 Indian birds — including 56 individuals of the Indian red-

junglefowl subspecies *G. g. murghi*, previously under-sampled — by microsatellite markers and mitochondrial D-loop sequence, reported average FST of 0.126 within G. g. murghi and 0.154 within G. g. domesticus, with more than 0.2 between the two groups, and concluded that Indian domestic chicken carries genetic contributions independently derived from G. g. murghi, not solely from admixture with an already-domesticated Southeast Asian population.

This is not yet a refutation in the sense §7.3 and §15.4–§15.6 used for sunflower's and horse's rival centers. Eda (2021, *Animal Frontiers* 11(3):52–58), reviewing both literatures, notes that more recent, larger genomic surveys have shifted the field's weight toward the single-subspecies, single-origin reading without eliminating the older Indian and multiple-maternal-lineage findings from the published record. Peters et al.'s (2022) own synthesis, drawing on Wang et al. (2020) among others, states directly that South Asian domestic chickens' apparent affinity to the local G. g. murghi subspecies is better read as later admixture with already-domesticated birds arriving from Southeast Asia, rather than as evidence of an independent local domestication event — a position that narrows, without formally retracting, Kanginakudru et al.'s (2008) own reading of the same general pattern.

A further, separate complication concerns tempo rather than geography, in the same spirit as this cycle's declared geography/tempo separation (§2.1, §18.5): reviews of the genomic literature report a deep divergence between the ancestral lineage of domestic chickens and present-day wild red junglefowl on the order of several tens of thousands of years — far older than any proposed domestication event — a pattern structurally similar to Bactrian camel's own deep divergence estimate (§19.3) and read the same way here: as evidence about ancestral population history, not as a claim about when domestication itself occurred.

20.5 A structurally new complication: disputes over authenticity, not only over location

Every prior 'contested center' case in this cycle — barley's Tibetan candidate (§2.7), maize's location dispute (§17.6), Bactrian camel's HI/HII split (§19.2–§19.6) — has involved disagreement about *where* a genuine domestication event happened, or about *how many* genuine centers there were. None involved active dispute about whether the underlying specimens were even correctly identified as the domesticate in question.

Chicken's older, more dispersed archaeological picture rested in part on exactly this kind of unexamined identification: Peters et al. (2022) re-identify a purportedly early Egyptian specimen as a duck, and treat two iconographic 'chicken' identifications as more plausibly representing wild junglefowl. This is a different order of correction from a refuted *center* (as with sunflower's second center or horse's three rival centers, §7.3, §15.4–§15.6): those refutations left the count of proposed centers intact and reduced it by excluding a specific, still-correctly-identified candidate location. Peters et al.'s corrections instead remove specimens from the evidentiary base entirely, which mechanically removes any center whose case rested substantially on them, without offering a specific replacement claim to weigh against a rival one.

This cycle's own §1.4 commitment — no invented figures, and no center admitted without a directly reported statistic behind it — already implies the correct response: a candidate center whose supporting specimens have been independently re-examined and reclassified cannot be carried forward into a C count on the strength of the original identification alone. This chapter treats Peters et al. (2022) as authoritative for the specimens they directly re-examined, and treats centers resting on specimens outside their reassessment (such as the Indus Valley and northern Chinese Neolithic claims, which were archaeobotanical/faunal impressions

rather than the iconographic and textual material Peters et al. concentrate on) as neither confirmed nor refuted by that paper specifically — an open evidentiary gap, not a resolved one, and reported as such rather than adjudicated here.

20.6 Attempting C, κ, D: why no PI is computed for chicken, and for a reason distinct from every prior 'not computed' case

§17.6 (maize) and §19.6 (Bactrian camel) both reported 'not computed' because the literature disputes *which* of several named locations hosts the single accepted center. Chicken finds a different obstruction.

On the current weight of evidence (§20.3–§20.4), C=1 is the best-supported reading: Wang et al.'s (2020) 863-genome result and Peters et al.'s (2022) zooarchaeological reassessment are mutually reinforcing on a broad region — mainland Southeast Asia and the immediately adjacent southwestern Chinese/northern Thai/Myanmar borderlands — in a manner structurally similar to dromedary's archaeology-genetics convergence (§18.3–§18.4). The older multiple-maternal-origins literature (Liu et al. 2006; Kanginakudru et al. 2008) has not been retracted, but on Eda's (2021) own reading is increasingly reinterpreted, at least for the Indian case, as post-domestication admixture rather than independent local domestication — the same move §7.3 and §15.4–§15.6 used to exclude a rival center, though here it is a trend in the literature's own weight of opinion rather than a single decisive refuting study, so it is reported as narrowing, not as closed, in the same register used for Bactrian camel's HI/HII narrowing (§19.3).

Why no κ is assigned here

As with Bactrian camel (§19.6's box), no source reviewed for this chapter reports a directly quantified fraction splitting a confirmed major center from a confirmed minor one, of the kind Naderi et al. (2008) supplied for goat or Morrell & Clegg for

barley. Kanginakudru et al.'s (2008) own FST values (0.126 within G. g. murghi, 0.154 within G. g. domesticus, >0.2 between groups) quantify population differentiation, not a fraction of studies or loci agreeing on a second confirmed center; repurposing an FST statistic as a κ value would be exactly the kind of invented weighting §11.5 and §19.6 have both declined. No κ is assigned.

Why no D̄ is computed either, even for C=1

This cycle's six prior PI=0 cases (§18.4's box) each reached the floor because a single, effectively unanimous, located center was in hand. Chicken differs from all six: neither of its two convergent evidentiary lines supplies a site-level coordinate. Peters et al.'s (2022) own accepted earliest site, Ban Non Wat, is reported at the level of Phimai District, Nakhon Ratchasima Province, central Thailand — the same kind of regional, not surveyed-point, precision this cycle declined to convert into a coordinate for Ayakagytma (§19.4). Wang et al.'s (2020) G. g. spadiceus source population is, by construction, a subspecies range spanning parts of three countries, not a point. A distance computation forcing either into an invented single coordinate would manufacture false precision the cited sources do not themselves supply. Since D̄ is undefined by convention only for C=1 with an actual single located point (§18.4), and no located point exists here even under the best-supported C=1 reading, this is reported as 'not computed', not as PI=0.

This is chicken's own distinct contribution to the 'not computed' category first opened by maize and Bactrian camel (§19.8): a case where the geographic count is the **least** contested part of the picture, yet the index still cannot be evaluated, because neither convergent evidentiary line reaches site-level coordinate resolution. §20.7 formalises this distinction, since §2.7's original prose

definition does not by itself distinguish 'not computed because location is disputed' from 'not computed because no coordinate exists to dispute'.

20.7 A formal restatement of the Domestication Polycentricity Index

§2.7 defined PI = C × κ × D̄ in prose, sufficient for seventeen crop/species-model combinations reported as single numbers or as an explicitly undefined case (§17.6, §19.6). Chicken (§20.6) exposes a distinction the prose definition does not itself make explicit: between a case that is undefined because of a live dispute over location, and one that is undefined because no source supplies the coordinate the formula requires at all. This section restates the index formally enough to keep the two apart, as a permanent addition to the index's own definition, without changing any value this cycle has already reported.

20.7.1 Center coordinates and the resolvability predicate

Let a case be associated with a proposed set of corroborated centers

$$X = \{x_1, \ldots, x_C\}$$

where each proposed center is either a resolved point on the terrestrial sphere (a reported latitude/longitude pair, tied to a named excavated site or an equivalent surveyed location) or an unresolved region (a subspecies range, a province, or a named broad zone without a single reported coordinate). Define a per-center resolvability indicator

$$r_i = 1 \; if \; x_i \; is \; a \; reported \; point; \; r_i = 0 \; otherwise.$$

The case is coordinate-resolvable, written R(X) = 1, only if every proposed center is individually resolvable:

$$R(X) = 1 \Leftrightarrow r_i = 1 \; for \; all \; i = 1, \ldots, C$$

This single predicate reproduces every 'not computed' decision this cycle has already made by inspection (maize, §17.6; Bactrian camel, §19.6; Ayakagytma's non-computation within §19.4) and

additionally separates chicken's case — R(X)=0 because *no* candidate center reaches point resolution, independent of how many centers are proposed — from a genuine location dispute, where R(X) can be 0 even for a single proposed center whose own location, not existence, is contested.

20.7.2 The Index as a partial function

With R(X) defined, the Index is restated as a partial function on the triple (C, κ, D̄):

$$PI\left(C, \kappa, \underline{D}\right) = \{C \times \kappa \times \underline{D} \;\; if\; R(X) = 1;\; 0 \;\; if\; C = 1\; (\underline{D} := 0);$$
$$\perp \;\; otherwise.$$

Each branch is read directly off §20.7.1's predicate rather than restated inside the equation itself: the first applies whenever R(X)=1 and κ is directly reported by the cited sources; the second whenever C=1 and the single center is unanimously corroborated, with D̄ set to 0 by convention (§2.7); the third applies otherwise — when neither condition is met.

The symbol ⊥ is deliberately not the number 0: §18.4's box already stressed that PI=0 is a genuine, informative floor value, not an absence of information, and conflating it with 'not computed' would understate exactly the six cases (§19.8) that worked hard, on the sources' own terms, to reach that floor honestly. Chicken (§20.6) returns ⊥ under the third clause, for the coordinate-resolvability reason rather than a live location dispute — a distinction the synthesis table in §20.8 records explicitly for the first time.

20.7.3 D̄ as an average over site-pairs, and interval propagation under a reported sensitivity range

For a resolvable case with C ≥ 2, §2.7's D̄ is the mean great-circle distance over all unordered center pairs:

$$\underline{D} = \frac{1}{C(C-1)/2} \Sigma_{i<j}\, d\left(x_i, x_j\right)$$

summed over all pairs i<j, divided by the number of pairs C(C−1)/2, where d(·,·) is the great-circle distance between two reported coordinate pairs — the same script-based computation used in code/Ch18_dromedary_distance_check.py and its analogues throughout Sections VII–XI.

Several cases (Bactrian camel, §19.5; the contested Tibetan barley center, §2.7) report D̄, or a D̄-like sensitivity figure, as a range rather than a single number, because the underlying candidate coordinates are themselves reported as alternative representative points rather than a single agreed site. This cycle has never proposed a statistical error model for such ranges — no cited source supplies a probability distribution over candidate coordinates, and inventing one (a Gaussian spread, a confidence interval) would itself violate §1.4. The correct treatment is interval, not statistical, propagation:

$$PI_{min} = C \times \kappa \times \underline{D}_{min}, \quad PI_{max} = C \times \kappa \times \underline{D}_{max}$$

reporting PI ∈ [PI_{min}, PI_{max}] directly from the sensitivity bounds the cited sources themselves supply, exactly as §19.5's 1,676.8–2,810.0 km sensitivity range would propagate into a PI range if Bactrian camel ever acquired a κ value. This is a restatement of existing practice, not a new number: no case in §19.8's table needs to be recomputed, since every resolvable case in that table used a single D̄ already, and the interval form reduces to the point form exactly when $\underline{D}_{min} = \underline{D}_{max}$.

20.7.4 Monotonicity, and what the formal restatement changes (and does not)

On the resolvable branch, PI is linear and strictly increasing in each of its three arguments holding the other two fixed and positive:

$$\frac{\partial PI}{\partial C} = \kappa \underline{D}, \quad \frac{\partial PI}{\partial \kappa} = C \underline{D}, \quad \frac{\partial PI}{\partial \underline{D}} = C\kappa, \quad all \geq 0.$$

None of this changes a single number this cycle has already published; §19.8's table is unaffected, and every case in it remains

on the resolvable branch it was already computed under. What the restatement adds is exactly what §20.6 needed and §2.7's prose definition did not supply: a way to say that chicken's failure to produce a PI is a different *kind* of non-result from maize's or Bactrian camel's, rather than reporting all three under the same undifferentiated 'not computed' label.

20.8 Cross-cycle synthesis: eighteen crop/species-model combinations across twelve sections

Adding chicken to §19.8's table extends the 'not computed' group to three entries, and, for the first time, distinguishes the branch each entry falls under per §20.7.2:

Crop/species (model)	C	κ	D̄ (km)	PI	Branch (§20.7.2)
Pig (core model)	2	1.000	6,525	13,050	resolvable
Common bean	2	0.902	3,658	6,601	resolvable
Water buffalo (core model)	2	1.000	2,914.7	5,829	resolvable
Cattle (core model)	2	1.000	2,758.7	5,517	resolvable
Squash (C. pepo)	2	1.000	2,282	4,565	resolvable
Barley	2	0.556	3,046	3,384	resolvable
Rice (C=2 model)	2	0.200	1,761	704	resolvable
Grapevine	2	0.897	305	547	resolvable
Goat (core model)	2	0.014	693.1	19.4	resolvable
Einkorn	1	1.000	0	0	resolvable,

Crop/species (model)	C	κ	D̄ (km)	PI	Branch (§20.7.2)
					unanimous
Rice (C=1 model)	1	1.000	0	0	resolvable, unanimous
Sunflower	1 (2nd center refuted)	1.000	0	0	resolvable, unanimous
Horse	1 (three rivals refuted)	1.000	0	0	resolvable, unanimous
Sheep	1 (single broad zone)	1.000	0	0	resolvable, unanimous
Dromedary	1 (archaeology-genetics convergence)	1.000	0	0	resolvable, unanimous
Maize	1 (location disputed)	n/a	531 (location only)	⊥	R(X)=0, live dispute
Bactrian camel	1 (location disputed)	n/a	1,676.8–2,810.0 (sensitivity only)	⊥	R(X)=0, live dispute
Chicken	1 (best-supported)	not assigned	no reported point on either convergent line	⊥	R(X)=0, no dispute, no point

The 'not computed' group now has three members. Two (maize, Bactrian camel) reached it because a real location dispute remains open. Chicken reaches it by a different, and in one sense more fundamental, route: not because its geography is disputed, but

because neither of its two mutually reinforcing evidentiary lines was ever built to supply a point coordinate in the first place. §20.7's R(X) predicate is what makes this a documented distinction rather than a rhetorical one.

20.9 Closing Section XII

Chicken passed §20.2's justification test for a new case type and, examined on its own evidentiary terms (§20.3–§20.6), returned an honest ⊥ of a kind this cycle had not yet produced. The index itself has been extended (§20.7) to say precisely what that ⊥ means, as a permanent addition to §2.7's own definition, applicable to every future case regardless of taxonomic kingdom.

Final stopping-rule declaration for Section XII

No Section XIII is committed to here. This chapter tested, and confirmed, that a new case type can be admitted to this cycle on methodological grounds alone, and that doing so can produce a genuine result — a formal extension of the index itself — even when no PI value is returned for the case that prompted it. Any further bird case, any further non-mammalian animal case, or any case from a taxonomic kingdom not yet examined would each need to repeat §20.2's justification from scratch, exactly as this chapter repeated it for the mammal-only cycle that preceded it. Naming a specific further candidate here without one currently in view would be the same unsupported invention this cycle has declined at every floor and ceiling reached so far.

This closes Section XII.

References newly cited in Chapter 20

Best, J., Fothergill, T., Sykes, N. et al. (2022). Redefining the timing and circumstances of the chicken's introduction to Europe and north-west Africa. Antiquity 96(388): 868–882.

Eda, M. (2021). Origin of the domestic chicken from modern biological and zooarchaeological approaches. Animal Frontiers 11(3): 52–58.

Fumihito, A., Miyake, T., Sumi, S., Takada, M., Ohno, S. & Kondo, N. (1994). One subspecies of the red junglefowl (Gallus gallus gallus) suffices as the matriarchic ancestor of all domestic breeds. Proceedings of the National Academy of Sciences USA 91: 12505–12509.

Kang, L., Qian, L., Zheng, M., Chen, L., Chen, H., Yang, L., You, L., Yang, B., Yan, M., Gu, Y., Wang, T., Schiessl, S.-V., An, H., Blischak, P., Liu, X., Lu, H., Zhang, D., Rao, Y., Jia, D., Zhou, D., Xiao, H., Wang, Y., Xiong, X., Mason, A.S., Pires, J.C., Snowdon, R.J., Hua, W. & Liu, Z. (2021). Genomic insights into the origin, domestication and diversification of Brassica juncea. Nature Genetics 53(9) (page range not confirmed in sources reviewed for this chapter).

Kanginakudru, S., Metta, M., Jakati, R. D. & Nagaraju, J. (2008). Genetic evidence from Indian red jungle fowl corroborates multiple domestication of modern day chicken. BMC Evolutionary Biology 8: 174.

Liu, Y.-P., Wu, G.-S., Yao, Y.-G., Li, Y., Luo, S.-J., Andersson, L. & Zhang, Y.-P. (2006). Multiple maternal origins of chickens: out of the Asian jungles. Molecular Phylogenetics and Evolution 38: 12–19.

Peters, J., Lebrasseur, O., Irving-Pease, E. K., Paxinos, P. D., Best, J., Smallman, R. et al. (2022). The biocultural origins and dispersal of domestic chickens. Proceedings of the National Academy of Sciences USA 119(24): e2121978119.

Wang, M.-S., Thakur, M., Peng, M.-S., et al. (2020). 863 genomes reveal the origin and domestication of chicken. Cell Research 30: 693–701.

Chapter 21 --- Turkey Domestication: One Resolved Center, One Confirmed but Unlocatable

21.1 A second bird case, re-earning §20.2's test

§20.9 closed Section XII without committing to a further chapter, and set an explicit condition on any that might follow: "Any further bird case ... would each need to repeat §20.2's justification from scratch." Turkey (*Meleagris gallopavo*) is a second bird case, so that condition applies here in full, and is met on grounds distinct from chicken's own justification, not by restating it.

Chicken (Chapter 20) was admitted because a large, genuinely single-origin genomic result sat against an older, not-retracted multiple-origins literature --- and, on inspection, returned R(X)=0 for a reason no earlier case had produced: neither of its two evidentiary lines was ever built to supply a point coordinate at all. Turkey is admitted for a different reason. It is doubly corroborated --- archaeology and genetics agree that no shared maternal lineage links Mesoamerica and the American Southwest --- and it produces a coordinate-resolvability pattern §20.7 has not yet catalogued: one of its two independently corroborated centers is a reported point tied to a named excavation, and the other is confirmed to exist, by exclusion of the alternatives, without ever having been assigned a candidate location by any source reviewed here.

Turkey meets §20.2's re-justification requirement for a second bird case on the resolvability grounds just described: a doubly-corroborated second center whose existence is certain but whose location the reviewed literature has never proposed. Cotton returns to Kingdom Plantae for the first time since grapevine (Chapter 10), testing whether the R(X) apparatus built across Sections XI–XII generalizes to this cycle's highest corroborated center count yet (C=4). Both chapters report only what their cited sources support;

no coordinate or κ is invented to force a pattern the sources do not themselves supply.

21.2 Two independent domestication events, corroborated by both evidentiary lines

Speller, Kemp, Wyatt, Monroe, Lipe, Arndt & Yang (2010, *PNAS* 107(7):2807–2812) analyzed mitochondrial DNA from 149 turkey bones and 29 coprolites recovered from 38 archaeological sites across the American Southwest, spanning roughly 200 BC to AD 1800. A single, genetically uniform lineage (haplogroup H1) dominates the Southwest domestic record from the Basketmaker II period onward. Critically, the study's own genetic comparison ruled out both previously proposed progenitors for this lineage: the South Mexican wild turkey (*M. g. gallopavo*, the confirmed Mesoamerican progenitor) and the local Southwest wild subspecies (*M. g. merriami*). A separate haplogroup (H2), consistent with limited local Merriam's introgression, occurs at low frequency alongside H1 at several sites.

Manin, Corona-M, Alexander, Craig, Thornton, Yang, Richards & Speller (2018, *Royal Society Open Science* 5(1):171613) extended the genetic sampling to 55 Mesoamerican specimens and reported no shared maternal haplotypes between the Mesoamerican and Southwest domestic populations at all --- a negative result that, combined with Speller et al.'s (2010) exclusion of cross-region ancestry, is the archaeogenetic basis for treating turkey as two independent domestication events rather than one center with a secondary dispersal, in the same doubly-corroborated sense this cycle has applied to pig (§11.3), cattle (§13.3) and water buffalo (§14.3).

21.3 The Mesoamerican center: a resolved point

The Mesoamerican domesticate's wild progenitor (*M. g. gallopavo*) and its domestic descendant form a single, genetically continuous clade (Speller et al. 2010), consistent with the historical understanding of central/southern Mexico as this species' domestication center. The clearest single-site evidence for domestic status --- medullary bone indicating egg-laying hens, whole eggs, and both adult and juvenile birds recovered from two domestic residences --- comes from the Mitla Fortress in the Central Valleys of Oaxaca, dated to the Classic–Early Postclassic period (Lapham, Feinman & Nicholas, 2016, *Journal of Archaeological Science: Reports* 10:534–546), placing secure domestic husbandry there by roughly 400–500 CE.

A separate line pushes the underlying husbandry or captive-rearing practice earlier still: Thornton et al. (2012, *PLoS ONE* 7(8):e42630) identified *M. gallopavo* remains --- a species non-native to the Maya lowlands --- at the Late Preclassic site of El Mirador, Guatemala (ca. 300 BC–AD 100), showing turkeys already captively reared and traded well outside their natural range a full millennium before the Oaxaca evidence. Both figures are reported here rather than adjudicated: the two studies answer different questions (secure domestic breeding at one site, versus earliest evidence of captive management and long-distance movement of the species), and this cycle's discipline (§1.4) is to report what each source supports rather than collapse them into one date.

For the real-coordinate check in §21.5, the Mesoamerican center is represented by the Oaxaca Valley findspot (Mitla), a named, excavated location with a reported coordinate --- satisfying §20.7.1's resolvability indicator, r=1.

21.4 The Southwest center: confirmed to exist, never assigned a location

The Southwest domestic lineage is not in doubt as a second, independent event: Speller et al. (2010) positively excluded both the Mesoamerican and the local wild subspecies as its source, and Manin et al. (2018) found no maternal-lineage overlap with Mesoamerica at all. What neither study, nor any later one reviewed here, supplies is a candidate geographic origin within the Southwest for that source population.

Speller et al.'s (2010) own assessment, stated plainly in their discussion, is that the available data could rule out the two previously proposed progenitors but could not pinpoint where the H1 lineage's true source population originated. Eight years and a larger Mesoamerican comparison sample later, Manin et al. (2018) reported the same gap in stronger terms: haplogroup H1 "has no wild equivalent recognized yet." The Southwest center is therefore a case this cycle has not previously produced: a center whose *existence* is doubly corroborated but whose *location* has never been proposed by any source, as opposed to maize or Bactrian camel, where a location is disputed between two or more explicitly named candidates.

The 38 sites sampled by Speller et al. (2010), together with the additional sites reported in later regional studies (the Mimbres Valley, southwestern New Mexico; Tijeras Pueblo and the middle San Juan region, New Mexico; Homol'ovi, Arizona; and Basketmaker-period sites in southeastern Utah and southwestern Colorado, including Turkey Pen Ruin), record where domestic turkeys were *kept and used*, not where the H1 lineage was first brought under domestication. Treating that findspot cluster as if it were the corroborated center would misrepresent exactly the gap the cited authors themselves flag.

21.5 A real-coordinate check --- and why it can only be partial

Computed via great-circle distance (code/Ch21_turkey_distance_check.py, same haversine convention as §6.4 and Section VII–XI's scripts, mean Earth radius 6,371.0088 km): the Oaxaca Valley findspot and the geographic centroid of the Southwest sample cluster (the Four Corners area spanning southeastern Utah, southwestern Colorado, northern Arizona and northwestern New Mexico) are **2,451.1 km** apart.

This figure is reported as an illustrative span only, in the same spirit as §6.4's 531 km for maize and §19.5's 1,676.8–2,810.0 km sensitivity range for Bactrian camel --- and with one further caveat those two cases did not need: it is not even a distance between two candidate *centers*. One endpoint (Oaxaca) is a corroborated center; the other (the Four Corners centroid) is the geographic middle of an assemblage of use-sites, not a proposed birthplace for the Southwest lineage. Reporting it as anything more precise would manufacture a center where the cited sources supply none.

21.6 Applying §20.7's predicate: a fourth route to ⊥

Formal statement, following §20.7.1–§20.7.2 directly

Let X = {x_Mesoamerica, x_Southwest}. x_Mesoamerica is a reported point (Oaxaca/Mitla; Lapham et al. 2016) so r_Mesoamerica = 1. x_Southwest has no reported point in any source reviewed here (Speller et al. 2010; Manin et al. 2018) so r_Southwest = 0. By §20.7.1, R(X) = 0, since R(X)=1 requires r_i=1 for every i. By §20.7.2's partial-function definition, PI(C,κ,D) = ⊥ for turkey: C=1 is false (two independent events are corroborated), and R(X)=1 is false, so neither the resolvable branch nor the C=1-unanimous branch applies.

This is a fourth distinct route to ⊥, alongside maize and Bactrian camel (a single center, location disputed between named

candidates) and chicken (zero resolved centers, no candidate ever proposed on either evidentiary line). Turkey adds the case §20.7.1's own text anticipated but this cycle had not yet instantiated: more than one corroborated center, with resolvability split unevenly between them.

21.7 Cross-cycle synthesis: the ‘not computed’ group reaches four members

Crop/species	C (corroborated)	Distance reported (km)	Branch (§20.7.2)
Maize	1 (location disputed)	531 (location only)	R(X)=0, single-center location dispute
Bactrian camel	1 (location disputed)	1,676.8–2,810.0 (sensitivity only)	R(X)=0, single-center location dispute
Chicken	1 (best-supported)	no reported point on either line	R(X)=0, zero resolved centers
Turkey	2 (doubly corroborated)	2,451.1 (illustrative span only)	R(X)=0, one resolved / one unresolved center

Every entry in the group now carries a distinct, named reason under §20.7's own taxonomy, rather than a single undifferentiated

‘not computed’ label. No PI value already published anywhere in Sections I–XII changes as a result (§20.7.4).

21.8 What Chapter 22 will check

Turkey tested whether the R(X) predicate could name a resolvability pattern this cycle had not yet produced; it could, cleanly, on the first genuinely new bird case admitted since chicken. Chapter 22 returns to plants and asks a different question of the same formal apparatus: whether it holds up against the highest corroborated center count this cycle has proposed for any single case, C=4, where the individual-center resolvability question turns out to matter just as much as it did here.

References newly cited in Chapter 21

Lapham, H.A., Feinman, G.M. & Nicholas, L.M. (2016). Turkey husbandry and use in Oaxaca, Mexico: A contextual study of turkey remains and SEM analysis of eggshell from the Mitla Fortress. Journal of Archaeological Science: Reports 10: 534–546.

Manin, A., Corona-M, E., Alexander, M., Craig, A., Thornton, E.K., Yang, D.Y., Richards, M. & Speller, C.F. (2018). Diversity of management strategies in Mesoamerican turkeys: archaeological, isotopic and genetic evidence. Royal Society Open Science 5(1): 171613.

Song, K. & Osborn, T.C. (1992). Polyphyletic origins of Brassica napus: new evidence based on organelle and nuclear RFLP analyses. Genome 35(6), 992–1001.

Speller, C.F., Kemp, B.M., Wyatt, S.D., Monroe, C., Lipe, W.D., Arndt, U.M. & Yang, D.Y. (2010). Ancient mitochondrial DNA analysis reveals complexity of indigenous North American turkey domestication. Proceedings of the National Academy of Sciences USA 107(7): 2807–2812.

Thornton, E.K. et al. (2012). Earliest Mexican turkeys (Meleagris gallopavo) in the Maya region: implications for pre-Hispanic animal trade and the timing of turkey domestication. PLoS ONE 7(8): e42630.

Chapter 22 --- Cotton: Four Independent Domestications, and a Predicate That Will Not Let Three Stand In for Four

22.1 Why cotton, and why here

Gossypium is unusual among this cycle's cases in a way none of the preceding twenty chapters has tested directly: the literature agrees, without live dispute, that four separate species were independently brought under domestication on four different landmasses. If corroborated, C=4 would be the highest center count this cycle has proposed for any single case. §21.1's stopping rule admitted cotton specifically to test whether §20.7's formal apparatus, built across the animal sections, holds together at that count --- and, as §22.4 will show, it does, but not in the way a simple four-way headline would suggest.

22.2 Four species, four independent domestications: the corroborated count

Two of the four are allotetraploids, native to the Western Hemisphere: *G. hirsutum* (upland cotton) and *G. barbadense* (Egyptian/Pima or Sea Island cotton). Yuan, Grover, Hu, Pan, Miller, Conover, Hunt, Udall & Wendel (2021, *Advanced Science* 8:2003634), resequencing 643 accessions spanning the wild-to-domesticated continuum of both species, confirmed that wild *G. hirsutum* and *G. barbadense* were independently domesticated and have remained phylogenetically distinct populations throughout their subsequent human-mediated dispersal across the American tropics.

The other two are diploids, native to the Old World: *G. arboreum* and *G. herbaceum*. Their status as independent domesticates was, in the authors' own words, long in question, since no wild form of *G. arboreum* has ever been identified and the two species are morphologically similar. Renny-Byfield, Page, Udall, Sanders, Peterson, Arick, Grover & Wendel (2016, *Genome Biology and Evolution* 8(6):1940–1947) resolved this using genome-wide repeat-content analysis and divergence-time estimates from roughly 7,000 orthologous genes, concluding that the two species separated long before either was domesticated --- evidence for two genuinely independent domestication events rather than one species giving rise to the other under cultivation.

No source reviewed here disputes the count itself: every genomic, phylogenomic and archaeobotanical study consulted agrees on four independent domestications. Following the einkorn convention (§2.7, where unanimous agreement across independent methods gives κ=1.0 without a fraction to report), κ=1.0 for cotton's center *count*. What divides the four cases sharply, as §22.3–§22.4 show, is not whether each center exists but whether each has ever been assigned a location precise enough to satisfy §20.7.1's resolvability indicator.

22.3 Two New World centers, both resolved to real coordinates

G. hirsutum: Brubaker & Wendel (1994, *American Journal of Botany* 81(10):1309–1326) identified the Yucatan Peninsula as the region where wild *G. hirsutum* was first brought under domestication by pre-Columbian peoples, a conclusion Yuan et al. (2021) confirm from genomic data: wild *G. hirsutum* was "initially domesticated in the Yucatan Peninsula," subsequently dispersing under cultivation across most of the American tropics over the following four to eight thousand years.

G. barbadense: the same Yuan et al. (2021) resequencing places its independent domestication in northwestern South America. The earliest secure material evidence for domesticated cotton in this region is the cotton textile and fiber assemblage from Huaca Prieta, in the Chicama Valley of Peru's north coast (Stephens, 1975, *American Antiquity* 40(4):406–419), among the oldest cotton textile finds anywhere in the Americas; Westengen, Huamán & Heun (2005, *Theoretical and Applied Genetics* 110:392–402) subsequently mapped the genetic diversity of early South American cotton to the same coastal zone.

Both centers are represented in §22.5's real-coordinate check by named, excavated or securely regionally anchored locations --- satisfying §20.7.1's resolvability indicator, r=1 for each.

22.4 Two Old World centers --- one resolved, one genuinely disputed

G. arboreum: the earliest direct material evidence of cotton fiber anywhere in the Old World comes from Neolithic Mehrgarh, in Balochistan, Pakistan --- mineralized cotton fibers recovered from a copper bead, dated to the sixth millennium BC (Moulherat, Tengberg, Haquet & Mille, 2002, *Journal of Archaeological Science* 29(12):1393–1401). This is consistent with the broader literature's placement of *G. arboreum*'s domestication in the Indus Valley/northwestern Indian subcontinent, and gives this center a named, excavated, coordinate-resolvable point --- r=1.

G. herbaceum is a different case entirely. Its wild progenitor (subsp. *africanum*) is confined to the savannahs of southern Africa (Botswana, Namibia, Zimbabwe and South Africa), a region multiple independent sources agree was never itself a site of domestication or even local use. The domestication event is instead placed broadly in northeastern Africa or Arabia, roughly 5,000 km from the wild population's actual range. Ryan, Dabrowski, Dapoigny, Gauthier, Douville, Tengberg, Kerfant, Mouton,

Desormeau, Zazzo & Bouchaud (2021, *Scientific Reports* 11:303) state the position plainly: *G. herbaceum* "was domesticated in Africa," but "the precise place of origin and the exact chronology remain unknown," with the earliest archaeological traces of cotton use located in northeastern Africa near the end of the first millennium BC. No source reviewed here narrows this to a named excavated site or a small candidate zone in the way Mehrgarh does for *G. arboreum*, or the way §6.3 and §19.2 do for maize's and Bactrian camel's competing candidates.

This is not a location dispute of the maize or Bactrian camel kind, where two or more named candidates compete for the same center. It is closer to the Southwest turkey center (§21.4): a domestication event whose existence is not seriously questioned, but for which no source has ever proposed a specific candidate coordinate at all --- r_herbaceum = 0.

22.5 A real-coordinate check on the three resolvable centers

Computed via great-circle distance (code/Ch22_cotton_distance_check.py, same haversine convention, mean Earth radius 6,371.0088 km) over the three centers that do satisfy §20.7.1's resolvability indicator:

G. hirsutum (Yucatan Peninsula) ↔ *G. barbadense* (Huaca Prieta, Peru): **3,390.5 km**.

G. hirsutum (Yucatan Peninsula) ↔ *G. arboreum* (Mehrgarh, Pakistan): **13,896.5 km**.

G. barbadense (Huaca Prieta, Peru) ↔ *G. arboreum* (Mehrgarh, Pakistan): **15,819.6 km**.

The mean of these three resolvable-pair distances is **11,035.6 km** --- by a wide margin the largest dispersion figure this cycle has computed for any case, resolvable or not (compare grapevine's 305 km or pig's 6,525 km, §20.8). It is reported here explicitly as an

illustrative three-center sensitivity figure, not as D̄ for a PI computation, for the reason §22.6 makes formal: the correctly specified case is C=4, and §20.7.1 does not permit substituting a resolvable subset for the full corroborated count.

22.6 Applying §20.7's predicate: the highest C yet proposed, and still ⊥

Formal statement, following §20.7.1–§20.7.2 directly

Let X = {x_hirsutum, x_barbadense, x_arboreum, x_herbaceum}, C=4. r_hirsutum = 1 (Yucatan Peninsula; Brubaker & Wendel 1994; Yuan et al. 2021). r_barbadense = 1 (Huaca Prieta, Peru; Stephens 1975; Westengen et al. 2005). r_arboreum = 1 (Mehrgarh, Pakistan; Moulherat et al. 2002). r_herbaceum = 0 (no reported point; Ryan et al. 2021).

By §20.7.1, R(X) = 0, since R(X)=1 requires r_i=1 for all i=1,...,C, and r_herbaceum fails. By §20.7.2, PI(C,κ,D̄) = ⊥ for cotton, on the resolvability branch: C=1 is false, so the unanimous-center clause does not apply, and R(X)=1 is false, so the resolvable clause does not apply either.

This is the cycle's fifth member of the 'not computed' group, and its first with C=4 --- the strongest corroborated center count this cycle has ever proposed for a single case, reaching ⊥ for exactly the reason §20.7.1 was written to make explicit: a high, undisputed C does not by itself buy resolvability. One weak link in the coordinate chain is enough.

A three-center PI restricted to *G. hirsutum*, *G. barbadense* and *G. arboreum* was deliberately not computed here. Doing so would understate cotton's own corroborated count from four to three, the same error §6.5 declined to make for maize by refusing to treat two disputed single-center candidates as two independently corroborated centers. The 11,035.6 km figure in §22.5 is reported as

a sensitivity check on the resolvable subset, exactly as §6.4's 531 km and §19.5's sensitivity range were, not as a substitute PI.

22.7 Cross-cycle synthesis: five cases now share the 'not computed' group, on four distinct grounds

Crop/species	C (corroborated)	Distance reported (km)	Branch (§20.7.2)
Maize	1 (location disputed)	531 (location only)	R(X)=0, single-center location dispute
Bactrian camel	1 (location disputed)	1,676.8–2,810.0 (sensitivity only)	R(X)=0, single-center location dispute
Chicken	1 (best-supported)	no reported point on either line	R(X)=0, zero resolved centers
Turkey	2 (doubly corroborated)	2,451.1 (illustrative span only)	R(X)=0, one resolved / one unresolved center
Cotton	4 (unanimous, no dispute)	11,035.6 (3-of-4 subset, illustrative only)	R(X)=0, three resolved / one unresolved center

Cotton and turkey share a branch --- "n of C centers resolved, at least one not" --- that did not exist in §20.8's table at all; §21.6 opened it, and §22.6 shows it is not a one-case curiosity, since it

recurs at a completely different taxonomic and geographic scale. No PI value published anywhere in Sections I–XIII changes as a result of either addition (§20.7.4).

22.8 What resolvability-splitting cases add to the cycle's own self-knowledge

Sections I–XII produced two kinds of undefined case: a disputed single center (maize, Bactrian camel) and a wholly unresolved case (chicken). Turkey and cotton together establish that the interesting boundary is not how many centers a case has, nor how strongly their existence is corroborated, but whether *every* one of them individually clears §20.7.1's bar. A four-center case with unanimous, undisputed support among specialists (cotton) and a two-center case with exactly the same doubly-corroborated support (turkey) both land at ⊥ for the identical structural reason: R(X) is a conjunction, not an average, so one unresolved center is sufficient to fail it regardless of how many other centers are individually well pinned down.

Final stopping-rule declaration for Section XIII

Turkey and cotton were both admitted, tested and reported on the terms §21.1 declared before either chapter was written. Both returned ⊥, for related but newly distinguished reasons, and both extended §20.7's own taxonomy of non-results rather than merely repeating an existing entry in it.

No Section XIV is committed to here. Any further case --- bird, plant, or from a kingdom not yet examined --- would need to repeat §20.2's justification from scratch, exactly as Chapter 21 repeated it for turkey. Naming a specific further candidate here without one currently in view would be the same unsupported invention this cycle has declined at every floor and ceiling reached so far.

This closes Section XIII.

References newly cited in Chapter 22

Brubaker, C.L. & Wendel, J.F. (1994). Reevaluating the origin of domesticated cotton (Gossypium hirsutum; Malvaceae) using nuclear restriction fragment length polymorphisms (RFLPs). American Journal of Botany 81(10): 1309–1326.

Moulherat, C., Tengberg, M., Haquet, J.-F. & Mille, B. (2002). First evidence of cotton at Neolithic Mehrgarh, Pakistan: analysis of mineralized fibres from a copper bead. Journal of Archaeological Science 29(12): 1393–1401.

Renny-Byfield, S., Page, J.T., Udall, J.A., Sanders, W.S., Peterson, D.G., Arick, M.A., Grover, C.E. & Wendel, J.F. (2016). Independent Domestication of Two Old World Cotton Species. Genome Biology and Evolution 8(6): 1940–1947.

Ryan, S.E., Dabrowski, V., Dapoigny, A., Gauthier, C., Douville, E., Tengberg, M., Kerfant, C., Mouton, M., Desormeau, X., Zazzo, A. & Bouchaud, C. (2021). Strontium isotope evidence for a trade network between southeastern Arabia and India during Antiquity. Scientific Reports 11: 303.

Stephens, S.G. (1975). A reexamination of the cotton remains from Huaca Prieta, north coastal Peru. American Antiquity 40(4): 406–419.

Westengen, O.T., Huamán, Z. & Heun, M. (2005). Genetic diversity and geographic pattern in early South American cotton domestication. Theoretical and Applied Genetics 110: 392–402.

Yuan, D., Grover, C.E., Hu, G., Pan, M., Miller, E.R., Conover, J.L., Hunt, S.P., Udall, J.A. & Wendel, J.F. (2021). Parallel and Intertwining Threads of Domestication in Allopolyploid Cotton. Advanced Science 8: 2003634.

Chapter 23 --- Donkey: A Sixth Path to the Single-Center Floor, and This Cycle's Cleanest Sample Size Yet

23.1 Admitted on its own, after Section XIII closed

§22.7's closing box left no further case named, and repeated §20.2's condition: any further case would need to re-earn its place from scratch. Donkey (*Equus asinus*) is admitted here on exactly that basis, not as a continuation of Section XIII. Its justification is narrow and specific: this cycle's single-center floor group (§19.8's table: einkorn, sunflower, horse, sheep, dromedary) has grown case by case, each entry reached through a different evidentiary route --- unanimous methods agreement, refuted rival centers, a single broad zone, archaeology-genetics convergence. Todd, Tonasso-Calvière, Chauvey et al. (2022, *Science* 377(6611):1172–1180) supply a sample size no other case in this cycle's floor group has matched — 207 modern and 31 ancient genomes against 15 wild equid comparators — and this chapter tests whether that scale changes anything about how the floor is reached, or simply confirms it more securely than a smaller sample could.

Donkey is reported on the same terms already used for dromedary (§18) and sheep (§16): the result, whichever way the evidence falls, is stated plainly, and no further case is committed to at this chapter's close.

23.2 A single domestication, at a scale this cycle has not previously sampled

Todd et al. (2022) constructed a genome panel of 207 modern and 31 ancient donkeys, together with 15 wild equid comparators, and report a strong phylogeographic structure in modern donkeys consistent with a single domestication in eastern Africa, roughly 5000 BCE (a little over 7,000 years before present). The study's own

summary is direct: a single domestication event, followed by expansions within Africa and into Eurasia, and a later return to Africa.

The authors further identify a previously unknown genetic lineage in the Levant, dated to roughly 200 BCE, which contributed increasing ancestry toward donkey populations in Asia — a secondary, post-domestication dispersal-and-admixture event, structurally analogous to the secondary lineages this cycle has already distinguished from primary domestication centers elsewhere (goat's minor signal, §17.4; chicken's admixture layers, §20.5). It does not compete with the single African origin as a second center; no source reviewed here reads it that way.

23.3 Why C=1 here is not a default assumption but a directly reported result

This cycle has treated C=1 conclusions carefully throughout, distinguishing a genuinely tested single center (dromedary, sheep, horse) from an assumption never seriously challenged. Donkey belongs to the first group: Todd et al. (2022) built their panel specifically to test population structure across the full range of modern and ancient donkey diversity, and the single-origin signal is the paper's own finding, not an absence of contrary evidence. Following the einkorn convention (§2.7), κ=1.0: no source reviewed here proposes a second, independently corroborated donkey domestication center.

23.3.1 A disclosed complication: what earlier mitochondrial evidence suggested, and how genome-wide data reconciled it

§23.2–§23.3's single-origin reading is Todd et al.'s (2022) own genome-wide result, but it was not the field's first word on the question, and the earlier record is disclosed here rather than left implicit. Beja-Pereira, England, Ferrand et al. (2004, Science 304:1781), sequencing mitochondrial control-region DNA from 256

donkeys across 52 countries, identified two well-differentiated maternal haplogroups (Clade I and Clade II) and read this, at the time, as evidence for two separate domestication events in northeast Africa — structurally the same kind of single-versus-multiple disagreement §4.2 and §4.7 reported for rice and African rice, arising here in the animal that would eventually anchor this cycle's cleanest single-center case.

Kimura, Marshall, Chen et al. (2011, Proceedings of the Royal Society B 278:50-57), sequencing ancient and historic museum specimens of both African wild ass subspecies, resolved half of that question: the Nubian wild ass (Equus africanus africanus) was confirmed as the direct ancestor of Clade I, while the Somali wild ass (Equus africanus somaliensis) showed enough mitochondrial divergence from both the Nubian wild ass and domestic donkeys that it could be excluded as Clade II's source — resolving one long-standing question (was the Nubian wild ass truly ancestral?) while explicitly leaving a second open (what, then, gave rise to Clade II?).

§23.2's Todd et al. (2022) is what closes the question Kimura et al. left open, and does so with a different kind of evidence rather than a larger sample of the same kind: 207 modern and 31 ancient nuclear genomes, not mitochondrial control-region sequence alone, resolving a single autosomal domestication signal beneath the two mitochondrial clades. Two well-differentiated maternal lineages are compatible with one nuclear domestication event if both lineages were already present in the founding wild population — the same resolution this cycle's dog chapter found between mitochondrial and nuclear evidence at §12.3, and the same structural move Jing et al. (2023) made for rice's three mitochondrial-era verdicts in §4.2. §23.3's $\kappa=1.0$ and §23.6's $C=1$ stand as Todd et al.'s own reported finding, not as a silent overruling of Beja-Pereira and Kimura's earlier, narrower reading;

both readings are accurate to the evidence available when each was published.

23.4 No coordinate-level center is reported, and none is manufactured here

As with sheep's single broad zone (§16.4), the domestication region here — eastern Africa, specifically Kenya and the Horn of Africa — is reported at a regional grain, not tied to a single named excavated site. §20.7.2's C=1-unanimous branch does not require R(X)=1 to return PI=0: for a single, unanimously corroborated center, the count and agreement are what the formula needs, and $\bar{D}$ is 0 by construction regardless of whether that one center is a point or a broad zone. No real-coordinate check is therefore computed or needed for this chapter, on the same grounds §16.4 already established for sheep.

23.5 PI=0, on the same floor as five earlier cases, for a sixth distinct reason

Formal statement, following §20.7.2 directly

C=1 (Todd et al. 2022, a directly tested and reported single-origin result). κ=1.0 (no dissenting center proposed in the literature reviewed). By §20.7.2's C=1-unanimous clause, $PI(C,\kappa,\bar{D}) = C \times \kappa \times \bar{D} = 1 \times 1.0 \times 0 = 0$, independent of R(X).

Donkey reaches the same PI=0 floor as einkorn (unanimous methods agreement), sunflower and horse (rival centers directly refuted), sheep (single broad zone) and dromedary (archaeology-genetics convergence) — a sixth distinct evidentiary route to the same number, on this cycle's largest sample size yet for any single-center case.

23.6 Cross-cycle synthesis update

Donkey is added to the PI=0 floor group first assembled at §8.2 and extended through §19.8: C=1 (directly tested, unanimous), κ=1.000, D̄=0, PI=0. The 'not computed' group (§22.7) is unchanged at five members; this chapter adds to the floor, not to the ceiling or to the disputed middle. No number already published anywhere in Sections I–XIII changes as a result.

This closes the chapter. No further case is committed to here.

References newly cited in Chapter 23

Todd, E.T., Tonasso-Calvière, L., Chauvey, L. et al. (2022). The genomic history and global expansion of domestic donkeys. Science 377(6611): 1172–1180.

Section XIV — Five New Cases Across Four Chapters: Potato, Sorghum, Two Chinese Millets, and Banana

Opened here on the author's decision to extend the cycle, per §23.6's own requirement: any extension needs a new, separately declared stopping rule.

Chapter 24 — Potato: A Single Andean Center, and a Species the Method Does Not Reach

24.1 A stopping rule for Section XIV, admitting four chapters and five species at once

§23.6 closed Chapter 23 without committing to a further case, on the same terms every section in this cycle has closed on. Section XIV is opened here on a single criterion, already stated informally when this extension was first proposed and restated formally below: a case is admitted only if it introduces a genuinely different shape of question from the twenty-two cases Appendix A already

catalogues, not merely another row inside a pattern this cycle has already resolved.

Stopping rule for Section XIV, declared before any of this section's four chapters is written

Four chapters, five species, are admitted this section.

1. Potato (Solanum tuberosum, Chapter 24) is admitted as a case whose own literature already argues for a clean single-origin result, tested here against the single-versus-multiple tension this cycle has now met repeatedly, and disclosing — outside the index's own case count, on the terms §4.7 already used for Oryza glaberrima — a second, taxonomically distinct question about a wild relative species managed, and possibly domesticated, far outside South America.

2. Sorghum (Sorghum bicolor, Chapter 25) is admitted as this cycle's first case since dog (§12.4) whose center-count, rather than its location, is what the cited literature has not settled.

3. Foxtail millet and broomcorn millet (Setaria italica and Panicum miliaceum, Chapter 26) are admitted together as a second East Asian, multi-species test beyond rice (§4), chosen because the two crops resolve differently under the identical method applied to both.

4. Banana (Musa spp., Chapter 27) is admitted as this section's structurally hardest case: a domestication process reported by its own literature as successive hybridization across several named wild taxa and regions, rather than a dispute over how many centers exist or where they sit — a case the C, κ, D̄ triple was not built to describe.

No PI, coordinate, or κ is invented anywhere in this section to force a case onto a branch its own sources do not support; where cited sources disagree with one another, that disagreement is

reported, not adjudicated. No Section XV is committed to at this section's close.

24.2 A monophyletic single origin, argued directly rather than assumed

Spooner, McLean, Ramsay, Waugh & Bryan (2005, PNAS 102(41):14694–14699) genotyped 362 wild and landrace potato individuals — 261 wild accessions across the Solanum brevicaule complex and 98 cultivated landraces — with 438 amplified fragment length polymorphisms. Their phylogenetic analysis supports a cladistic split between a "northern" component of the wild complex, centered in Peru, and a "southern" component in Bolivia and Argentina, and finds the cultivated landraces monophyletic within the northern component alone: a single domestication, not the multiple independent origins that most prior twentieth-century hypotheses (reviewed in Spooner et al. 2005 itself) had proposed. Later taxonomic revision folded the ancestral wild taxon into what is now named Solanum candolleanum, without altering the geographic result: a wild population native to the region around Lake Titicaca, on the Peru–Bolivia border, in the southern Peruvian highlands.

24.3 A disclosed historical complication: two centers proposed a century ago, and how later work resolved them

The single-origin reading is not the field's first word on the question, and the earlier record is disclosed here rather than left implicit, following this cycle's own convention (§23.3.1). Vavilov's collecting expeditions of the late 1920s, continued by Juzepczuk and Bukasov, described two centers of potato varietal diversity — a Peru–Bolivia highland center and a second center on the southern coast of Chile — a genuinely two-center hypothesis, structurally the same shape this cycle has already met for maize (§6.3), grapevine (§10.2.1) and cotton (§22.4). Spooner et al. (2005) address this directly: the Chilean landraces are read as secondarily derived from

the Andean lineage, after hybridization with the Bolivian and Argentinian wild species Solanum tarijense, rather than as an independent domestication event. The two-center hypothesis is not corroborated as a second center under this cycle's own standard; it is a secondary hybridization-and-differentiation event, structurally the same move already catalogued for goat's minor signal (§17.4), chicken's admixture layers (§20.5), and donkey's Levantine lineage (§23.2).

24.4 A disclosed, unresolved tension with more recent reviews

A 2025 review of potato genomic resources (Kyriakidou, Achakkagari, Tai and colleagues, writing in the Canadian Journal of Plant Science) states plainly that potato domestication "involved multiple independent domestication events and ongoing gene flow between cultivated and wild populations," citing Särkinen et al.'s 2019 taxonomic monograph of Solanum and Bozan et al.'s 2023 phylogenomic work. This sits in direct tension with Spooner et al.'s (2005) monophyly result, and no source reviewed here resolves the tension: the review does not supply a second corroborated coordinate center comparable in evidentiary weight to Spooner et al.'s own AFLP dataset, and Bozan et al. (2023), as cited by later reviews of the same genomic resequencing tradition (Zhang et al. 2025), is itself concerned primarily with post-domestication introgression from wild species into diploid and tetraploid landraces — the same kind of secondary gene flow §24.3 already distinguished from an independent domestication center. This tension is disclosed and left open rather than adjudicated, on the same no-invented-data grounds §1.4 declared for this entire cycle: this chapter does not manufacture a second center's coordinates to force a resolution neither cited source itself provides.

24.5 Outside the index's own count: a taxonomically distinct wild relative, possibly domesticated far outside South America

Pavlik, del Rio, Bamberg & Louderback (2024, American Journal of Botany) report genetic evidence that Solanum jamesii — the Four Corners potato, a wild species entirely distinct from S. tuberosum's own S. brevicaule/candolleanum lineage — was transported by Ancestral Puebloan groups far north of its natural range across the Colorado Plateau, with populations at sites hundreds of kilometers from the species' core distribution in the Mogollon region of the American Southwest. The study's own authors describe the Southwest as "an important, overlooked secondary region of domestication" for this separate species, on evidentiary grounds — anthropogenic transport, cultivation at archaeological sites, and founder-effect genetic signatures — structurally comparable to those §4.7 already used to disclose Oryza glaberrima outside rice's own case count, and Kinder, Adams & Wilson (2017, Journal of Ethnobiology) independently documented cultivation evidence for the same species among Ancestral Puebloan groups. S. jamesii is reported here on exactly those terms: a genuinely distinct question about a different species, disclosed for its relevance to the domestication of tuber-bearing Solanum as a genus, and excluded from this chapter's own C, κ, D̄ computation, which concerns only S. tuberosum.

24.6 PI=0, joining the floor's now-eight-member group

Formal statement, following §20.7.2 directly

C=1 (Spooner et al. 2005, a directly tested monophyly result for the northern Solanum brevicaule/candolleanum clade near Lake Titicaca, southern Peru). κ=1.0, following the einkorn convention (§2.7): no source reviewed here reports a second corroborated domestication center with its own coordinate, for either the Vavilov two-center hypothesis (§24.3, resolved as secondary

hybridization) or the more recent multiple-origins claim (§24.4, disclosed but not itself coordinate-resolved). By §20.7.2's C=1-unanimous clause, $PI(C,\kappa,\bar{D}) = C \times \kappa \times \bar{D} = 1 \times 1.0 \times 0 = 0$, independent of R(X).

Potato reaches the same PI=0 floor as einkorn, sunflower, horse, rice (C=1 model), sheep, dromedary and donkey — a seventh distinct evidentiary route to the same number, on grounds closest to donkey's own: a directly tested monophyly result with a disclosed, unresolved tension in the more recent literature that does not itself rise to a second corroborated center.

24.7 Cross-cycle synthesis update

Potato is added to the PI=0 floor group first assembled at §8.2 and extended through §23.6: C=1 (directly tested, monophyletic), κ=1.000, $\bar{D}$=0, PI=0. Appendix A.2 grows from seven to eight members. Solanum jamesii is not added to any table in Appendix A, on the same grounds Oryza glaberrima was excluded from it: a genuinely distinct question, disclosed rather than computed. No number already published anywhere in Sections I–XIII or Chapter 23 changes as a result.

References newly cited in Chapter 24

Spooner, D.M., McLean, K., Ramsay, G., Waugh, R. & Bryan, G.J. (2005). A single domestication for potato based on multilocus amplified fragment length polymorphism genotyping. Proceedings of the National Academy of Sciences 102(41): 14694–14699.

Kyriakidou, M., Achakkagari, S.R., Tai, H.H. et al. (2025). Genomic and pangenomic resources for potato improvement: harnessing diversity from wild relatives. Canadian Journal of Plant Science.

Zhang, C. et al. (2025). A genomic variation map provides insights into potato evolution and key agronomic traits. Plant Communications / ScienceDirect.

Pavlik, B.M., del Rio, A., Bamberg, J. & Louderback, L.A. (2024). Evidence for human-caused founder effect in populations of Solanum jamesii at archaeological sites: II. Genetic sequencing establishes ancient transport across the Southwest USA. American Journal of Botany.

Kinder, D.H., Adams, K.R. & Wilson, H.J. (2017). Solanum jamesii: Evidence for Cultivation of Wild Potato Tubers by Ancestral Puebloan Groups. Journal of Ethnobiology 37(2): 218–240.

Chapter 25 — Sorghum: A Disputed Center Count, Not a Disputed Location

25.1 What §24.1 admitted sorghum to test

§24.1 admitted sorghum for a specific, narrow reason: it is this cycle's first case since dog (§12.4) whose open question is how many centers exist, not where a single center sits. This chapter tests that claim against the cited literature directly, rather than restating it.

Sorghum is reported on the same terms already used for dog (§12): a well-corroborated core case is stated plainly, any further proposed center is tested against this cycle's two-independent-line corroboration standard rather than accepted on one line's say-so, and no PI is invented to resolve a disagreement the cited sources do not themselves resolve.

25.2 The core, doubly-corroborated case: eastern Sudan

Clark & Stemler (1975, Nature 254:588–591) first reported impressions of domesticated sorghum spikelets in ceramics from Neolithic central Sudan. Winchell, Stevens, Murphy, Champion & Fuller (2017, Current Anthropology 58(5)) substantially strengthened this with spikelet-morphology evidence from ceramic impressions of the Butana Group, in the far eastern Sahel near the

Atbara and Gash rivers, dated to the fourth millennium BCE — archaeological evidence, independent of genetics, for a domestication process already underway in eastern Sudan by roughly 3000 BCE, consistent with the earlier archaeobotanical synthesis of Fuller & Stevens (2018). On the genetic side, Smith, Nicholson, Kistler, Mace, Clapham, Stevens et al. (2019, Nature Plants 5:369–379) sequenced ancient sorghum DNA and reported a domestication history of gradual, continuous diversity decline rather than a sharp bottleneck — a different genomic signature from other founder cereals reviewed earlier in this cycle (§2, §4), but one the authors read as consistent with a single primary domestication centered in this same north-east African region, with bicolor established as the ancestral cultivated race from which other races subsequently diverged (Ananda et al. 2020, as reported in later reviews of the Smith et al. dataset).

25.3 A disclosed, unresolved center-count dispute: the guinea-margaritiferum lineage

Kimber (2000) and Mace, Tai, Gilding et al. (2013, Nature Communications 4:2320) both raise the possibility of an independent, later domestication event underlying the guinea and margaritiferum sorghum races, geographically associated with West Africa rather than the Nile valley. This is not the same shape of disagreement maize or Bactrian camel presented: it is not a dispute over where a single center sits, but over whether a second, distinct center exists at all — the same shape of question this cycle first met with dog (§12.2–§12.4). Unlike sorghum's Sudanese core case, the guinea-margaritiferum hypothesis is not doubly corroborated to this cycle's own standard: Mace et al. (2013) report it as a genomic signal consistent with, but not decisive for, an independent origin, and no archaeological line reviewed here independently corroborates a distinct West African center on the terms §25.2 established for Sudan. Racial diversification following

a single domestication and geographic diversification implying a second, independent one are not the same claim, and the cited sources themselves do not agree on which describes guinea-margaritiferum.

25.4 Why no PI is computed, and why this is not the same non-computation as maize's or Bactrian camel's

§20.7.1's resolvability predicate was built to separate a disputed location (R(X)=0 despite a corroborated center count) from a case where the center count itself is unsettled. Maize (§6.5) and Bactrian camel (§19.6) are both C=1, single-center-location disputes: a domestication event is not doubted, only its precise geographic point. Sorghum's disagreement is different in kind: Sudan's C=1 status is not in doubt on the corroboration standard §25.2 established, but whether a second center should be added to that C is exactly what Kimber (2000) and Mace et al. (2013) leave open, and what no later source reviewed here closes. Following §12.4's own resolution for dog, this chapter declines to assign a κ to either reading of guinea-margaritiferum — not out of caution for its own sake, but because doing so would require adjudicating a live scientific disagreement rather than reporting one, exactly the move §1.4's discipline exists to prevent.

Formal statement, following §12.4's own resolution

Disputed C: 1 (Sudan core case only, corroborated by both archaeology and genetics) versus a proposed but not doubly-corroborated 2 (adding the guinea-margaritiferum lineage as a second, West African center). κ is not assigned to either reading. PI is not computed, on the same grounds §12.4 declined to compute one for dog: the disagreement concerns the center count itself, not a resolved model's location.

25.5 Cross-cycle synthesis update

Sorghum joins dog as the second member of Appendix A.4's non-standard exclusion group — cases excluded not by §20.7.2's R(X) predicate, which presupposes an agreed center count, but by a live disagreement over that count itself. This is a distinct route from every member of A.3's five-case group (§22.7), all of which agree on C and disagree only on location or on coordinate resolvability. No number already published anywhere in this cycle changes as a result; this chapter adds a second member to a group of one, not a new group.

References newly cited in Chapter 25

Clark, J.D. & Stemler, A. (1975). Early domesticated sorghum from Central Sudan. Nature 254: 588–591.

Winchell, F., Stevens, C.J., Murphy, C., Champion, L. & Fuller, D.Q. (2017). Evidence for Sorghum Domestication in Fourth Millennium BC Eastern Sudan: Spikelet Morphology from Ceramic Impressions of the Butana Group. Current Anthropology 58(5): 673–683.

Fuller, D.Q. & Stevens, C.J. (2018). Sorghum domestication and diversification: a current archaeobotanical perspective. In Mercuri, D'Andrea, Fornaciari & Hoelzmann (eds.), Plants and People in the African Past.

Smith, O., Nicholson, W.V., Kistler, L., Mace, E., Clapham, A., Rose, P., Stevens, R., Ware, R., Samavedam, S., Barker, G., Jordan, D., Fuller, D.Q. & Allaby, R.G. (2019). A domestication history of dynamic adaptation and genomic deterioration in Sorghum. Nature Plants 5: 369–379.

Mace, E.S., Tai, S., Gilding, E.K. et al. (2013). Whole-genome sequencing reveals untapped genetic potential in Africa's indigenous cereal crop sorghum. Nature Communications 4: 2320.

Kimber, C.T. (2000). Origins of domesticated sorghum and its early diffusion to India and China. In Smith, C.W. & Frederiksen, R.A. (eds.), Sorghum: Origin, History, Technology, and Production.

Chapter 26 — Two Chinese Millets: A Second East Asian Multi-Species Test

26.1 A second East Asian case, for a different reason than rice

Rice (§4) tested this cycle's method against three incompatible genetic verdicts about a single species. Foxtail millet (Setaria italica) and broomcorn millet (Panicum miliaceum) are admitted here as a different kind of East Asian test: two distinct, independently domesticated species, excavated together at the same North China sites, that this chapter's identical method resolves onto two different branches of §20.7.2's partial function.

Both species are reported on the terms §3.6–§3.7 already used for chickpea and lentil: examined together because they share a landscape, not an evidentiary profile. Foxtail millet is tested first for a single-origin reading; broomcorn millet is tested separately and reported under §20.7.2's location-dispute branch if its archaeological and genetic centers diverge. No PI is invented to force an agreement the lines do not themselves reach.

26.2 Foxtail millet: a Chinese origin, and an older rival hypothesis not supported by later evidence

Molecular studies spanning isozyme, prolamin, rDNA, RAPD, AFLP, genomic RFLP, mitochondrial RFLP and transposon-display markers — reviewed together in Kajuna and colleagues' synthesis of foxtail millet crop evolution — converge on China as foxtail millet's center of diversity, with local landrace groups differentiating only after domestication, and recent archaeological

evidence (§26.3 below) supports the same reading. A minority hypothesis, proposed by Kawase & Sakamoto and based on the presence of genetically less specialized, morphologically primitive accessions between Afghanistan and India, located foxtail millet's origin there instead. No later molecular or archaeological source reviewed here corroborates the Afghanistan–India hypothesis as a second, independent center; it stands as a proposed and effectively refuted rival, structurally the same shape sunflower's second-center claim took in §7.3 and horse's three rival centers took in §15.5, rather than as a genuinely disputed second center on sorghum's terms (§25.3).

Formal statement for foxtail millet, following §20.7.2 directly

C=1 (China, molecular consensus). κ=1.0: the Kawase & Sakamoto rival hypothesis is not corroborated by later molecular or archaeological evidence reviewed here, following the same refuted-rival convention already applied to sunflower (§7.3) and horse (§15.5). PI(C,κ,D̄) = 1 × 1.0 × 0 = 0, independent of R(X).

26.3 Broomcorn millet: an archaeological center and a genetic signal that do not coincide

Lu, Zhang, Wu, Zhu, Yang, Weng, Huang, Ge, Wang & Chen (2009, PNAS 106(18):7367–7372) reported phytolith and biomolecular evidence identifying broomcorn millet at the Cishan site, on the eastern foothills of the Taihang Mountains near Wu'an, Hebei — the type site of the Cishan culture — dated to as early as roughly 10,000 calibrated years before present, making it, on the archaeological evidence, the earliest identified cultivated grain crop in East Asia and the type site for the culture that bears its name. Independently, Hunt, Rudzinski, Jones and colleagues' genetic study of broomcorn millet diversity, using chloroplast and nuclear markers, reports a signal pointing toward the western Loess Plateau — several hundred kilometers west of Cishan, on the North

China Plain — as at least one region of primary domestication, and as the likely source of the crop's later westward expansion into Inner Asia from the third millennium BCE. The two evidentiary lines, one archaeological and one genetic, point to different parts of northern China; neither source reviewed here reconciles them, and this chapter does not invent a reconciliation.

26.4 A real-coordinate check, reported as illustrative only

Cishan (36.5757°N, 114.1180°E, Wu'an, Hebei — the type site's own reported coordinates) and a representative point within the western Loess Plateau, Tianshui, Gansu (34.5809°N, 105.7249°E — a representative point chosen here, not a coordinate reported by Hunt et al. themselves, who describe a region rather than a single site, on the same disclosed-representative-point convention §15.5 used for horse's Volga-Don homeland zone), lie 790.5 km apart on a mean Earth radius of 6,371.0088 km. This is reported as an illustrative span only, on the same terms §21.5 reported turkey's Mesoamerica-to-Southwest distance and §22.5 reported cotton's three-center mean: neither location is a corroborated second center in the sense §20.7.1 requires, since the archaeological and genetic evidentiary lines have not themselves agreed to name two centers — they disagree about where the one process they each describe took place.

Formal statement for broomcorn millet, following §20.7.2 directly

C=1 (a single domestication process is not in dispute), but R(X)=0: the archaeological center (Cishan, a resolved point) and the genetic signal (western Loess Plateau, an unresolved region reported here only via a disclosed representative point) do not coincide, and no source reviewed here adjudicates between them. By §20.7.2's third clause, PI(C,κ,D̄) = ⊥. The illustrative 790.5 km

span (§26.4) is reported as a sensitivity figure only, on the same terms as B.8's turkey span and B.9's cotton span, not as a PI D.

26.5 Cross-cycle synthesis update

Foxtail millet joins the PI=0 floor group (Appendix A.2), growing it from eight to nine members, on the same refuted-rival grounds as sunflower and horse. Broomcorn millet joins the R(X)=0 location-dispute portion of Appendix A.3, growing it from five to six members — a single-center case whose archaeological and genetic evidentiary lines disagree about that one center's location, structurally closest to maize (§6.5) among the cases already catalogued there, though reached through phytolith-versus-chloroplast evidence rather than through two competing archaeological complexes. No number already published anywhere in this cycle changes as a result of either addition.

References newly cited in Chapter 26

Lu, H., Zhang, J., Wu, N., Zhu, K.B., Yang, X., Weng, D., Huang, T., Ge, Y., Wang, J. & Chen, Y. (2009). Earliest domestication of common millet (Panicum miliaceum) in East Asia extended to 10,000 years ago. Proceedings of the National Academy of Sciences 106(18): 7367–7372.

Hunt, H.V., Rudzinski, A., Jones, M.K. et al. Genetic evidence for a western Chinese origin of broomcorn millet (Panicum miliaceum).

Kaur, P. et al. (2014). Polyphyletic origin of Brassica juncea with B. rapa and B. nigra (Brassicaceae) participating as cytoplasm donor parents in independent hybridization events. American Journal of Botany 101(7), 1157–1166.

Kawase, M. & Sakamoto, S. Origins and geographic differentiation of foxtail millet (as reviewed in later syntheses of foxtail millet crop evolution).

Chapter 27 — Banana: A Domestication Process the Index Was Not Built to Count

27.1 This section's structurally hardest case

§24.1 admitted banana as the case that would close Section XIV on a sixth and newly distinct route to ⊥. This chapter tests that claim by reporting what the cited genomic literature itself says banana domestication was — not a discrete choice among candidate centers, but a sequence of hybridization events across named taxa and regions — before asking what that means for §20.7's formal apparatus.

Banana is reported on the terms its own literature reports it: a sequence of hybridization events, not a single wild-to-domesticate transition with one or several candidate centers. If the cited sources support a coherent C, κ, D̄ triple despite that structure, this chapter computes one; if not, that is reported as plainly as dog's disputed count (§12.4), with the specific reason the case fails A.3's five grounds or A.4's dog-shaped exclusion. This closes Section XIV; no Section XV is committed to here.

27.2 The first step: hybridization in New Guinea

Genomic and archaeobotanical evidence converges on New Guinea as the site of banana's initial domestication step. Kuk Swamp, in the Wahgi Valley of the Western Highlands Province of Papua New Guinea (5.7825°S, 144.3300°E), has yielded phytolith evidence for banana cultivation from roughly 6,900 to 6,400 years ago, among the earliest agricultural evidence anywhere in the island. Martin, Cenci, Roúx et al. (2023, The Plant Journal) and the more recent Musa ancestor-genome assembly of Rouard, Martin, Chase et al. (2025, Nature Communications) both report that this initial step

was not a straightforward domestication of a single wild species, but a hybridization between Musa acuminata subspecies banksii (and possibly zebrina) and a separate species, Musa schizocarpa, native to New Guinea and previously unsuspected to have contributed to cultivated banana at all.

27.3 Successive steps: hybridization across Southeast Asia

As early cultivars diffused from New Guinea through Southeast Asia, further hybridizations occurred with additional wild Musa taxa native to each region in turn: Musa acuminata ssp. zebrina in Java, ssp. malaccensis on the Malay Peninsula and in Sumatra, ssp. burmannica in southern Indo-Burma, and Musa balbisiana across a range from India to South China and, in some reconstructions, the Philippines. Sardos, Perrier, Doutrelepont et al. and the wider genome-ancestry-mosaic literature (Martin et al. 2020, 2023) report cultivar genomes as mosaics of three to as many as seven to nine ancestral genetic pools, including at least two contributors whose wild source population has not yet been identified. Rouard, Martin, Chase et al. (2025) sequenced several of these previously uncharacterized wild genetic groups directly, resolving one as Musa acuminata ssp. halabanensis and leaving a further contributor only partially resolved.

27.4 Why the C, κ, D̄ triple does not describe this case

§20.7.1's resolvability predicate presupposes a set of proposed centers $X = \{x_1,\ldots,x\_C\}$, each a candidate origin point for the same domestication event, disagreeing at most about which of C locations is correct or how many centers exist. Banana's own literature does not describe candidate alternatives for a single event: it describes a documented sequence of at least two, and by the fullest genomic accounting as many as eight or nine, real hybridization events across different named regions, each contributing genetic material that persists in modern cultivars. This

is not a case where C is disputed, as with dog (§12.4) and sorghum (§25.4); nor is it a case where a single center's location is disputed, as with maize (§6.5) and broomcorn millet (§26.3); nor is it a case where centers are proposed but not coordinate-resolvable, as with chicken, turkey and cotton (§20.6, §21.6, §22.6). It is a case where the underlying process itself — a compounding sequence of admixture events across a widening geographic range, rather than a wild-to-domesticate transition at one or several discrete points in time and space — does not fit the index's own model of what a "center" is. Cotton (§22.6) came closest to this shape among cases already catalogued, with four independent domestications of four different species; banana differs from cotton's case in kind, not only degree, because cotton's four domestications are four separable single-species events, each individually describable by §20.7.1's predicate, while a single cultivated banana genome is itself already a mosaic of multiple wild contributors before any C can be assigned to it at all.

27.5 An illustrative geographic span, reported as a sensitivity figure only

Following §21.5's and §22.5's own convention for reporting a span without computing a PI from it, the great-circle distance from Kuk Swamp, New Guinea (5.7825°S, 144.3300°E), to Guwahati, Assam (26.14°N, 91.73°E) — already used elsewhere in this cycle (§14.3) as a representative point within Musa balbisiana's reported range in eastern India — comes to 6,685.7 km on a mean Earth radius of 6,371.0088 km. This is reported purely to illustrate the geographic scale of the hybridization sequence §27.3 describes, not as a $\bar{D}$ between two corroborated centers of the same event.

Formal statement: no PI computed, on grounds distinct from every case in Appendix A.3 or A.4

Banana is excluded from §20.7.2's partial function altogether, rather than returning ⊥ under its third clause. The predicate R(X) presupposes a proposed center set X for one domestication event; banana's own literature reports a documented sequence of at least two and as many as eight or nine hybridization events across different named taxa and regions, contributing to a single mosaic cultivar genome. No C is assigned, because no single event is being counted. This is reported here as a sixth, structurally distinct route to non-computation, joining maize and Bactrian camel's location disputes (§20.7.2, R(X)=0), chicken's zero-resolved-centers case (§20.6), turkey and cotton's mixed-resolvability cases (§21.6, §22.6), and dog and sorghum's disputed-count cases (§12.4, §25.4) as a case this cycle's formal apparatus does not reach at all.

27.6 Cross-cycle synthesis update, and the close of Section XIV

Banana is catalogued in a new Appendix A.5, following the precedent §A.4 set for dog: a case outside A.3's five (now six) coordinate-resolvability grounds and outside A.4's disputed-count grounds, reported on its own terms because the open question is neither a location nor a count, but whether the index's own model of a domestication event applies to the case at all. No number already published anywhere in this cycle, including elsewhere in this section, changes as a result.

This closes Section XIV. Five species across four chapters have been added: potato (Appendix A.2, floor group, eighth member), sorghum (Appendix A.4, disputed-count group, second member), foxtail millet (Appendix A.2, floor group, ninth member), broomcorn millet (Appendix A.3, location-dispute group, sixth member), and banana (a new Appendix A.5, on grounds no earlier case in this cycle has produced). No Section XV is committed to here.

References newly cited in Chapter 27

Martin, G., Baurens, F.C., Cenci, A. et al. (2020, and 2023 Interspecific introgression patterns reveal the origins of worldwide cultivated bananas in New Guinea). The Plant Journal.

Rouard, M., Martin, G., Chase, R. et al. (2025). Unravelling genomic drivers of speciation in Musa through genome assemblies of wild banana ancestors. Nature Communications.

Sardos, J., Perrier, X., Doutrelepont, H. et al. Genome ancestry mosaics reveal multiple and cryptic contributors to cultivated banana.

Denham, T.P., Haberle, S.G., Lentfer, C. et al. (2003). Origins of Agriculture at Kuk Swamp in the Highlands of New Guinea. Science 301: 189–193.

Chapter 28 — Cat (Felis catus): A Domestication Whose Consensus Location Changed While This Cycle Was Being Written

28.1 A second bird-shaped problem, this time a mammal

Chicken (Chapter 20) forced this cycle to admit a fourth outcome type: convergent geography without a computable index, because two evidentiary lines pointed at the same broad region without ever supplying a site-level coordinate. Cat forces a fifth. Its literature does not converge — it has, within the span of this cycle's own composition, reversed itself. A 2007 single-origin result and a long-standing rival Egyptian hypothesis have both just been challenged by a 2025 genomic study proposing a third region neither had named. This chapter is written deliberately close to that reversal, and says so throughout rather than quietly picking a winner.

The same data commitments carry over unchanged: no invented figures, disagreement reported rather than resolved by authorial preference, and every computed or attempted quantity traceable to a specific cited source.

28.2 The 2007 model: a single Near Eastern origin, five founders

Driscoll, Menotti-Raymond, Roca, Hupe, Johnson, Geffen, Harley, Delibes, Pontier, Kitchener, Yamaguchi, O'Brien & Macdonald (2007, *Science* 317:519–523) genotyped 979 domestic cats and wild individuals from all five subspecies of *Felis silvestris* — European, Near Eastern (*lybica*), Central Asian (*ornata*), southern African (*cafra*), and Chinese desert (*bieti*) wildcats — using mitochondrial sequence and microsatellite data. Their result placed domestication in the Near East, coincident with the spread of early agricultural villages in the Fertile Crescent, and traced the world's domestic cat population to at least five founding matrilines drawn from Near Eastern wildcats specifically, later dispersed by human agency.

The strongest independent anchor for a Near Eastern reading is archaeological rather than genetic: a joint human–cat burial at Shillourokambos, Cyprus, dated to approximately 9,500 years before present (Vigne et al. 2004). Cyprus lies outside the natural range of *F. lybica* — a wildcat could only have reached the island by boat — so the burial is evidence that a tamed or camp-following cat had already travelled with people by that date, not itself a claim about where the taming began.

28.3 A long-standing rival: Pharaonic Egypt, roughly 3,500 years ago

Egyptian cat iconography and mummification are separately extensive, and a second hypothesis — an independent or contributing Egyptian domestication center around 3,500 years ago — has circulated in the literature alongside the Near Eastern one for decades. The most recent comprehensive genomic study to address the question directly summarises the pre-existing state of the field

in these terms: archaeozoological and iconographic evidence pointed to two possible centers of domestication, the Neolithic Levant around 9,500 years ago and Pharaonic Egypt around 3,500 years ago, with genuine uncertainty over which — if either alone — was correct (De Martino et al. 2025). This is the two-center picture the present chapter's working note took as its starting point.

28.4 De Martino et al. (2025, *Science*): a third region, and a much later European arrival

De Martino, Larson and colleagues analysed 87 ancient and modern cat genomes, including 70 new low-coverage ancient genomes spanning roughly 9000 BCE to the 19th century CE and 17 higher-coverage modern and museum wildcat genomes from Europe, North Africa and Anatolia. Two findings directly overturn rather than adjudicate between the Levant/Egypt pair:

First, nuclear genome-wide analysis places the ancestry of today's domestic cats in North African wildcat populations (the paper's title names North Africa explicitly), not in the Levantine or Egyptian lineages the older two-center picture had assumed as the only candidates.

Second, domestic cats do not appear to have dispersed into Europe with Neolithic farmers at all. The earliest cat in the dataset genetically identifiable as a true domestic or African wildcat lineage in Europe is a Sardinian specimen radiocarbon-dated to the second century CE — roughly 2,000 years ago — probably introduced from North Africa and plausibly connected to Roman-period movement rather than to the Neolithic package. Cat remains and depictions from earlier in the European record are read by this study as genetically European wildcat, reflecting contact and possible hybridization rather than an established domestic population.

This is a direct, disclosed departure from an earlier mitochondrial-DNA literature (Ottoni et al. 2017) that had read a Near Eastern

mitochondrial lineage's spread into Europe as tracking the Neolithic expansion. The newer nuclear study does not merely add a third candidate to the older two; it removes the evidentiary basis for treating either Levant-to-Europe or Egypt-to-Europe as a settled Neolithic-era dispersal route, on grounds structurally similar to the correction chicken's own record received from Peters et al. (2022, §20.3) — a later, larger, methodologically stronger study substantially rewriting rather than merely supplementing an earlier consensus.

28.5 Why this case returns R(X) = 0, for a reason distinct from every earlier ⊥ instance

Three regions have now been named across this literature — Levant, Egypt, North Africa — and this cycle's own predicate (§20.7.1–§20.7.2) requires asking whether any is pinned to a real coordinate the way einkorn's Karacadağ or Telarmachay (§29.3, below) are. None is. In every source reviewed for this chapter, each of the three candidate origins is reported as a region or a cultural period (the Fertile Crescent; Pharaonic Egypt; the North African range of *F. l. lybica*), never as a single excavated point comparable in kind to this cycle's other resolvable cases. This is a different failure mode from every prior ⊥ case:

Unlike maize and Bactrian camel (§17.6, §19.6), where rival hypotheses *do* supply competing point coordinates and R(X) = 0 reflects a live choice between them, cat's rival hypotheses supply no coordinates to choose between in the first place.

Unlike chicken (§20.6–§20.7), where two evidentiary lines converge on one broad region without a point, cat's evidentiary lines disagree with each other about which broad region is correct, and the most recent and methodologically strongest of them directly contradicts the two older ones rather than confirming a shared reading.

C is therefore reported as unresolved among three named regions, none individually locatable at the resolution this index requires; κ is not assigned and D̄ is not computed; PI is ⊥, on the same disclosed, non-committal footing as maize, Bactrian camel, and chicken before it, but added here as a fifth distinct route to that same symbol.

28.6 Synthesis note

Case	Named candidate regions	Best current reading	Why ⊥	Source
Cat	Levant (~9,500 BP); Pharaonic Egypt (~3,500 BP); North Africa (favoured by the most recent nuclear study)	North African origin; European dispersal ~2,000 BP, not Neolithic	No candidate region is reported at point-coordinate resolution in any source reviewed	Ch.28, §28.2–§28.5

This is added to Appendix A.3 as a seventh ⊥ case, under a newly disclosed sub-reason distinct from the location-dispute and convergence reasons already recorded there (§28.7 below carries this into the appendix itself).

References newly cited in Chapter 28

Driscoll, C.A., Menotti-Raymond, M., Roca, A.L., Hupe, K., Johnson, W.E., Geffen, E., Harley, E.H., Delibes, M., Pontier, D., Kitchener, A.C., Yamaguchi, N., O'Brien, S.J. & Macdonald, D.W.

(2007). The Near Eastern Origin of Cat Domestication. *Science* 317(5837): 519–523.

De Martino, M. et al. (2025). The dispersal of domestic cats from North Africa to Europe around 2000 years ago. *Science* 390(6776).

Ottoni, C. et al. (2017). The palaeogenetics of cat dispersal in the ancient world. *Nature Ecology & Evolution* 1: 0139.

Vigne, J.-D., Guilaine, J., Debue, K., Haye, L. & Gérard, P. (2004). Early taming of the cat in Cyprus. *Science* 304(5668): 259.

Chapter 29 — Llama and Alpaca (Lama glama, Vicugna pacos): Two Domestications in One Region, and a Post-Conquest Merger

29.1 Two species, two wild progenitors, one recurring source of confusion

South America has four extant camelids: two wild — guanaco (*Lama guanicoe*) and vicuña (*Vicugna vicugna*) — and two domestic — llama (*Lama glama*) and alpaca (*Vicugna pacos*). For most of the twentieth century the ancestry of the two domestic forms was genuinely unsettled, with at least four competing hypotheses reviewed in the literature: guanaco→llama and vicuña→alpaca as separate lineages; guanaco→llama with alpaca as a llama×vicuña hybrid; both domestic forms from guanaco alone; or both from now-extinct wild precursors. The near-extirpation of purebred herds during the Spanish conquest, and subsequent free interbreeding, made the modern population a poor guide to the founding relationships on its own.

29.2 Resolving the founder question: Kadwell et al. (2001) and its genomic confirmation

Kadwell, Fernandez, Stanley, Baldi, Wheeler, Rosadio & Bruford (2001, *Proceedings of the Royal Society B*) used mitochondrial and

microsatellite DNA across all four species to settle the ancestry question: llama derives from guanaco, and alpaca derives from vicuña — not, as an earlier and once-influential reading had proposed, from guanaco with vicuña playing no domesticatory role. Marín, Zapata, González, Bonacic, Wheeler, Casey, Bruford, Palma, Poulin, Alliende & Spotorno (2007) and, at full genomic resolution, Marín et al. / the 2020 reference-genome study (Fan et al. 2020, *Genome Biology* 21:159) confirm this phylogenomically: llama and guanaco genomes group together, as do alpaca and vicuña, with the domestication relationship no longer seriously contested at the species level. What remains open, and is this chapter's actual subject, is *where* each of the two domestications happened.

29.3 Alpaca: the Telarmachay hypothesis, and a live doubt about the evidence itself

The most detailed and longest-studied candidate site for early camelid management is the Telarmachay rock shelter, in the puna of Junín in the Peruvian central Andes, at 11°11′S, 75°52′W, 4,420 m above sea level. Lavallée, Julien and Wheeler's decades of excavation there proposed a gradual sequence: predominantly vicuña and guanaco hunting from roughly 9,000–7,200 BP, increasing specialisation in vicuña and guanaco between 7,200–6,000 BP, and — on the strength of a shift toward neonatal camelid remains and an incisor morphology matching modern alpacas — a proposed domestication signal around 7,100–6,000 BP (Wheeler 1984, 1985). The rock shelter's occupation sequence has since been redated by AMS radiocarbon to 9.1–8.0 through 3.8–3.0 kyr BP (Le Neün et al. 2023b), and the wet-puna, Junín-centered hypothesis remains the most consistently cited location for early alpaca domestication in the literature reviewed for this chapter.

This is not, however, an undisputed reading of the evidence at Telarmachay itself. Le Neün, Dufour, Goepfert, Wheeler & Cucchi

(2023, and in a 2026 follow-up study) applied first-phalanx morphometrics to the Telarmachay faunal assemblage and found that most specimens fall within the size range of both wild modern vicuñas and domesticated highland alpacas — a result the authors themselves describe as making bone-size evidence alone an unconvincing basis for claiming early domestication at the site, independent of the incisor-morphology argument Wheeler's original case rested on.

This is a different kind of open question from anything §17–§26 encountered: it is not a dispute over *where* alpaca domestication happened (no rival location is proposed), and not a dispute over *how many* centers there are (no second alpaca-specific center is proposed either). It is a live methodological dispute over whether the cited osteological evidence at the one proposed location actually distinguishes early domestication from continued wild hunting. Because no rival location and no rival center count are in play, this chapter still assigns C = 1 for alpaca and places it, provisionally, at the PI = 0 floor alongside einkorn and chickpea — but flags the assignment as resting on a single site whose own most recent morphometric reanalysis calls the underlying identification into question, a caveat carried into Appendix A.2 rather than left here.

29.4 Llama: a named region, not a named point

The parallel case for llama is archaeologically and genetically real but geographically coarser. Zooarchaeological and isotopic work in northwest Argentina and northern Chile documents llama domestication from guanaco in the dry puna, at elevations of 3,200 m and above, between approximately 5,000 and 3,800 BP (Mengoni-Goñalons & Yacobaccio 2006, reviewed in Wheeler 2012). Díaz-Maroto, Rey-Iglesia, Cartajena, Núñez, Westbury, Varas, Moraga, Campos, Orozco-terWengel, Marín & Hansen (2021, *eLife* 10:e63390) generated ancient mitochondrial genomes from camelid

remains at the Tulán ravine sites (Tulán-52, -54, -85, -94) near the Salar de Atacama, in the vicinity of San Pedro de Atacama, dated 3,500–2,400 BP, confirming guanaco ancestry for llama-sized specimens at that locality and finding evidence of bidirectional pre-conquest hybridization between llama and vicuña lineages.

No source reviewed for this chapter reports a single decimal-degree excavation point offered as *the* llama domestication locus, comparable to Telarmachay's role for alpaca; the cited literature instead names a region (northwest Argentina and northern Chile, dry puna, ≥3,200 m) and a cluster of sites within it. San Pedro de Atacama (22°54′S, 68°12′W) is used below only as an illustrative anchor for that cluster, on the same footing as the illustrative-only distances this cycle has already used for Bactrian camel (§19.5) and the Chinese millets (§26.4) — not as a claim that this is the domestication point itself.

The great-circle distance from Telarmachay to San Pedro de Atacama, computed the same way as every other distance in this cycle, is 1,536.6 km. This figure is reported here as a sensitivity/illustrative figure only: it measures the separation between one well-defined alpaca-associated site and one representative locality within llama's much larger named region, not a Polycentricity Index for either species, since neither term of the C, κ, D̄ triple resolves for llama on the same footing it does for alpaca.

29.5 Why no PI is computed for either species, and how this differs from goat's minor second signal

Goat's second, minor signal (§17.4) is this cycle's model for a real, quantified, small κ against a large D̄ — a genuinely corroborated but highly unequal second center. Llama and alpaca do not fit that model, because in neither case is a *second* center for the *same* species proposed at all: each is a single-progenitor, single-region case. The

open question for alpaca is evidentiary (does the cited osteology at the one proposed site actually show domestication, §29.3); the open question for llama is locational precision (a named region without a published point, §29.4) — the same fifth ⊥ reason Chapter 28 introduced for cat, of which llama is this cycle's second instance. Alpaca is provisionally floor-group (PI = 0, with the caveat disclosed above); llama is ⊥, alongside cat, maize, Bactrian camel, chicken, turkey, and cotton.

29.6 Post-conquest hybridization is a separate phenomenon from either founding event

Fan et al. (2020) report introgression between the two domestic lineages far higher in alpaca (36%) than in llama (5%), dated close to the Spanish conquest, roughly 500 years ago — a bottleneck-and-remixing event that postdates both proposed founding domestications by several thousand years. This is included here for completeness and because it is the reason Kadwell et al. (2001) opens by calling llama and alpaca ancestry "controversial": the post-conquest admixture is real and well-dated, but it is evidence about the last five centuries of these two lineages' history, not about where or when either was first domesticated, and this chapter does not let it stand in for either question.

29.7 Synthesis note

Case	C	Location evidence	Status	Source
Alpaca	1 (vicuña, wet-puna hypothesis)	Telarmachay, Junín, Peru (11°11′S, 75°52′W)	Provisional PI = 0 floor; site's own recent morphometric reanalysis disputes the	Ch.29, §29.3

Case	C	Location evidence	Status	Source
			domesticati on reading	
Llama	1 (guanaco, dry-puna hypothesis)	NW Argentina / N Chile, ≥3,200 m; Tulán ravine cluster near San Pedro de Atacama, illustrative only	⊥, no point-level coordinate reported for the domesticati on locus itself	Ch.29, §29.4

Illustrative-only distance, Telarmachay to San Pedro de Atacama: 1,536.6 km (§29.4; not a Polycentricity Index).

References newly cited in Chapter 29

Kadwell, M., Fernandez, M., Stanley, H.F., Baldi, R., Wheeler, J.C., Rosadio, R. & Bruford, M.W. (2001). Genetic analysis reveals the wild ancestors of the llama and the alpaca. *Proceedings of the Royal Society B* 268(1485): 2575–2584.

Fan, R. et al. (2020). Genomic analysis of the domestication and post-Spanish conquest evolution of the llama and alpaca. *Genome Biology* 21: 159.

Wheeler, J.C. (1984, 1985). Publications on the Telarmachay faunal sequence; reviewed in Wheeler (1995) and in Le Neün et al. (2023, 2026).

Le Neün, M., Dufour, E., Goepfert, N., Wheeler, J.C. & Cucchi, T. (2023). Documenting past South American camelid diversity at

Telarmachay (Puna of Junín, Peru) using first phalanges morphometrics. *Revista de Arqueologia* 36(3): 26–37; follow-up study, *Quaternary Science Reviews* (2026), New insights into the domestication process of South American camelids at Telarmachay (Peru) from 9,000 to 4,500 years BP.

Denham, T. (2025). Forgetting cane grasses: Switching temporal focus to reveal mosaics of Saccharum diversity. Plants, People, Planet 7(3), 590–602.

Diamond, J. (2002). Evolution, consequences and future of plant and animal domestication. Nature 418, 700–707.

Díaz-Maroto, P., Rey-Iglesia, A., Cartajena, I., Núñez, L., Westbury, M.V., Varas, V., Moraga, M., Campos, P.F., Orozco-terWengel, P., Marín, J.C. & Hansen, A.J. (2021). Ancient DNA reveals the lost domestication history of South American camelids in Northern Chile and across the Andes. *eLife* 10: e63390.

Mengoni-Goñalons, G.L. & Yacobaccio, H.D. (2006). The domestication of South American camelids: a view from the South-Central Andes. In *Documenting Domestication*, ed. Zeder, Bradley, Emshwiller & Smith.

Chapter 30 — Yeast (Saccharomyces cerevisiae): One Wild Origin, Several Independent Domestications

30.1 A third case admitted after Chapter 29, on its own evidentiary merits

Chapter 28 and Chapter 29 were admitted after Section XIV closed, each re-earning §2.7's discipline on its own evidentiary record rather than fitting a plan drawn in advance. Yeast (Saccharomyces cerevisiae) is admitted here on the same footing, and for a reason distinct from both: cat and llama (§28.5, §29.5) fail this cycle's resolvability predicate because no candidate region resolves to a

point; yeast's wild origin does resolve to a region, corroborated independently by two separate large-scale sequencing programs, but the domestication side of the question does not resolve to a single event at all. The same data commitments carry over unchanged: no invented figures, disagreement reported rather than resolved by authorial preference, and every computed or attempted quantity traceable to a specific cited source.

30.2 A single wild geographic origin: the out-of-China result

Peter et al. (2018, Nature) whole-genome sequenced and phenotyped 1,011 S. cerevisiae isolates drawn from wild and human-associated sources worldwide. The greatest genomic diversity among all sampled lineages was found in strains from Taiwan, mainland China, and other regions of East Asia, a pattern the authors read as evidence for a single geographic origin of the species in East Asia rather than multiple, independently founded wild lineages arising in parallel across separate continents. The same study estimates that the species began dispersing worldwide from that region roughly 15,000 years ago, well before any of the domestication events discussed below.

Duan, Han, Wang, Liu, Shi, Li, Zhang & Bai (2018, Nature Communications), sampling 106 wild and 160 fermentation-associated isolates collected across China specifically, reached the same regional conclusion independently and sharpened it: China, or more broadly Far East Asia, is read as the most likely center of origin not only of the wild species but specifically of its domesticated populations. On the C, κ, D̄ vocabulary this cycle applies elsewhere, the wild-origin question resolves cleanly to one region, doubly corroborated by two independently assembled sampling programs — closer in structure to horse's single confirmed Volga–Don center (§15.5) than to any of this cycle's disputed-location or disputed-count cases. No source reviewed for

this chapter, however, narrows that region to a single excavated or sampled point comparable to Karacadağ (einkorn, §2.2) or Telarmachay (alpaca, §29.3): every account read here reports a broad region (East Asia; China/Far East Asia), never a coordinate, and no illustrative distance is computed in this chapter as a result — the same disclosed omission this cycle already applied to chicken (§20.6), rather than a manufactured anchor point standing in for a source that does not supply one.

30.3 What a single wild origin does not settle: several independently dated domestication events

A single wild-origin region is where this case starts to diverge from every earlier single-origin result in this cycle. Peter et al. (2018) report that wine yeast and sake yeast carry the genomic signatures of domestication from different ancestral lineages, acquired thousands of years apart: markers consistent with domestication appear in sake yeast by around 4,000 years ago, and in wine yeast only by around 1,500 years ago. These are not two readings of one founding event — they are two separately dated, separately lineaged domestications drawing on the same underlying wild diversity pool at different points in human history, for different fermentation traditions.

Duan et al. (2018) add a further layer directly relevant to how these founding events happened. Their domesticated isolates resolve into two major groups, associated respectively with solid-state and liquid-state fermentation traditions, and both groups appear to descend from heterozygous ancestors formed by outcrossing between diverse wild isolates — that is, each domesticated lineage is read as its own admixture event within the wild population's standing diversity, not as a single strain gradually brought under cultivation and then spread. This is a different kind of internal structure from anything a two-parent hybrid origin (grapevine, §10; common bean, §9) or a single-lineage domestication (einkorn, §2.2)

supplies: the founding step itself is reported as a recombination among several wild strains, repeated independently for different fermentation niches.

30.4 A convergent industrial signature: Gallone et al. (2016) and the five-lineage beer picture

Gallone, Steensels, Prahl, Soriaga, Saels, Herrera-Malaver, Merlevede, Roncoroni, Voordeckers, Miraglia et al. (2016, Cell) sequenced 157 industrial S. cerevisiae isolates — 102 beer strains, 19 wine strains, 11 spirit strains, 7 sake strains, 7 strains from spontaneous fermentations, 5 bioethanol strains, 4 bread strains, and 2 laboratory strains — and resolved today's industrial yeasts into five sublineages, genetically and phenotypically separated from wild strains, each tracing to only a few ancestors through its own pattern of domestication and subsequent divergence. Domestication signatures are reported as most pronounced in beer strains specifically, which the authors attribute to beer yeast's continuous residence within an industrial niche, with only limited genetic admixture back into wild stocks — a structural analogue, at the level of an individual industrial lineage, to this cycle's own repeated observation (goat, §17.4; pig, §11.4) that continuous isolation from a wild-type population, not simply time since founding, is what a strong domestication signature actually tracks.

30.5 Why the C, κ, D̈ triple does not describe this case, and how it differs from cat, llama, and banana

This cycle's resolvability predicate (§20.7.1–§20.7.2) presupposes a proposed center set $X = \{x_1,...,x\_C\}$ for one domestication event, disagreeing at most about which of C locations is correct or how many centers exist. Yeast's own literature does not supply a disagreement of that shape. Unlike cat and llama (§28.5, §29.5), where the obstacle is that no candidate region resolves to a point at all, yeast's wild origin does resolve to a region, on convergent

evidence from two independent sequencing programs (§30.2). The obstacle here is that the event being asked about is not singular: sake, wine, beer, bread, and bioethanol lineages are reported as separately founded, separately dated domestications drawn from one wild source population, not as rival location claims for one shared founding event. Unlike banana (§27.4), where multiple hybridization events accumulate into a single mosaic cultivar genome, yeast's multiple domestications remain genetically distinct lineages — wine yeast is not partly sake yeast the way a cultivated banana genome is partly several wild taxa at once. There is accordingly no single "the domesticated yeast" whose center or centers this index's C term could count, and no C is assigned here for the same underlying reason banana received none: the predicate's own model of what a domestication event is does not apply to a case structured as repeated, independent founding events from one wild source rather than one event with contested or multiple centers.

This is reported as a case in Appendix A.5's category — outside the index's domain altogether — but on grounds distinct from banana's own: banana's difficulty is cross-taxon admixture compounding into one genome; yeast's difficulty is temporal and cultural multiplicity of separately founded lineages from one, otherwise resolvable, wild-origin region. No PI is computed, and no number published anywhere else in this cycle changes as a result.

30.6 Synthesis note

Case	Why no C is assigned	Source
Yeast	Wild origin resolves to one region (East Asia/China; Peter et al. 2018, Duan et al. 2018), unlike banana — but sake, wine, beer, bread and bioethanol lineages are separately founded, separately dated	Ch.30, §30.2–§30.5

Case	Why no C is assigned	Source
	domestications from that one source, not rival centers for one event; §20.7.1's predicate presupposes a single proposed center set for a single event, which does not apply here either.	

No illustrative distance is reported for this chapter, unlike banana's Kuk Swamp–Assam span (§27.5) or turkey's and cotton's own (§21.5, §22.5): no source reviewed here anchors either the wild-origin region or any individual domestication event to a decimal-degree point, so none is manufactured to stand in for one.

References newly cited in Chapter 30

Peter, J. et al. (2018). Genome evolution across 1,011 Saccharomyces cerevisiae isolates. Nature 556(7701): 339–344.

Duan, S.-F., Han, P.-J., Wang, Q.-M., Liu, W.-Q., Shi, J.-Y., Li, K., Zhang, X.-L. & Bai, F.-Y. (2018). The origin and adaptive evolution of domesticated populations of yeast from Far East Asia. Nature Communications 9: 2690.

Gallone, B., Steensels, J., Prahl, T., Soriaga, L., Saels, V., Herrera-Malaver, B., Merlevede, A., Roncoroni, M., Voordeckers, K., Miraglia, L. et al. (2016). Domestication and Divergence of Saccharomyces cerevisiae Beer Yeasts. Cell 166(6): 1397–1410.

Chapter 31 — Honey Bee (Apis mellifera): A Domesticate Without a Genetic Boundary

31.1 A case admitted for what it breaks, not what it repeats

Chapters 28–30 were admitted after Section XIV closed, each re-earning §2.7's discipline on its own evidentiary record rather than fitting a plan drawn in advance (§30.1). Honey bee (Apis mellifera)

is admitted here on the same footing, for a reason none of the preceding thirty chapters supplies. Every one of them — whatever its outcome, a corroborated non-zero PI (§8.2, Appendix A.1), a C=1 floor by one of six distinct routes (Appendix A.2), an unresolved location (Appendix A.3), a disputed center count (Appendix A.4), or a domestication process the index's own model does not describe (Appendix A.5: banana, yeast) — presupposes that a population genetically distinguishable from its wild source exists for the resolvability predicate (§20.7.1–§20.7.2) to be tested against. Honey bee's own literature does not clearly supply one across most of its recorded history of human association. The same data commitments carry over unchanged from every prior chapter: no invented figures, disagreement reported rather than resolved by authorial preference, and every computed or attempted quantity traceable to a specific cited source.

31.2 The wild-origin dispute, kept separate from the domestication question

As with dog's wolf-origin geography (§12.2–§12.3), this chapter treats the question of where the wild species itself originated as distinct from the question of domestication, and does not let one substitute for the other. Whitfield, Behura, Berlocher, Clark, Johnston, Sheppard, Smith, Suarez, Weaver & Tsutsui (2006), genotyping 1,136 nuclear SNPs across 341 individuals, read the data as evidence of an African origin for A. mellifera, with the M, C, and O lineages representing two to three subsequent expansions into Eurasia. Han, Wallberg & Webster (2012), reanalysing the same underlying question with an expanded sampling design, found no strong support for the African-origin reading and instead reported a pattern more consistent with an origin close to the region where Apis's Asian sister species occur — Western or Central Asia rather than East Africa. Wallberg, Han, Wellhagen, Dahle, Kawata, Haddad et al. (2014), sequencing 140 genomes from 14 worldwide

populations at 8.3 million SNPs, likewise found no evidence for an African origin and read their data as more consistent with Han et al.'s reconstruction. Higher raw genetic diversity in African populations has been cited on the other side of the dispute, but no source reviewed here resolves this into an agreed single answer, and none of the three studies sampled populations spanning the species' full lineage range.

This dispute concerns where the wild species itself arose, long before any human involvement is proposed by any source reviewed. It is not, on its own terms, a domestication-center dispute in this cycle's sense, and this chapter does not attempt to force it into one: unlike maize's or Bactrian camel's rival domestication-location hypotheses (§6.3, §19.2), no source here proposes rival human management centers at all, only rival readings of the wild species' own biogeographic history. Chapter 31 sets this question aside for the same reason Chapter 12 set aside the wolf-origin dispute before turning to the dog domestication event itself: it is a genuine, live disagreement, but not the one this chapter was admitted to test.

31.3 The evidentiary record of human association: chemical, iconographic, and archaeological

The record of humans exploiting A. mellifera is long, real, and increasingly well dated, independent of where the resolution of §31.2's dispute eventually lands. Roffet-Salque, Regert, Evershed et al. (2015), analysing lipid residues in more than 6,000 pottery samples from over 150 Old World archaeological sites, identified a distinctive beeswax chemical signature across Neolithic Europe, the Near East, and North Africa, continuously and in places extensively from at least the seventh millennium BC — including, at one site in Turkey, evidence dated to around 6,500 BC, among the earliest secure evidence for bee-product use by farming communities anywhere reviewed. The authors read the association as beginning

at, or close to, the earliest onset of agriculture in the region, and describe it as possible early evidence for the beginnings of a domestication process without claiming the process was completed within their own dataset. Independently of this chemical record, ancient Egyptian bee iconography is attested from the Old Kingdom, around 2400 BC, depicting what appears to be managed hive-keeping rather than incidental honey-hunting.

The clearest single instance of large-scale, dated, physically excavated apiculture comes from a much later period and a specific site: Mazar & Panitz-Cohen (2007) and Bloch, Francoy, Wachtel, Panitz-Cohen, Fuchs & Mazar (2010) report an apiary at Tel Rehov (32.457°N, 35.498°E), in Israel's Beit She'an Valley, dated to the mid-10th to early 9th century BC. Thirty cylindrical clay hives survived intact, with physical and stratigraphic evidence for an original installation of 100 to 200 hives arranged in orderly rows — an industrial-scale operation by any standard this cycle has applied elsewhere, roughly three millennia before the present.

31.4 A translocation the source literature itself quantifies, reported rather than recomputed here

What Bloch et al. (2010) add to Mazar & Panitz-Cohen's excavation is not only a date but a genetic identification: ancient DNA recovered from the preserved bee remains at Tel Rehov identifies the colonies as belonging to, or closely resembling, the Anatolian subspecies (A. m. anatoliaca), rather than the subspecies native to the Levant. The inhabitants of Tel Rehov are read as having imported bee stock from several hundred kilometres away — plausibly, the authors suggest, because Anatolian bees were less aggressive and produced substantially higher honey yields than the local population — rather than managing a wholly local wild population in place. Independent support for the plausibility of exactly this kind of long-distance transfer comes from an eighth-century BC Assyrian stele, which records bees being carried from

the Taurus Mountains of southern Turkey to the land of Suhu, on the middle Euphrates, over a route the secondary literature reports as being of a comparable distance to the roughly 400 km (250 mi) separating the Taurus range from Tel Rehov itself.

This 400 km figure is reported here as it appears in the literature reviewed, not recomputed from first coordinates: no source consulted for this chapter names a single excavated or sampled point within the Taurus range comparable to Karacadağ for einkorn (§2.2) or Telarmachay for alpaca (§29.3), so no great-circle distance is independently calculated here, in the same spirit as chicken's (§20.6) and yeast's (§30.2) own disclosed omissions where a source reports only a region rather than a point. What the figure supports, reported rather than computed, is that Iron Age apiculture in the Levant already involved real, long-distance translocation of managed colonies — a genuinely domesticate-like behaviour, centuries before any comparable genetic signature is detectable in the species as a whole (§31.5).

31.5 Why no genetic boundary separates ‘domesticated’ from ‘wild’ for most of this record

Every prior animal case in this cycle — pig, dog, cattle, water buffalo, horse, sheep, goat, dromedary, Bactrian camel, chicken, turkey, cat, llama, alpaca — is a vertebrate whose domesticated populations are genetically distinguishable, to some reported degree, from their wild source. Honey bee is not: Wallberg et al. (2014), reporting the most extensive worldwide genomic survey reviewed for this chapter, find that contemporary populations retain high genetic diversity and read this explicitly as evidence for the absence of a domestication bottleneck of the kind found in every other managed animal this cycle has examined. Rangel, Traver, Stoner, Hatter, Trevelline, Garza, Shepherd, Seeley & Wenzel (2020), sampling wild and managed colonies side by side in Pennsylvania, report that managed colonies are not reliably

genetically distinguishable from nearby wild ones on standard population-genetic grounds; queens mate on the wing with drones drawn indifferently from both populations, and until the recent arrival of the parasitic mite Varroa destructor, gene flow between managed hives and free-living colonies was essentially unrestricted across most of the species' introduced and native range alike. Carpenter & Harpur (2021), reviewing the US literature on this question directly, note that despite centuries of documented management, honey bee has not previously received the kind of systematic domestication-history review routinely applied to other managed species — itself a symptom of how poorly the vertebrate-derived domestication vocabulary this cycle has used throughout fits an insect whose free-living and human-kept populations have rarely been reproductively separated at all.

Panziera, Requier, Chantawannakul, Pirk & Blacquière (2022) sharpen the contrast further: where domestication in other organisms typically reduces genetic diversity and fitness relative to the wild ancestor, honey bee management practices — large-scale hive movement, cross-regional introductions, queen trading, and selective breeding programmes — are reported as actively reducing diversity in both managed and wild populations at once, precisely because the two remain interconnected rather than genetically separated by the management itself. The one clearly documented case of a real, measurable domestication-associated genetic signature in this species comes from Lin, Zhu, Zhuang, Wang, Zhang, Gao, Niu & Ji (2023), who report strong, lineage-level genetic divergence in the Dongbei bee, a Chinese population intentionally introduced beyond A. mellifera's natural range and locally managed for approximately 100 years — a signature the authors estimate, from linkage-disequilibrium decay, as equivalent to roughly 2.5 million years of divergence under ordinary natural selection. This is a real, dated, quantified domestication effect,

drawn directly from its own source; it is also the only one of its kind identified in the literature reviewed for this chapter, confined to one recent, specifically documented population under a specifically documented, intensive local breeding regime, rather than a signature carried across the species' multi-millennial exploitation history reported in §31.3.

31.6 Applying §20.7's predicate: a seventh, categorically distinct route to ⊥

Formal statement, following §20.7.2 directly. The resolvability predicate presupposes a proposed center set $X = \{x_1,\ldots,x\_C\}$, each x_i representing a candidate locus for one domestication event, with $R(X)$ testing whether each candidate resolves to a usable point. Honey bee's literature does not fail this predicate the way any of the six prior ⊥ cases did: not maize's or Bactrian camel's shape (§6.5, §19.6), since no rival, named candidate locations are in dispute here at all; not chicken's (§20.6), since the obstacle is not that no candidate region achieves point resolution; not turkey's or cotton's (§21.6, §22.6), since this is not a case where some centers resolve and others do not; not cat's or llama's (§28.5, §29.5), since the obstacle is not that named regions exist but none reaches point-coordinate resolution; not banana's (§27.4), since there is no cross-taxon hybridization compounding into a single mosaic genome; and not yeast's (§30.5), since there is no single resolved wild-origin region from which several separately dated domestications can be enumerated — §31.2's wild-origin dispute is itself unresolved, and, more fundamentally, it is not the obstacle here at all.

The obstacle instead is prior to all of these: §20.7.1's predicate presupposes that a domesticated population — a candidate x_i's own referent — exists as a genetically bounded object distinguishable from the wild source population it was drawn from. For all but the most recent, most locally documented fraction of this species' recorded management history (§31.5), the literature reviewed here

reports the opposite: continuous gene flow, no detectable bottleneck at the species level, and a domestication-associated genetic signature confirmed in only one population, introduced within living historical memory under an intensively documented breeding regime. R(X) is not returning ⊥ because a center cannot be located; C itself cannot be responsibly assigned, because the entity C would be counting instances of — a domesticated A. mellifera population separable from its wild source — is not the entity most of this species' own documented history of human management actually produced. This is the same underlying move §27.4 and §30.5 already made for banana and yeast: reporting that the predicate's own object does not apply, rather than manufacturing a number to fill the gap. It is reported as a case in Appendix A.5's category on that basis, on a third and distinct ground from either.

31.7 What behavioural translocation without genetic domestication implies for the cycle as a whole

Read together, §31.3–§31.6 describe something this cycle has not previously separated so cleanly: a documented, dated, in one case (§31.4) even distance-quantified record of humans moving, housing, and managing a species at real geographic scale — beeswax exploitation from the 7th millennium BC, Old Kingdom iconography by 2400 BC, industrial apiculture with cross-regional colony import by the 10th–9th century BC — running for close to nine thousand years without producing, across most of that record, the genetically bounded population that every other case in this cycle has treated as domestication's minimal signature. Where such a signature does appear (§31.5, Dongbei bee), it is not a residue of that long history at all, but an artefact of one recent, specifically documented, intensively managed population. This does not mean A. mellifera is undomesticated in any everyday sense — the behavioural record in §31.3 speaks for itself — only that behavioural domestication and genetic domestication, treated as

inseparable by the predicate this cycle has applied to every prior species, come apart completely in this one, for reasons that are about honey bee's own biology (mating on the wing, ready reversion of managed colonies to free-living status, minimal reproductive isolation between kept and wild stock) rather than about the quality or completeness of the evidence reviewed.

31.8 Synthesis note

Case	Why no C is assigned	Source
Honey Bee	Documented behavioural/logistical management for roughly nine thousand years (beeswax exploitation from the 7th millennium BC, Old Kingdom iconography, Tel Rehov's dated, distance-quantified colony import) without a corresponding species-wide genetic domestication bottleneck; the one confirmed domestication-associated genetic signature (Dongbei bee, Lin et al. 2023) is confined to a single, recently introduced, intensively managed population. §20.7.1's predicate presupposes a genetically bounded domesticated population as its object; for most of this species' management history, no source reviewed here reports one.	Ch.31, §31.3–§31.6

No PI is computed, and no number published anywhere else in this cycle changes as a result. Honey bee joins banana and yeast in Appendix A.5, on a third, distinct ground; it is also this cycle's first case drawn from Insecta rather than Vertebrata, its thirty-third species overall, and its sixteenth from kingdom Animalia — the first of the sixteen that is not a vertebrate.

References newly cited in Chapter 31

Whitfield, C.W., Behura, S.K., Berlocher, S.H., Clark, A.G., Johnston, J.S., Sheppard, W.S., Smith, D.R., Suarez, A.V., Weaver, D. & Tsutsui, N.D. (2006). Thrice out of Africa: ancient and recent expansions of the honey bee, Apis mellifera. Science 314(5799): 642–645.

Han, F., Wallberg, A. & Webster, M.T. (2012). From where did the Western honeybee (Apis mellifera) originate? Ecology and Evolution 2(8): 1949–1957.

Wallberg, A., Han, F., Wellhagen, G., Dahle, B., Kawata, M., Haddad, N. et al. (2014). A worldwide survey of genome sequence variation provides insight into the evolutionary history of the honeybee Apis mellifera. Nature Genetics 46(10): 1081–1088.

Roffet-Salque, M., Regert, M., Evershed, R.P. et al. (2015). Widespread exploitation of the honeybee by early Neolithic farmers. Nature 527: 226–230.

Mazar, A. & Panitz-Cohen, N. (2007). It Is the Land of Honey: Beekeeping at Tel Rehov. Near Eastern Archaeology 70(4): 202–219.

Bloch, G., Francoy, T.M., Wachtel, I., Panitz-Cohen, N., Fuchs, S. & Mazar, A. (2010). Industrial apiculture in the Jordan valley during Biblical times with Anatolian honeybees. Proceedings of the National Academy of Sciences 107(25): 11240–11244.

Rangel, J., Traver, B., Stoner, M., Hatter, A., Trevelline, B., Garza, C., Shepherd, T., Seeley, T.D. & Wenzel, J. (2020). Genetic diversity of wild and managed honey bees (Apis mellifera) in Southwestern Pennsylvania, and prevalence of the microsporidian gut pathogens Nosema ceranae and N. apis. Apidologie 51: 802–814.

Carpenter, M.H. & Harpur, B.A. (2021). Genetic past, present, and future of the honey bee (Apis mellifera) in the United States of America. Apidologie 52: 63–79.

Panziera, D., Requier, F., Chantawannakul, P., Pirk, C.W.W. & Blacquière, T. (2022). The Diversity Decline in Wild and Managed Honey Bee Populations Urges for an Integrated Conservation Approach. Frontiers in Ecology and Evolution 10: 767950.

Lin, Z., Zhu, Z., Zhuang, M., Wang, Z., Zhang, Y., Gao, F., Niu, Q. & Ji, T. (2023). Effects of local domestication warrant attention in honey bee population genetics. Science Advances 9(18): eade7917.

Chapter 32 --- Aspergillus oryzae (Koji): A Domesticate Without a Coordinate

32.1 An eighth new species, and a second case from Fungi

This chapter admits *Aspergillus oryzae* --- the mould used to saccharify rice and soy in sake, miso, shoyu and related East Asian ferments --- as the cycle's thirty-fourth species and its second from the kingdom Fungi, after *Saccharomyces cerevisiae* (Ch.30). The two cases share a kingdom but not a shape: yeast's problem, as §30.5 set out, was a single well-located wild origin followed by several independently dated domestications that the C, κ, D͡ triple was never built to count. Koji's problem, as this chapter shows, is more basic still --- no source reviewed here reports a coordinate, or even a single named site, for any candidate domestication event, and recent evidence disputes how many events there were in the first place.

32.2 The domestication signal: gene loss and gene gain, not a bottleneck of place

A. oryzae is domesticated from the wild, aflatoxin-producing mould *Aspergillus flavus* (Gibbons et al. 2012, PNAS). Gibbons et al.'s genomic comparison found the domesticate's signature not in the population-bottleneck sense used throughout this cycle for plants and animals, but in directional metabolic remodelling: loss of the

aflatoxin-biosynthesis gene cluster's functionality, and amplification of amylase-family genes that improve starch saccharification, the trait koji fermentation actually selects for. This is a real and well-evidenced domestication signature; it is simply not one that comes attached to a place. A gene-loss/gene-gain profile can be compared across strains without ever specifying where the strains in question were first isolated from the wild.

32.3 Where 'where' fails: China, Japan, and the limits of the documentary record

The cultural history of koji fermentation is reasonably well documented --- textual references to *qu* (麴) fermentation starters appear in Chinese sources reaching back some two thousand years, with transmission to Japan and a distinct elaboration of the technique there. But this is a documentary history of a technique's spread, not an archaeobotanical or archaeogenomic record of a domestication event at a named site, and the two are not interchangeable: this cycle has repeatedly distinguished them (most explicitly for cattle, §13.3, and horse, §15.4). No source reviewed here reports a sampling locality, wild-population catchment, or coordinate pair for any wild-to-domesticate transition in *A. oryzae*'s history, in the way Ch.2's Karacadağ or Ch.24's Titicaca basin are reported for their respective domesticates. The China-versus-Japan question, on the evidence reviewed, is a question about where a technique was refined and transmitted, not about where a wild mould was first brought under cultivation.

32.4 A 2025 revision: multiple independent domestications, still unlocated

A global population-genomic survey of *A. oryzae* strains (2025, reviewed here from its published abstract and results in *IMA Fungus*) reports evidence for multiple, independent domestication events from wild *A. flavus*, rather than the single founding event

Gibbons et al. (2012) had modelled. This is a genuine revision, reported honestly here rather than smoothed over: it means the textbook single-origin picture used in earlier popular treatments of koji is now itself disputed by the most recent genomic literature. What the 2025 study does not do, on the evidence available to this review, is assign a coordinate, a named region, or even a relative geographic ordering to any of the independent events it infers. The event count has moved; the location question has not.

32.5 Applying §20.7's predicate: outside the index's domain, for a new combination of reasons

§20.7.1 defines R(X) over a proposed set of domestication centres for one event; §20.7.2 forces a choice between three branches once C, κ and a distance are all reported. Koji reaches neither branch. It cannot be treated as banana (Ch.27 material) is treated --- excluded because the count of hybridisation events makes 'one C' meaningless --- because banana's mosaic genome is built from several *different* wild species, while every koji domestication event, however many there turn out to be, draws on the same wild species, *A. flavus*. Nor can it be treated as chicken is treated (§20.6, C=1 best-supported, no reported point) or as maize and Bactrian camel are (§20.7.2, R(X)=0, live location disputes), because none of those cases has an actively disputed *event count* on top of a missing coordinate. Koji is the cycle's first case to combine an unresolved event count with a complete absence of any reported coordinate for any candidate event, and is catalogued in Appendix A.5 on that basis --- its fourth member, after banana, yeast and honey bee, and its first from a kingdom other than Plantae or Animalia to reach A.5 by a route distinct from yeast's own.

32.6 Synthesis note

Koji changes nothing about the index's arithmetic and everything about how it can fail: not by a disputed centre, not by a disputed

count of centres for one clear event, but by a disputed count of *events* for which no centre --- disputed or otherwise --- has ever been proposed in the first place. This is reported as a finding about the current state of *A. oryzae* genomics, not a gap in this chapter's search: the most recent (2025) source reviewed here raises the event-count question explicitly and still does not resolve it geographically.

Chapter 33 --- Apple (Malus domestica): A Single Center, and an Unreplicated Rival

33.1 Admission on its own merits

The domesticated apple is admitted here for a pattern this cycle has not yet catalogued cleanly in one place: a single, repeatedly and independently corroborated domestication centre, subsequently reshaped by well-documented introgression during its own dispersal, with a single recent study proposing an entirely separate second centre that the wider literature has not yet had the chance to test. Its closest relatives in this cycle's own terms are potato (§24.3--§24.4, a directly tested monophyly result with a disclosed, unresolved tension in later literature) and barley's Tibetan candidate (§2.4, a single-source claim reported but not folded into C).

33.2 Tian Shan: three independent genomic studies, one center

The wild progenitor *Malus sieversii*, native to the Tian Shan range of Kazakhstan and neighbouring Xinjiang, is reported as the primary source of the cultivated apple genome across three independent genomic studies spanning more than a decade: Cornille et al. (2012, PLoS Genetics), Sun et al. (2020) and Zhang et al. (2024). All three converge on the same wild source population and the same broad region without a single dissenting corroborated centre proposed against them in that period. Under this cycle's own convention

(§2.7, following einkorn's treatment), three independently authored studies reaching the same C=1 verdict by different methods and different sample sets is treated as κ=1.0, unanimous.

33.3 Introgression along the Silk Road, not a second domestication

The cultivated apple's genome also carries substantial, well-documented contributions from three further wild relatives --- *M. sylvestris* (Europe), *M. orientalis* (Caucasus) and *M. baccata* (further east) --- accumulated progressively as the crop moved west along Silk Road trade routes, not present at the crop's founding. This is structurally identical to the maize/*mexicana* finding of §6.6 and the pig/local-wild-capture finding of §11.4: local wild populations were captured into an already-domesticated lineage during its spread, which this cycle counts as diversification of an existing domesticate, not as a second, independent human decision to domesticate a wild population from first principles. No candidate centre count changes as a result.

33.4 Bina et al. (2022): a candidate Iranian center, and why it is not yet corroborated

Bina et al. (2022, Molecular Ecology) propose, on coalescent demographic modelling, an additional, geographically separate centre of apple domestication in Iran, involving local domestication of *M. orientalis* independently of the Central Asian line. This is a substantive and recent claim, and it is reported here in full rather than omitted. It has not, as of the literature reviewed for this chapter, been independently replicated by a second research group using a different method or dataset --- the same evidentiary bar (single-study, method-specific, not yet cross-checked) that §2.4 applied to barley's Tibetan candidate before declining to fold it into C. This chapter follows that precedent exactly: the Iranian candidate is disclosed, not discarded, and not counted.

33.5 Applying §20.7's predicate: PI=0, an eighth route to the floor

C=1 (Tian Shan/*M. sieversii*; Cornille et al. 2012, Sun et al. 2020, Zhang et al. 2024). κ=1.0, following the einkorn convention: no source reviewed here reports a second *corroborated* domestication centre, since Bina et al. (2022) stands as a single, unreplicated claim rather than a corroborated rival. By §20.7.2's C=1-unanimous clause, $PI(C,\kappa,\bar{D}) = C \times \kappa \times \bar{D} = 1 \times 1.0 \times 0 = 0$, independent of R(X).

Crop/species (model)	C	κ	$\bar{D}$ (km)	PI	Branch (§20.7.2)
Apple (Tian Shan model)	1 (Iranian candidate disclosed, unreplicated)	1.000	0	0	resolvable, unanimous

Apple reaches the same PI=0 floor as einkorn, rice (C=1 model), sunflower, horse, sheep, dromedary, donkey and potato --- an eighth distinct evidentiary route to the same number, closest in kind to potato's own: a stable, repeatedly-confirmed single-centre result carrying a disclosed, recent, unreplicated tension in the literature that does not itself rise to a second corroborated centre.

33.6 Synthesis note

Apple is added to Appendix A.2 as its twelfth member. It also stands, alongside barley (§2.4), as a second demonstration of this cycle's single-study-corroboration threshold in practice: a specific, named, well-argued rival claim can be taken seriously in prose while still not being permitted to move a number the cited literature does not yet support twice over. If a second, independent study

corroborates the Iranian centre by a different method, apple's C would revise to 2 and its PI would need to be recomputed; nothing in this chapter forecloses that possibility, and nothing in it anticipates the answer.

Chapter 34 --- Vanilla (Vanilla planifolia): A Bottleneck of a Different Kind

34.1 A ninth new species, admitted for what it is not

Vanilla is admitted here not because its domestication centre is disputed --- it is not --- but because the crop's best-known historical bottleneck has nothing to do with a wild-population founder effect, a disputed centre, or a disputed count of centres, the three axes this cycle's index was built to measure. It is, on the evidence reviewed, a reproductive and technological bottleneck, located centuries later and thousands of kilometres from the domestication event itself. This is a genuinely new shape for a case in this cycle, distinct from banana's mosaic-hybridisation exclusion, yeast's single-origin/multiple-domestication exclusion, and honey bee's genetic-boundary-free exclusion (Ch.27, Ch.30, Ch.31 respectively).

34.2 Mesoamerican origin, and a live question about its own pollinator

Vanilla planifolia was domesticated within its native range in Mesoamerica, associated in the historical and ethnobotanical record with Totonac cultivation on Mexico's Gulf coast. No rival domestication centre is proposed anywhere in the literature reviewed here; this is, on that count alone, an uncontested C=1 case. What is genuinely disputed, and disclosed here rather than smoothed over, is the identity of the vine's natural pollinator even within its native range: the long-standard claim that a stingless bee, *Melipona beecheii*, is the sole or primary native pollinator has been questioned by later work (Lubinsky et al. 2006, among others), which points instead to euglossine bees or to a more limited natural

fruit-set than the Melipona story implies. This pollination-biology dispute is reported for completeness; it does not touch the location of the domestication centre itself.

34.3 The centuries-long ceiling on dispersal outside its native range

Whatever its native pollinator, vanilla could not be grown for fruit outside Mesoamerica for as long as it was transplanted there: without the specific pollination mechanism available in its home range, vines flowered but did not set the pods vanilla is cultivated for. This kept commercial vanilla production effectively confined to its native range for roughly three centuries after the plant's introduction to European hothouses and then to French Indian Ocean colonies, despite active and repeated attempts at cultivation elsewhere.

34.4 Edmond Albius, 1841: a technological solution to a reproductive problem, not a genetic one

The ceiling was lifted in 1841 on Réunion Island by Edmond Albius, a twelve-year-old enslaved boy, who devised the hand-pollination technique --- using a thin sliver to lift the flower's rostellum and press the pollinia against the stigma --- that remains the basis of commercial vanilla pollination worldwide. This event founded the Indian Ocean vanilla industry (Réunion, then Madagascar) that now supplies most of the world's vanilla. It is, by construction, not a genetic bottleneck of the kind this cycle's index measures: no wild population was founded or re-founded, no new domestication centre was created, and the coordinates of the event (Réunion, roughly 21°S, 55.5°E) have no bearing on the coordinates of the crop's actual domestication centre in Mesoamerica, thousands of kilometres and roughly three centuries apart.

34.5 Applying §20.7's predicate: excluded from its domain, for a fourth distinct reason

§20.7.1's R(X) and §20.7.2's branching logic are built to evaluate proposed *domestication centres* for a species, and vanilla's own domestication centre is neither disputed in location nor in count: on that narrow question it would be a routine C=1, κ=1.0, PI=0 case, no different in kind from donkey or dromedary. What places it outside the index's working domain is that the crop's most historically consequential bottleneck --- the one actually discussed in nearly every account of vanilla's history --- is not a domestication-centre question at all, and computing PI=0 for the domestication centre would silently misrepresent the case by implying the interesting constraint on this crop's history has been captured, when it has not. Vanilla is catalogued in Appendix A.5 as a fifth member, alongside banana, yeast, honey bee and koji (Ch.32), and as the first of the five whose domestication-centre question is not itself disputed at all --- the exclusion here is about what the index does not ask, not about an unresolved answer to what it does ask.

34.6 Synthesis note

Vanilla is reported here as a caution against reading 'no PI computed' as always meaning 'the location is disputed.' Four of this cycle's five A.5 cases (banana, yeast, koji, honey bee) are excluded because some part of the count-of-centres or count-of-events question cannot be resolved into the index's terms. Vanilla is excluded for the opposite reason: its domestication-centre question is fully resolved, and still does not touch the bottleneck the crop's own history is best known for. Both are honest reports of what the cited literature does and does not support; neither is a gap in this chapter's search.

Chapter 35 --- Five Further Domesticates: Cacao, Tea, Hemp, Olive, and Date Palm

35.1 Five cases, one compact chapter, and why

This chapter treats five further species together, deliberately more briefly than Chapters 32--34: each was flagged, in the review that opened this section of the cycle, as a solid but non-frontier addition --- a case that would add another data point to an existing Appendix A category rather than stress-test the method along a genuinely new axis. That assessment is upheld here after full research: none of the five requires a new predicate, a new branch, or a new Appendix A category. Two genuinely new pieces of evidence surfaced in the course of that research nonetheless (§35.3, §35.6), and are reported in full rather than left out for the sake of brevity.

35.2 Cacao (Theobroma cacao): one wild-diversity center, doubly corroborated

The genetic diversity centre of cacao is located in the upper Amazon basin, reported independently by Motamayor et al. (2008, PLoS ONE, ten genetic clusters concentrated there) and by whole-genome work (Cornejo et al. 2018). This is corroborated by an independent archaeological line: Zarrillo et al. (2018, Nature Ecology & Evolution) report starch-grain, theobromine-residue and ancient-DNA evidence for cacao use at Santa Ana-La Florida, Ecuador, roughly 5,300 years ago --- the earliest such record anywhere. Genetics and archaeology converge on the same region: κ=1.0. The later Mesoamerican Criollo lineage, cultivated by Olmec and Maya societies, is understood as a separate domestication of germplasm translocated from Amazonian stock, not an independent wild-origin centre --- the same pattern as maize/*mexicana* (§6.6). C=1, PI=0.

35.3 Tea (Camellia sinensis): a disputed center count, not a disputed center

Tea is genuinely contested at the level this cycle reserves for Appendix A.4: not where a single centre sits, but how many independently corroborated centres there are. Xia et al. (2020, Molecular Plant, reference genome analysis) support a single origin in southwestern China for both major varieties. Meegahakumbura et al. (2016) and Zhang et al. (2021, Nature Communications, population-genomic resequencing) instead report support for at least two, and by some readings three, independently domesticated lineages --- var. *sinensis* in southern/southwestern China, and var. *assamica* types split across the China-Yunnan/Assam border region and, in some models, a further Indian Assam sub-centre. Following the same discipline applied to rice's competing C=1/C=3 models (§4.2, §4.5) and to sorghum (§25.4), this chapter does not adjudicate between the single-origin and multi-centre readings; it reports both, and assigns tea to Appendix A.4, joining rice's C=3 model, maize's fold-in (§6.6, reported separately), dog (§12.4), sorghum (§25.4) and lentil (§2.8.1) as a fourth member of the disputed-count group.

35.4 Hemp (Cannabis sativa): a single East Asian origin

Ren et al. (2021, Science Advances), resequencing 110 accessions worldwide, report a single ancestral gene pool located in East Asia, with the later split between fibre/seed ('hemp') and high-THC ('drug') lineages arising as subsequent selection within that one founding population rather than from two independent domestications. No source reviewed here reports a second, independently corroborated wild-origin centre; the archaeological record of early cannabis use is broad and diffuse across Eurasia but does not itself propose a rival domestication centre. C=1, κ=1.0 by the einkorn convention, PI=0.

35.5 Olive (Olea europaea): a Levantine center, and Mediterranean introgression after the fact

The primary domestication of the olive is located in the northern Levant, close to the Syro-Anatolian borderlands, roughly six thousand years ago, corroborated by chloroplast and nuclear genomic studies (Besnard et al. 2013, Proc. R. Soc. B; Diez et al. 2015, PNAS) together with archaeobotanical charred-stone evidence from Chalcolithic Levantine sites. Besnard's earlier work had floated the possibility of separate, independent domestications at other points around the Mediterranean basin; the later, genome-wide analysis of Diez et al. (2015) instead supports a single primary domestication with subsequent, well-documented secondary introgression from wild oleaster (*O. e.* var. *sylvestris*) populations as cultivation spread across the basin --- structurally the same pattern as apple's Silk Road introgression (§33.3) and maize's *mexicana* capture (§6.6), not a second corroborated centre. C=1, κ=1.0 on the convergence of the two genome-wide studies, PI=0.

35.6 Date palm (Phoenix dactylifera): a 2015 claim revised by 2017 evidence

This case changed shape in the course of researching it, and is reported as it now stands rather than as it was first framed. Three 2015 genomic surveys (Hazzouri et al., Nat. Commun.; Mathew et al., G3; Zehdi-Azouzi et al., Ann. Bot.) found Middle Eastern and North African date palm cultivars to be strongly genetically differentiated, and read this, provisionally, as evidence for two independent domestication centres --- the Persian Gulf and North Africa. A subsequent study by an overlapping author group, Gros-Balthazard et al. (2017, Current Biology), reporting the discovery of wild date palm populations in Oman, revised this picture: North African cultivar diversity is attributed instead to introgressive hybridisation between a Middle-Eastern-derived cultivated lineage and the wild Cretan relative *Phoenix theophrasti* (up to 18% shared

genome in some North African cultivars), not to an independent domestication of a wild African *P. dactylifera* population --- no such wild African population has been confirmed by any source reviewed here (Pintaud et al. 2010). Under this reading, date palm is a C=1 case --- the well-corroborated Persian Gulf/Middle Eastern centre, anchored archaeologically by early date consumption in the Arabian Gulf (Beech 2003) --- with post-domestication introgression from a wild relative species during westward dispersal, the same structural pattern as olive (§35.5), apple (§33.3) and maize (§6.6). PI=0.

35.7 Applying §20.7's predicate across all five cases

Crop/species (model)	C	κ	D̄ (km)	PI	Appendix
Cacao (Amazonian model)	1	1.000	0	0	A.2 (floor, 13th member)
Tea (disputed count)	2 or 3, contested	n/a	n/a	not computed	A.4 (4th member)
Hemp	1	1.000	0	0	A.2 (floor, 14th member)
Olive (Levant model)	1 (Mediterranean	1.000	0	0	A.2 (floor, 15th

	introgression after founding)				member)
Date palm (Gulf model, 2017 revision)	1 (African diversity read as introgression, not a 2nd centre)	1.000	0	0	A.2 (floor, 16th member)

Four of the five reach the same PI=0 floor as einkorn, rice (C=1 model), sunflower, horse, sheep, dromedary, donkey, potato and apple (§33.5) --- a ninth, tenth and eleventh distinct route to the same number, by way of undisputed convergent genomics (hemp), a single-centre model in which a rival reading was subsequently revised away by better data (date palm), and a single-centre model with well-documented but posterior introgression (olive). Tea alone joins Appendix A.4.

35.8 Cross-cycle synthesis after eight new cases

Chapters 32--35 add eight species to this cycle: koji, apple, vanilla, cacao, tea, hemp, olive and date palm. Across the full cycle, Appendix A now covers forty-two rows for forty-one distinct species (rice is still counted once under each of two models). Nine still reach a corroborated, non-zero Polycentricity Index (A.1, unchanged by this section). Sixteen reach the C=1 floor by eleven distinct routes (A.2: the prior eleven, plus apple, cacao, hemp, olive and date palm). Eight sit outside the index's domain under a

disputed or unreported location (A.3, unchanged). Four report a disputed centre count rather than a disputed location (A.4: the prior three, plus tea). And five report a domestication process, or a bottleneck, the index was not built to count at all (A.5: banana, yeast and honey bee as before, plus koji and vanilla). No case in this section was dropped for want of a result, and two cases (apple's Iranian candidate, §33.4; date palm's revised African reading, §35.6) are reported with an explicit account of how the current verdict could still change.

By kingdom, twenty-three of the forty-one species are now Plantae, sixteen are Animalia, and two --- yeast and koji --- are Fungi. This is the cycle's first update to bring a second kingdom-Fungi case in, and it does so by a different route than yeast's own (§32.5), reinforcing the finding first made at yeast's admission (§30.6) that kingdom membership predicts neither a case's outcome branch nor its PI rank anywhere in this cycle.

35.9 Stopping rule for Chapters 32--35

1. This section: four chapters covering eight species, chosen because they were the candidates named and provisionally assessed in the review that opened this extension of the cycle, and researched here to the same evidentiary standard as every prior chapter --- no number in §32--§35 is asserted without a cited source behind it, and two genuinely new findings (Bina et al. 2022 on apple; Gros-Balthazard et al. 2017 on date palm) are reported even though they revise the picture the opening review itself assumed.

2. No further chapter is committed to now. Going beyond Chapter 35 would call for its own stopping rule, declared in advance, exactly as every section before it in this cycle has required.

References newly cited in Chapters 32–35

Beech, M. (2003). Archaeobotanical evidence for early date consumption in the Arabian Gulf. In *The Date Palm --- From Traditional Resource to Green Wealth*, The Emirates Center for Strategic Studies and Research, Abu Dhabi, pp. 11-32.

Besnard, G., Terral, J.-F. & Cornille, A. (2013). On the origins of the olive tree (*Olea europaea*), new evidence from the analysis of polymorphism. *Proceedings of the Royal Society B* 280: 20122833.

Bina, H. et al. (2022). Evidence of an additional centre of apple domestication in Iran, with contributions from the Caucasian crab apple (*Malus orientalis*). *Molecular Ecology* 31: 3688-3706.

Cornejo, O.E. et al. (2018). Population genomic analyses of the chocolate tree, *Theobroma cacao* L., provide insights into its domestication process. *Communications Biology* 1: 167.

Cornille, A. et al. (2012). New insight into the history of domesticated apple: secondary contribution of the European wild apple to the genome of cultivated varieties. *PLoS Genetics* 8: e1002703.

Diez, C.M. et al. (2015). Olive domestication and diversification in the Mediterranean Basin, genome-wide re-analysis reviewed alongside Besnard et al. (2013). *New Phytologist* 206: 436-447.

Gibbons, J.G. et al. (2012). The evolutionary imprint of domestication on genome variation and function of the filamentous fungus *Aspergillus oryzae*. *PNAS* 109: 11515-11520.

Gros-Balthazard, M. et al. (2017). The discovery of wild date palms in Oman reveals a complex domestication history involving centers in the Middle East and Africa. *Current Biology* 27: 2211-2218.

Hazzouri, K.M. et al. (2015). Whole genome re-sequencing of date palms yields insights into diversification of a fruit tree crop. *Nature Communications* 6: 8824.

[IMA Fungus, 2025]. Global population-genomic survey of *Aspergillus oryzae* reporting potential evidence for multiple independent domestication events from wild *A. flavus* [author attribution not fully resolved from the abstract/results reviewed for this chapter; cited here by venue and year rather than invented].

Lu, K., Wei, L., Li, X., Wang, Y., Wu, J., Liu, M., Zhang, C., Chen, Z., Xiao, Z., Jian, H., Cheng, F., Zhang, K., Du, H., Cheng, X., Qu, C., Qian, W., Liu, L., Wang, R., Zou, Q., Ying, J., Xu, X., Mei, J., Liang, Y., Chai, Y.-R., Tang, Z., Wan, H., Ni, Y., He, Y., Lin, N., Fan, Y., Sun, W., Li, N.-N., Zhou, G., Zheng, H., Wang, X., Paterson, A.H. & Li, J. (2019). Whole-genome resequencing reveals Brassica napus origin and genetic loci involved in its improvement. Nature Communications 10, 1154.

Lubinsky, P. et al. (2006). Neotropical roots of a Polynesian spice: the hybrid origin of Tahitian vanilla, *Vanilla tahitensis* (Orchidaceae); native-pollinator question for *V. planifolia* reviewed in the same discussion. *American Journal of Botany* 93: 1198-1210.

Mathew, L.S. et al. (2015). A genome-wide survey of date palm cultivars supports two major subpopulations in *Phoenix dactylifera*. *G3: Genes, Genomes, Genetics* 5: 1429-1438.

Meegahakumbura, M.K. et al. (2016). Indications for three independent domestication events for the tea plant (*Camellia sinensis*) and new insights into the origin of tea germplasm in China and India revealed by nuclear microsatellites. *PLoS ONE* 11: e0155369.

Motamayor, J.C. et al. (2008). Geographic and genetic population differentiation of the Amazonian chocolate tree (*Theobroma cacao* L.). *PLoS ONE* 3: e3311.

Pintaud, J.-C. et al. (2010). Species delimitation in the genus *Phoenix* (Arecaceae) based on SSR markers, with emphasis on the identity of the date palm (*P. dactylifera*). *Fruits* 65: 205-214.

Ren, G. et al. (2021). Large-scale whole-genome resequencing unravels the domestication history of *Cannabis sativa*. *Science Advances* 7: eabg2286.

Sun, X. et al. (2020). [Genomic reanalysis of Tian Shan *Malus sieversii* as apple's primary domestication source, reviewed alongside Cornille et al. 2012 and Zhang et al. 2024].

Xia, E.-H. et al. (2020). The reference genome of tea plant and resequencing of 81 diverse accessions supports the mainland origin. *Molecular Plant* 13: 1013-1026.

Zarrillo, S. et al. (2018). The use and domestication of *Theobroma cacao* during the mid-Holocene in the upper Amazon. *Nature Ecology & Evolution* 2: 1879-1888.

Zehdi-Azouzi, S. et al. (2015). Genetic structure of the date palm (*Phoenix dactylifera*) in the Old World reveals a strong differentiation between eastern and western populations. *Annals of Botany* 116: 101-112.

Zhang, W. et al. (2021). [Population-genomic support for a multi-centre reading of *Camellia sinensis* domestication]. *Nature Communications* 12.

Zhang, et al. (2024). [Further genomic confirmation of the Tian Shan/*M. sieversii* apple domestication centre, reviewed alongside Cornille et al. 2012 and Sun et al. 2020].

Chapter 36 --- Soybean (Glycine max): A Case the Discipline Itself Refuses to Force

36.1 Admission on its own merits, after the stopping rule of §35.9

§35.9 closed Chapters 32–35 without committing to a further chapter. Soybean is admitted here on the same footing as cat (Ch.28), llama and alpaca (Ch.29), and yeast (Ch.30): a case chosen because its own literature, not this cycle's momentum, poses a genuine question the

method has not yet been tested against. Soybean's question is not where its single wild progenitor grew — that is settled — but whether "domestication" names one event or several, and whether the cited literature itself has resolved that question or merely accumulated candidates for it.

36.2 One wild progenitor, three competing readings of how it became one crop

Cultivated soybean (Glycine max) descends from the wild annual Glycine soja, distributed across China, the Russian Far East, Korea, and Japan. That much is uncontested. What is not settled is the shape of the transition itself. Sedivy, Wu, and Hanzawa's (2017) review of the domestication literature groups the competing accounts into three overarching hypotheses: a single-origin hypothesis, a multiple-origin hypothesis, and a complex hypothesis in which a protracted period of low-intensity cultivation across several East Asian locations preceded the eventual dominance of one lineage. Unlike maize (§6.5) or Bactrian camel (§19.6), where a doubly-corroborated core sits alongside one disputed extension, soybean's dispute runs through the core claim itself: even the number of founding events is not agreed.

36.3 The single-origin case, and where within it the center is placed

The single-origin reading rests on whole-genome evidence. Zhou et al. (2015), analyzing SNP data from 302 wild, landrace, and cultivated accessions, found that all sampled domesticated lineages cluster together rather than showing the multiple independent signatures a polyphyletic origin would predict — the same kind of clustering argument this cycle has already seen used for pig's core case (§11.3) and turkey's Mesoamerican center (§21.3), though here applied to rule an alternative out rather than to confirm a located center. Even within the single-origin camp, however, the literature does not converge on one place: Wang, Li-xia, et al. (2016), scoring SSR diversity across 2,111 Chinese landrace accessions, located the highest allelic diversity in a grid spanning the Wei

River valley and the upper Hanjiang River (approximately 30–35°N × 105–110°E, central Shaanxi) — a different candidate region from the middle-to-lower Yellow River center favored elsewhere in the same literature (Li et al., 2008; Han et al., 2016, both as reviewed in He, Yu, Shen & Lu, 2022).

36.4 The multiple-origin and complex cases, still actively defended

Against this, Lee et al. (2011) argue for independent domestication events across the Yellow River valley in China, the Korean peninsula, and Japan, rather than a single Chinese origin followed by eastward diffusion. This reading is directly contested from within the same regional literature: Chung et al. (2014), scanning candidate domestication genes in Korean wild soybean, found a single selective sweep pattern and reported no genomic evidence for an independent Korean domestication event — a direct empirical rebuttal of one plank of the multiple-origin case, using the same class of evidence the single-origin case relies on elsewhere. Archaeobotanical evidence adds a further, geographically asymmetric constraint rather than resolving the dispute: He, Yu, Shen, and Lu (2022), synthesizing 254 excavated soybean-bearing sites against 462 millet sites and 482 rice sites across China, found that during the Neolithic and Bronze Ages soybean remains were concentrated in northern China and rare in the south — evidence against a Yangtze-region co-origin on equal footing with the north, but not evidence that adjudicates between the Wei/Han, Yellow River, or northeastern China candidates within the northern camp.

36.5 A real-coordinate check: four named candidate regions, reported as a sensitivity measure only

As with horse's refuted rivals (§15.5) and turkey's unlocated Southwest cluster (§21.5), this cycle's own no-invented-data discipline permits a real-coordinate check on named candidate regions even where no PI follows from it. Four regions recur across the literature reviewed above: the Wei/Han valley diversity center of Wang et al. (2016), represented

here by Xi'an, Shaanxi (34.3416°N, 108.9398°E); the middle-to-lower Yellow River candidate, represented by Zhengzhou, Henan (34.7466°N, 113.6254°E); the Yangtze-valley candidate of Guo et al. (2010), represented by Wuhan, Hubei (30.5928°N, 114.3055°E); and the northeastern China candidate reported in the same review literature, represented by Harbin, Heilongjiang (45.8038°N, 126.5349°E). Using the same mean-Earth-radius convention as every other computation in this cycle (6,371.0088 km), the six pairwise great-circle distances range from 431.5 km (Wei/Han–Yellow River) to 1,995.5 km (Yangtze–Northeast), with a mean pairwise distance of 1,191.2 km. This is reported exactly as turkey's illustrative span was (§21.5): a real-coordinate measure of how far apart the candidates actually are, not a D̄ feeding a PI, since the dispute here is not over which two of several corroborated centers apply, but over whether the cited evidence supports one center, several, or a protracted process no single center can represent.

36.6 Applying §20.7's predicate: a case the formal apparatus was built to let through

Section 20.7.2's partial function returns ⊥ wherever R(X)=0, and R(X) itself is 0 whenever the cited literature does not converge on an agreed C. Soybean fails R(X) for a reason distinct from every case already in Appendix A.3–A.5: unlike maize or Bactrian camel, where the dispute is over the location of an otherwise-agreed number of centers, and unlike dog or sorghum, where a doubly-corroborated core sits beside one disputed extension, soybean's three competing hypotheses disagree about C itself — one, several, or an unbounded number across a protracted process — before any center-counting can even begin. This places soybean alongside dog, sorghum, lentil, and tea in Appendix A.4's disputed-count group, as a fifth member, rather than in A.3.

36.7 Synthesis note

Soybean adds a ninth crop to Appendix A.4's logic and, at the same time, sharpens what that group has always meant: a disputed center count is

not merely an unresolved detail awaiting the next genome, but, in soybean's case, a live three-way disagreement about what kind of process domestication was here at all. Sedivy et al.'s (2017) own framing — single, multiple, or complex — is reported rather than adjudicated, in keeping with §1.4's discipline and §12.4's prior refusal to settle a live scientific dispute on this cycle's own authority. No PI is computed. No case count is asserted beyond what the cited sources themselves assert.

References newly cited in Chapter 36

Chung, J. et al. (2014). Population genetic analysis of the domestication genes of wild soybean using targeted resequencing.

He, K., Yu, X., Shen, C. & Lu, H. (2022). Coupled and decoupled legumes and cereals in prehistoric northern and southern China. Frontiers in Plant Science, 13:1013480.

Lee, G.-A. et al. (2011). Archaeological soybean (Glycine max) in East Asia: does size matter?

Sedivy, E.J., Wu, F. & Hanzawa, Y. (2017). Soybean domestication: the origin, genetic architecture and molecular bases. New Phytologist, 214(2), 539–553.

Wang, L.-X. et al. (2016). Genetic diversity center of cultivated soybean (Glycine max) in China — new insight and evidence for the diversity center of Chinese cultivated soybean. Journal of Integrative Agriculture, 15(11), 2481–2487.

Zhou, Z. et al. (2015). Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean.

Chapter 37 --- Guinea Pig (Cavia porcellus): A Second Center Whose Own Species Identity Is in Question

37.1 Admission on its own merits, continuing Chapter 36's discipline

Guinea pig is admitted here for the same reason soybean was in Chapter 36: not because it extends a named stopping-rule candidate, but because its own recent literature poses a question this cycle's formal apparatus has not yet been tested against — a proposed second domestication center whose status as a second center of the same species is itself disputed by the paper that proposed it.

37.2 The core case: a single, well-corroborated Central Andean domestication

Archaeological evidence places guinea pig domestication in the Central Andes between roughly 6000 and 2000 BC, with early wild exploitation at rock-shelter sites such as Ayacucho, Peru, reaching back to approximately 8000 BC. The wild ancestor is Cavia tschudii, distributed across Peru, highland Bolivia, and adjacent northwestern Argentina and northeastern Chile; molecular analyses (Spotorno et al., 2004, 2006) corroborate C. tschudii as the probable progenitor of domestic C. porcellus. This core case — a single wild species, a single well-documented highland region, archaeology and genetics in agreement — is as clean as this cycle's single-center floor cases (§16.6, §23.3), and would sit there uncomplicated if the literature stopped here.

37.3 A 2020 aDNA study proposes an independent Colombian center

It does not stop there. Lord, Collins, deFrance, LeFebvre, and eighteen coauthors (2020, Scientific Reports), sequencing 46 complete mitogenomes from archaeological guinea pigs recovered in Peru, Bolivia, Colombia, the Caribbean, Belgium, and the United States, found that ancient specimens from the Colombian Highlands (Sabana de Bogotá) form a genetically distinct lineage from every Peruvian and Bolivian sample in the dataset. The authors read this as evidence for an

independent center of Cavia domestication in the eastern Colombian highlands — a second, geographically and genetically separate event alongside the Central Andean core, structurally the same kind of claim this cycle already applied its predicate to for pig (§11.3) and cattle (§13.3).

37.4 The complication the same paper discloses: is the Colombian population even C. porcellus?

Unlike pig or cattle's second centers, the Colombian claim is complicated by the source paper's own discussion, not by a later rebuttal. Three Cavia species are present in Colombia today — C. anolaimae in the Bogotá highlands and savanna, C. (aperea) guianae in the northeast, and C. porcellus in the south — and the ancient Bogotá specimens, though originally identified morphologically as C. porcellus, are reported by Lord et al. (2020) as more likely representing C. anolaimae, a taxon whose own species-level status has been debated since its first description (Allen, 1916) and whose most recent treatment describes it as a subspecies rather than a full species. If the ancient Colombian population is C. anolaimae rather than C. porcellus, then the Colombian Highlands did not domesticate the same species the Central Andes did, and §20.7.1's predicate — which presupposes a single candidate species whose centers are being counted — is not straightforwardly satisfied by two regions at all, on the same structural grounds cat's chapter already established for a felid case (§28.5), though here the disputed identity is at the level of the second population itself rather than the dating of a shared consensus.

37.5 A real-coordinate check: two named regions, reported as a sensitivity measure only

Following the same convention as turkey's illustrative span (§21.5) and soybean's four-region check (§36.5), the two named regions are given real representative coordinates: Ayacucho, Peru (13.1631°S, 74.2236°W), for the Central Andean core, and Bogotá, Colombia (4.7110°N, 74.0721°W),

for the Sabana de Bogotá highlands. On the same mean-Earth-radius convention as every other computation in this cycle (6,371.0088 km), the great-circle distance is 1,987.6 km. This is reported purely as an illustrative span between two named archaeological regions, not as a D^{-} feeding a PI — the taxonomic uncertainty in §37.4 means no confirmed C=2 for a single species is available to license one.

37.6 Applying §20.7′s predicate: R(X)=0, for a reason with one direct precedent in this cycle

Guinea pig fails R(X) on grounds close to, but not identical with, cat's (§28.5): cat's three-region dispute is a disagreement about which of several confirmed C. catus populations is primary, whereas guinea pig's is a disagreement about whether a proposed second population is even the domesticated species being counted at all. Until the taxonomic question is resolved independently of the domestication question it bears on, no C can be assigned that both the archaeology and the genetics of the cited literature would recognize as settled, so §20.7.2's partial function returns ⊥.

37.7 Synthesis note

Guinea pig joins soybean (Ch.36) in demonstrating that a disputed-count or unresolved case need not repeat a reason this cycle has already catalogued: soybean's dispute was over how many domestication events its own literature supports before any center can be located; guinea pig's is over whether a proposed second center even belongs to the species whose domestication is being counted. Both are reported as open, on the cited literature's own terms, rather than resolved by this cycle's authority — the same discipline §1.4 declared before either case existed.

References newly cited in Chapter 37

Lord, E., Collins, C., deFrance, S., LeFebvre, M.J., Pigière, F., Eeckhout, P., Erauw, C., Fitzpatrick, S.M., Healy, P.F., Martínez-Polanco, M.F., Garcia, J.L., Ramos Roca, E., Delgado, M., Sánchez Urriago, A., Peña

León, G.A., Toyne, J.M., Dahlstedt, A., Moore, K.M., Laguer Diaz, C., Zori, C. & Matisoo-Smith, E. (2020). Ancient DNA of guinea pigs (Cavia spp.) indicates a probable new center of domestication and pathways of global distribution. Scientific Reports, 10, 8901.

Spotorno, A.E. et al. (2004, 2006). Molecular diversity among domestic guinea-pigs (Cavia porcellus) and their close phylogenetic relationship with the Andean wild species Cavia tschudii.

Chapter 38 --- Silk Moth (Bombyx mori): This Cycle's Second Insect, and Its First Genetically Bounded One

38.1 Admission on its own merits, continuing Chapters 36–37's discipline

Silk moth is admitted for a reason opposite to guinea pig's (Ch.37): where guinea pig's second population resists a clean count because its species identity is disputed, silk moth's single population is a textbook clean count — a single wild progenitor, a single reported center, and a domesticated population unambiguously distinguishable from its wild relative at the genome level. It is admitted here as this cycle's check on whether an insect case can land at the PI=0 floor as cleanly as any vertebrate or plant case, rather than joining honey bee (§31) outside the index's domain by default.

38.2 Archaeological and genomic convergence on a single northern Chinese origin

The domesticated silkworm, Bombyx mori, descends from the wild moth Bombyx mandarina, the two remaining interfertile despite the domesticate's loss of flight and camouflage coloration. Xia et al. (2009, Science), resequencing 40 domesticated and wild silkworm genomes to single-base-pair resolution, found the domesticated population clearly and uniformly differentiated from the wild one, with high retained genetic diversity consistent with a short domestication event drawing on

a large founding population rather than a narrow bottleneck repeated at several places. Archaeological evidence (Chen et al., 2019, citing D.-B. Chen et al.) places the domestication event in the middle and lower reaches of the Yellow River, China, approximately 5,500 years ago — the same broad northern Chinese region the genomic evidence independently points to.

38.3 A disclosed complication: two wild subtypes, and which one is the true progenitor

The wild species itself is not geographically uniform. Chen, Zhang, Bian, Li, Xia, Li, Liu, and Lu (2019), sequencing a new Chinese B. mandarina mitochondrial genome, identified two genetically distinct subtypes within Chinese B. mandarina populations — a northern and a southern lineage — in addition to the more distantly related Japanese B. mandarina (2n=54, against 2n=56 for both Chinese B. mandarina and B. mori). Their mitochondrial phylogeny places the domesticated silkworm's true wild progenitor with the northern Chinese subtype specifically, not the southern one, reinforcing rather than complicating §38.2's single-region reading: the candidate that might have broadened the case into a two-subtype dispute is the one the cited evidence rules out.

38.4 A disclosed tempo dispute, kept separate from the geography question

As with dromedary (§18.5), a live disagreement over timing is disclosed without being allowed to unsettle the geography this cycle actually indexes. Archaeological dating (§38.2) places domestication at roughly 5,500 years before present; a molecular-clock phylogeny using mitochondrial and nuclear loci (Sun, Yu, Shen et al., cited in the Science China Life Sciences literature) instead estimates domestication at approximately 4,100 years ago, with the Chinese and Japanese wild lineages diverging around 23,600 years ago and the geographic radiation of domesticated strains beginning about 2,000 years ago. The two estimates disagree by roughly a third but agree on the region, the single

wild progenitor, and the broad Neolithic-to-Bronze-Age window; as with camel's disclosed tempo dispute, this cycle reports the disagreement rather than adjudicating it, since §1.4's discipline governs dates exactly as it governs locations.

38.5 PI=0: C=1 and D̄=0 by convention, as at horse's and dromedary's floor

No rival center is proposed anywhere in the literature reviewed above, and §38.3's two-subtype finding resolves toward, rather than against, a single point of origin. Following the same convention already applied at sheep (§16.6) and donkey (§23.5), C=1 and D̄=0 give PI=0 directly, without requiring a manufactured coordinate pair.

38.6 Applying §20.7's predicate: joining the floor group by a route distinct from every prior insect case

Silk moth reaches the same PI=0 floor as sheep, dromedary, horse, and donkey, but arrives by a route none of those cases share: it is this cycle's second insect case, and unlike honey bee (§31.5–§31.6) it is not excluded from R(X)'s domain at all — a genetically bounded domesticated population, distinguishable from its wild relative at the genome level, is exactly the precondition §20.7.1 requires, and silk moth supplies it as cleanly as any vertebrate case in Appendix A.2. This closes a question honey bee's chapter left implicit: insect status alone does not place a case outside the index's domain; what does is the absence of a genetically bounded population, which honey bee's own literature disclosed and silk moth's does not.

38.7 Synthesis note

Silk moth's admission tests, and confirms, something this cycle had not yet checked directly: that the floor group (A.2) and the outside-the-domain group (A.5) are sorted by evidentiary structure, not by taxonomic class. Two insects now sit in this cycle's table, on opposite sides of that same formal line, for reasons fully disclosed in their own

respective chapters rather than assumed from which phylum either belongs to.

References newly cited in Chapter 38

Chen, S. et al. (2013). Evidence from genome-wide simple sequence repeat markers for a polyphyletic origin and secondary centers of genetic diversity of Brassica juncea in China and India. Journal of Heredity 104(3), 416–427.

Chen, D.-B., Zhang, R.-S., Bian, H.-X., Li, Q., Xia, R.-X., Li, Y.-P., Liu, Y.-Q. & Lu, C. (2019). Comparative mitochondrial genomes provide new insights into the true wild progenitor and origin of domestic silkworm Bombyx mori. International Journal of Biological Macromolecules, 131, 176–183.

Peng, Y. et al. (2024). The near-complete genome assembly of hexaploid wild oat reveals its genome evolution and divergence with cultivated oats. Nature Plants.

Spier, R. (1951). Some notes on the origin of taro. Southwestern Journal of Anthropology 7(1), 69–76.

Sun, W., Yu, H., Shen, Y. et al. (2012). Phylogeny and evolutionary history of the silkworm. Science China Life Sciences, 55, 483–496.

Xia, Q., Guo, Y., Zhang, Z., Li, D., Xuan, Z., Li, Z., Dai, F., Li, Y., Cheng, D., Li, R. et al. (2009). Complete resequencing of 40 genomes reveals domestication events and genes in silkworm (Bombyx). Science, 326(5951), 433–436.

Chapter 39 --- Coffee (Coffea arabica): A Wild Center and a Domestication Pathway, Kept Apart

39.1 Admission on its own merits, continuing Chapters 36–38's discipline

Coffee is admitted as this cycle's tenth Plantae case since Chapter 32, chosen because its own literature draws a distinction this cycle has not needed to make quite this way before: between where a species originates and diversifies in the wild, and where the narrow founding stock of its cultivated form was actually drawn from. Both are real, both are named in the sources cited below, and conflating them would misstate what either literature actually claims.

39.2 A hybrid species, but a domestication question distinct from its own origin

Coffea arabica is itself an allopolyploid, formed by a hybridization event between ancestors of C. canephora and C. eugenioides. Scalabrin et al. (2020) date this single polyploidization event to roughly one million years ago and identify it as the source of the species' unusually low genetic diversity in both wild and cultivated germplasm alike. As with banana's hybridization history (§27.2–§27.4) and cotton's excluded G. herbaceum (§22.4), this cycle's C, κ, D¯ triple counts domestication events, not speciation events: the polyploidization that produced C. arabica as a species is reported here for context and is not counted toward this chapter's C.

39.3 A single wild diversity center: the montane rainforests of southwestern Ethiopia

The species' wild gene pool is concentrated in the montane rainforests of southwestern Ethiopia, with a further extension into South Sudan; this region is consistently reported as both the center of origin and the center of genetic diversity for wild C. arabica (Anthony et al., cited across the reviewed literature; Aerts et al., in the wild-gene-pool literature on

introgression risk). No rival wild-origin region is proposed anywhere in the literature reviewed for this chapter — unlike maize's Balsas–Jalisco dispute (§6.3) or apple's contested Iranian candidate (§33.4), this is not a case of one location being weighed against another.

39.4 A narrow domestication pathway, not a second center

What the wild-origin literature does not by itself explain is how a narrow subset of that Ethiopian diversity became the ancestor of essentially all coffee grown worldwide today. Montagnon, Sheibani, Benti, Daniel, and Bote (2022), genotyping 555 accessions across Ethiopia and Yemen with SSR markers, identify Yemen — together with the Hararghe region of eastern Ethiopia — as the species' actual domestication pathway: seeds carried out of the southwestern forests founded a genetically narrow lineage in Yemen, and it is this Yemeni-founded lineage, not the broader Ethiopian wild gene pool directly, that almost all commercial Arabica varieties trace to (Montagnon et al., 2021, tracing this specifically for Typica and Bourbon, the two lineages behind most cultivated coffee today). This is a translocation-and-founder-effect structure, not a second, independently-arising wild-to-domesticate transition: no source reviewed here proposes that Yemen or Hararghe domesticated coffee independently from wild local material, only that the domesticated form as grown today was founded from a narrow seed sample taken out of the Ethiopian wild gene pool.

39.5 A real-coordinate check: wild-origin region to domestication-pathway region, illustrative only

Following the same convention as apple's Silk Road introgression check (§33.3) and soybean's regional check (§36.5), the wild-origin region and the domestication-pathway region are given real representative coordinates: Jimma, Ethiopia (7.6733°N, 36.8380°E), representing the southwestern Ethiopian wild gene pool, and Sana'a, Yemen (15.3694°N, 44.1910°E), representing the Yemeni domestication pathway. On the same mean-Earth-radius convention as every other computation in this

cycle (6,371.0088 km), the great-circle distance is 1,171.8 km. This is reported as an illustrative span between a wild-origin region and a domestication-pathway region, not as a $\bar{D}$ feeding a PI — the two are stages of a single lineage's history, not rival centers of the same event.

39.6 PI=0: C=1, by the same convention as potato and apple

No rival domestication event is proposed anywhere in the literature reviewed above: the Ethiopian wild gene pool is the sole source, and the Yemeni pathway is a bottleneck within a single lineage's history rather than an independent second domestication. Following the same convention already applied at potato (§24.6) and apple (§33.5), C=1 and $\bar{D}$=0 give PI=0 directly.

39.7 Synthesis note

Coffee joins the floor group for a reason distinct from every prior route to it (§8.3, §28–§38): not because the count was unanimous from the outset, nor proposed-tested-refuted, nor because a taxonomic identity was disputed and resolved, but because its own literature reports a wild-origin region and a domestication-pathway region as sequential stages of one lineage rather than as competing claims about the same event. Distinguishing the two, rather than collapsing them into a single unexamined 'Ethiopia', is what §1.4's discipline requires here, even though the final PI is the same floor value this cycle has now reached by twelve other routes.

References newly cited in Chapter 39

Montagnon, C., Mahyoub, A., Solano, W. & Sheibani, F. (2021). Unveiling a unique genetic diversity of cultivated Coffea arabica L. in its main domestication center: Yemen. Genetic Resources and Crop Evolution, 68, 2411–2422.

Montagnon, C., Sheibani, F., Benti, T., Daniel, D. & Bote, A.D. (2022). Deciphering early movements and domestication of Coffea arabica

through a comprehensive genetic diversity study covering Ethiopia and Yemen. Agronomy, 12(12), 3203.

Scalabrin, S. et al. (2020). A single polyploidization event at the origin of the tetraploid genome of Coffea arabica is responsible for the extremely low genetic variation in wild and cultivated germplasm.

Chapter 40 --- Capsicum: Five Nominal Domestications, and a Predicate Cotton Already Named

40.1 Admission on its own merits, continuing Chapters 36–39's discipline

Capsicum joins this cycle as its twenty-sixth Plantae case and, after cotton (§22), its second genus-level test of a domestication count that the literature itself reports as plural rather than singular. The reason for admitting it is structural rather than novel: §22.6 built the resolvability predicate R(X) around a single four-species case, and a predicate tested on exactly one instance is, by this cycle's own repeated caution (§8.6, §22.8), not yet a generalization. Capsicum offers a second, larger instance — five nominally independent domestications rather than four — and, unlike cotton, one whose own literature disputes not only where one center sits but whether one of the five species is an independent domestication at all. Admitting it tests whether R(X) still returns a clean ⊥ when the obstacle is not a single unresolved center but several different kinds of obstacle at once.

40.2 Five domesticated species: the consensus view, and how it is supported

The field's standing consensus recognizes five domesticated Capsicum species: C. annuum, C. baccatum, C. chinense, C. frutescens and C. pubescens, each derived from a geographically distinct wild source and each independently brought under cultivation somewhere in the Neotropics beginning at least ten thousand years ago (Kraft et al. 2014).

The most direct genomic support for treating these as genuinely separate domestications, rather than one species subdivided late by trade, comes from Liu et al.'s (2023) graph-pan-genome study of 500 accessions: population-differentiation statistics (FST) between every pair of the five domesticated groups and their nearest wild relatives exceed 0.29 in every comparison, with most pairs above 0.37 — a level of genome-wide divergence the authors read as corroborating independent domestication events rather than a single event followed by later diversification.

Archaeobotanical corroboration for at least three of the five (annuum, baccatum, chinense) reaches back to starch-grain and macrofossil evidence recovered from sites across Mexico, coastal Peru, and the Amazon lowlands respectively (Perry et al. 2007; Pickersgill 1969), giving this chapter, like cotton's (§22.2), a corroborated species count before any question of geographic resolution is asked.

40.3 C. annuum: a corroborated center with an internal disagreement about exactly where

C. annuum's domestication locus is the best-documented of the five. Kraft et al. (2014) combine species distribution modeling, historical paleobiolinguistics (the reconstructed Proto-Otomanguean word for chili), microsatellite genetic data, and archaeobotanical macroremains from Coxcatlán Cave in the Tehuacán Valley, Puebla, and from the Ocampo caves, Tamaulipas, to argue for central-east Mexico as the best-supported single locus, with northeastern Mexico named as a genetically-favored but archaeologically weaker alternative the same study does not fully exclude. A decade later, Chiou et al. (2024) revisit the question with a larger archaeological seed-morphometric dataset and ecological niche models spanning 20,000 years, and report that the balance of evidence now favors southern Mexico over the Tehuacán-centered picture Kraft et al. had proposed. This chapter reports both positions rather than adjudicating between them, in keeping with §1.4's own discipline: a corroborated center, with the corroborating literature itself disagreeing about a several-hundred-kilometer range within Mexico.

40.4 C. baccatum: Bolivia and southern Peru, archaeologically dated

C. baccatum's wild form is restricted to dry environments of south-central Bolivia and southern Peru, and its domestication is the best archaeologically dated of the five: Pickersgill (1969) reports C. baccatum remains at Huaca Prieta and the nearby Paredones site dated to 7600–6500 BC, with the bulk of securely domesticated-type material dated to around 4500 BC, and further material with clear domestication morphology from Punta Grande and Ancón dated to 2000–500 BC. The consensus locus is the lowlands of Bolivia and the inter-Andean valleys of southern Peru (Pickersgill 1969) — a real but genuinely regional area, not a single excavated site, for which this chapter uses the Cochabamba valley as a representative coordinate (§40.7), following the same convention coffee used for Jimma (§39.5).

40.5 C. pubescens: a cultigen with no known wild form, but a locatable ancestral gene pool

C. pubescens is not known in the wild at all; it exists only as a cultigen, and its ancestry has to be inferred from its closest living wild relatives rather than read directly off a wild-to-domesticate transition. Palombo, Weiss-Schneeweiss & Carrizo García (2024), using genome-wide RAD-sequencing across the species and its putative wild relatives, confirm C. pubescens as a well-defined monotypic lineage sister to C. cardenasii and C. eximium, detect hybridization events between C. pubescens and both, and place the center of origin of its ancestral gene pool in the central-western Bolivia highlands, south-east to north-west of La Paz. This chapter treats that inferred gene-pool center, represented by La Paz, as the closest available proxy for a domestication locus this species can offer — with the caveat, stated once here and not repeated at every subsequent mention, that a gene-pool center inferred from wild relatives is not the same evidentiary object as an archaeologically dated domestication site, and is reported as such.

40.6 C. chinense and C. frutescens: the two that do not resolve — one to a point, one to independence itself

The remaining two species fail this chapter's resolvability bar for two different reasons. C. chinense's center of origin is consistently named as the Amazon basin, reached via the same archaeological sequence that dates baccatum's own spread to the Peruvian coast at roughly the time pottery arrives there (Pickersgill 1969), but no source reviewed here narrows that to a point coordinate any more precise than the basin itself. This chapter does not manufacture a representative point for a region that broad, and reports chinense as location-unresolved rather than invent one. C. frutescens fails on a different and more serious ground: its own independence as a domestication event is disputed, not only its location. The classical view places it in the Amazon basin with later dispersal to the Caribbean, structurally parallel to chinense; but Chiou et al.'s (2024) own morphometric quadratic discriminant analysis of modern and archaeological Capsicum seeds finds a continuum between C. frutescens and C. annuum rather than a clean separation, and reads this as support for treating frutescens as part of a broader C. annuum domestication spectrum rather than as a fully independent fifth species — a position the same study is careful to describe as a hypothesis their data support, not a settled reclassification. This chapter reports both positions, exactly as §1.4 requires, and notes that frutescens is consequently the first Capsicum case where the open question is a disputed count (the shape this cycle has previously used for dog, sorghum, lentil, tea, and soybean; Appendix A.4) layered onto a disputed location (the shape cotton and turkey used; Appendix A.3), rather than either alone.

40.7 A real-coordinate check among the three point-resolvable centers — illustrative only

Following coffee's own convention (§39.5) and cotton's before it (§22.5), the three centers this chapter can anchor to real coordinates — Tehuacán Valley, Puebla (18.4661°N, 97.3928°W) for C. annuum; the Cochabamba

valley, Bolivia (17.3895°S, 66.1568°W) as a representative point for C. baccatum's Bolivia/southern-Peru locus; and La Paz (16.5000°S, 68.1500°W) as a representative point for C. pubescens's inferred gene-pool center — are checked pairwise via great-circle distance (code/Ch40_capsicum_distance_check.py): annuum–baccatum, 5,249.8 km; annuum–pubescens, 5,035.4 km; baccatum–pubescens, 233.9 km.

The short baccatum–pubescens distance is worth flagging rather than passing over: both loci sit in the same broad Bolivian highland-to-valley corridor, which is consistent with the geographic proximity of their wild source populations reported independently in each species' own literature, and is not itself evidence for or against treating them as one event rather than two — the genomic differentiation reported by Liu et al. (2023, §40.2) is the evidence that actually bears on that question. This three-point check is reported as illustrative only, exactly as §39.5's and §22.5's own checks were: it is not a D̄ over five centers, because two of the five are not point-resolvable at all (§40.6).

40.8 Why R(X)=0: a compound failure, not cotton's single one

§22.6 found cotton at ⊥ for one reason: R(X) is a conjunction over all proposed centers (§20.7.2), and one of cotton's four — the Old World center contested between two candidate regions — failed to resolve to a point while the other three succeeded cleanly. Capsicum fails the same conjunction, but compounds three distinct obstacles rather than presenting one: (a) C. chinense has no point-coordinate anywhere in the literature reviewed, only a basin-scale region (§40.6); (b) C. pubescens has no wild form at all, so its 'center' is a gene-pool inference from wild relatives rather than an archaeological domestication locus (§40.5) — the same structural difficulty banana posed for a different reason (§27.6); (c) C. frutescens's status as a fifth independent domestication event is itself disputed in the current literature, not merely its location (§40.6) — a disputed-count problem this cycle has previously kept in Appendix A.4,

not A.3. Because R(X) is a conjunction rather than an average (§22.6's own phrasing), any one of these three would already be sufficient to return ⊥; Capsicum returns it three times over. This is disclosed as a genuinely new combination this cycle has not produced before — not a stronger or weaker result than cotton's, only a compound one — and is exactly the kind of case §22.8 anticipated when it asked what a second multi-species genus would add to this cycle's self-knowledge of its own predicate.

40.9 Placement in the master synthesis (Appendix A.3)

Capsicum is added to Appendix A.3 as a single case, following the same convention cotton's own four species were counted under in that table (§22's own row), and for the same reason: R(X)=0 is a property of the case, not of each candidate center separately, so Capsicum enters the master synthesis as one row representing all five nominal species, with its compound reasoning (§40.8) recorded in the table's own branch column rather than collapsed into cotton's single-obstacle phrasing.

40.10 Synthesis note

Two genus-level, multi-species tests of R(X) now exist in this cycle: cotton (§22) and Capsicum (this chapter). The predicate held for both — neither was forced to a number it could not support — but for structurally different reasons, which is itself the finding worth stating plainly: R(X)'s conjunction returns the same clean ⊥ whether the obstacle is one unresolved center among otherwise-solid ones, as with cotton, or three different kinds of obstacle compounding at once, as with Capsicum. A predicate that behaves identically under both shapes of failure is doing what §20.7 designed it to do.

References newly cited in Chapter 40

Chiou, K.L., Lira-Noriega, A. et al. (2024). Interdisciplinary insights into the cultural and chronological context of chili pepper (Capsicum

annuum var. annuum L.) domestication in Mexico. Proceedings of the National Academy of Sciences, 121(47), e2413764121.

Kraft, K.H., Brown, C.H., Nabhan, G.P., Luedeling, E., de Jesús Luna Ruiz, J., Coppens d'Eeckenbrugge, G., Hijmans, R.J. & Gepts, P. (2014). Multiple lines of evidence for the origin of domesticated chili pepper, Capsicum annuum, in Mexico. Proceedings of the National Academy of Sciences, 111(17), 6165–6170.

Liu, F., Zhao, J., Sun, H., Xiong, C., Sun, X., Wang, X., Wang, Z., Jarret, R., Wang, J., Tang, B., Xu, H., Hu, B., Suo, H., Yang, B., Ou, L., Li, X., Zhou, S., Yang, S., Liu, Z., Yuan, F., Pei, Z., Ma, Y., Dai, X., Wu, S., Fei, Z. & Zou, X. (2023). Genomes of cultivated and wild Capsicum species provide insights into pepper domestication and population differentiation. Nature Communications, 14, 5487.

Palombo, N.E., Weiss-Schneeweiss, H. & Carrizo García, C. (2024). Evolutionary relationships, hybridization and diversification under domestication of the locoto chile (Capsicum pubescens) and its wild relatives. Frontiers in Plant Science, 15, 1353991.

Perry, L., Dickau, R., Zarrillo, S., Holst, I., Pearsall, D.M., Piperno, D.R., Berman, M.J., Cooke, R.G., Rademaker, K., Ranere, A.J., Raymond, J.S., Sandweiss, D.H., Scaramelli, F., Tarble, K. & Zeidler, J.A. (2007). Starch fossils and the domestication and dispersal of chili peppers (Capsicum spp. L.) in the Americas. Science, 315, 986–988.

Pickersgill, B. (1969). The archaeological record of chili peppers (Capsicum spp.) and the sequence of plant domestication in Peru. American Antiquity, 34, 54–61.

Chapter 41 — Pea (Pisum sativum): A Founder Crop With Two Domesticated Groups, Neither Independently Pinned to a Point

41.1 Admission on its own merits, continuing Chapters 36–40's discipline

Pea joins this cycle as a founder crop of the original Fertile Crescent package already introduced in Chapter 2 (wheat and barley) and revisited throughout Section I, but it has not until now been given its own chapter. The reason for admitting it separately is the same reason cotton (§22) and Capsicum (§40) were admitted as genus-level tests rather than folded into a single-line mention: the current genomic literature on pea does not treat it as a single-origin founder crop alongside einkorn. It reports two genetically independent domesticated groups, Pisum sativum subsp. sativum and Pisum sativum subsp. abyssinicum, derived from different wild gene pools (Trněný et al. 2018; Hellwig, Abbo & Ophir 2022). This chapter asks the same question already asked of turkey (§21) and cotton (§22): what does R(X) return when a species-level domestication count is doubly corroborated but the locations behind that count are not equally well resolved?

41.2 Two domesticated groups, genomically distinguished

Trněný et al. (2018), using 11,343 genome-wide SNP markers across 154 wild accessions (134 P. sativum subsp. elatius, 20 P. fulvum) and 74 domesticated accessions (64 P. sativum landraces, 10 P. abyssinicum), find that cultivated P. sativum and the Ethiopian pea (P. abyssinicum) trace to different P. elatius gene pools, and explicitly reject the competing hypothesis that P. abyssinicum arose from hybridization between P. sativum subsp. elatius and P. fulvum. Hellwig, Abbo & Ophir (2022) independently corroborate this with RAD-seq data from 494 accessions: of 32 genomic regions carrying a detectable selection signature, 29 are found only in P. sativum subsp. sativum and 3 only in P. abyssinicum,

with no region shared between the two domesticated groups and no haplotype-pattern similarity within any region examined. Both studies converge on the same reading — two domestication events, not one event followed by later regional divergence — using independent marker sets and independent statistical approaches, the same two-independent-methods structure §2.2 required for einkorn before treating its own single-origin result as settled.

41.3 P. sativum subsp. sativum: an inherited location, not an independently tested one

Archaeobotanical convention places pea's initial domestication in the Fertile Crescent alongside einkorn, emmer, barley, lentil, chickpea, and flax, with early legume remains recovered from PPNA and PPNB sites across the same corridor — Tell Abu Hureyra, Jericho, Çayönü, Cafer Höyük, and Ali Kosh among them (Zohary & Hopf 2000; Weeden 2018; Riehl, Zeidi & Conard 2013). This attribution, however, rests on pea's membership in the founder-crop package identified by the "core area" hypothesis (Lev-Yadun, Gopher & Abbo 2000; already discussed at §2.3), not on a pea-specific replication of the kind Heun et al. (1997) and Kilian et al. (2007) independently carried out for einkorn. No source reviewed here reports an AFLP-, SNP-, or resequencing-based study that tests wild P. sativum subsp. elatius population structure against cultivated pea and returns a single candidate wild population the way Heun et al. returned Karacadağ for einkorn. The closest available genetic study, Smýkal et al. (2018), characterizes wild P. sativum subsp. elatius population structure across fourteen populations sampled in the northern part of the Fertile Crescent — real DARTseq data (18,397 SNP markers; AMOVA attributing 63% of allelic variance between populations) — but its own stated aim is describing that region's population structure for conservation purposes, not testing competing domestication-locus hypotheses the way §2.2's einkorn studies did. This chapter therefore reports pea's Fertile-Crescent attribution as inherited from the general founder-crop-package hypothesis rather than independently confirmed for

pea itself, and does not manufacture a level of point-precision the pea-specific literature does not support.

41.4 P. abyssinicum: a regional highland attribution, independently corroborated as a separate event

P. abyssinicum is restricted to the highlands of Ethiopia and southern Yemen (Maxted & Ambrose 2001; Trněný et al. 2018), where it survives today chiefly as the landrace crop known locally as Dekoko, concentrated in the Tigray highlands and the northern part of the former Wollo province (Gebremichael et al. 2025). Unlike P. sativum subsp. sativum's inherited attribution (§41.3), P. abyssinicum's status as an independent domestication event is directly tested rather than assumed: both Trněný et al. (2018)'s gene-pool assignment and Hellwig, Abbo & Ophir (2022)'s non-overlapping selection signatures speak specifically to this species, not to the founder-crop package as a whole. Its location, however, is reported at the same regional grain as P. sativum's — "Ethiopia and Yemen," or, in the more recent agronomic literature, the Tigray highlands — without a single archaeobotanically or genetically dated point comparable to Karacadağ.

41.5 A real-coordinate check between the two regional attributions — illustrative only

Following the convention already used for coffee (§39.5), cotton (§22.5) and Capsicum (§40.7), a great-circle distance is computed (code/Ch41_pea_distance_check.py) between the two regions' representative points: Karacadağ, SE Turkey (37.67°N, 39.83°E) — the same coordinate §2.2 uses for einkorn, reused here only because it is the point already established in this cycle for the "core area" hypothesis pea's own attribution inherits, not because any pea-specific study names it — and Mekelle, Tigray (13.4967°N, 39.4753°E), a representative point for the Ethiopian highland region P. abyssinicum is reported to occupy. The computed distance is 2,688.2 km. This number is reported exactly as Capsicum's three-point check was (§40.7): illustrative only, since neither

endpoint is a point-resolved domestication locus in its own right, only a representative marker for a broad region named in the literature. No D̄ is computed for use in a PI value on the strength of this single illustrative pair.

41.6 Why R(X)=0: two corroborated events, zero point-resolved centers

§20.7.2's R(X) predicate requires each proposed center to resolve to a real coordinate before a PI value can be computed. Pea's case is structurally distinct from every prior double-center case in this table. Turkey (§21) had one resolved center and one unresolved center. Cotton (§22) had three resolved and one unresolved. Capsicum (§40) had a compound failure across three different obstacles among five candidate centers. Pea, by contrast, has C=2 independently corroborated domestication events — as well-supported at the level of "is this real and how many" as any case in this cycle, per §41.2 — with neither center independently resolved to a point: P. sativum subsp. sativum's location is inherited from a package-level hypothesis never directly tested against pea's own wild population data (§41.3), and P. abyssinicum's location, though its status as a separate event is directly tested, is only regionally reported (§41.4). This is a new sub-reason for landing at ⊥, distinct from cat's "no candidate region locatable at point resolution" (§28, Appendix A.3) because pea's count is not in dispute the way cat's three-rival-region problem left the count itself open — and distinct from llama's "single center but no point-level coordinate" (§29, Appendix A.3) because pea has two corroborated centers, not one. Pea is reported here as this cycle's first case where a doubly-corroborated count meets a doubly-unresolved geography.

41.7 Placement in the master synthesis (Appendix A.3)

Pea is added to Appendix A.3 as a two-center case with an illustrative, not evidentiary, distance figure, and with its own branch label — "R(X)=0, two corroborated centers, neither independently point-resolved" — to keep it distinct from turkey's and cotton's partial-

resolution branches and from cat's and llama's single-center branches already tabulated there.

41.8 Synthesis note

Sections I through this chapter have now produced five distinct routes to R(X)=0 among cases with more than one proposed center: one resolved against one unresolved (turkey), three resolved against one unresolved (cotton), a three-way compound failure across five centers (Capsicum), and now two corroborated centers where neither was ever independently tested for its own location (pea). That the predicate returns the same clean ⊥ across four structurally different failures, rather than a graded or ambiguous result, continues to be the finding this cycle keeps re-deriving rather than assuming (§22.8, §40.10): a conjunction over unresolved coordinates fails identically regardless of why any one coordinate is unresolved.

References newly cited in Chapter 41

Gebremichael, H. et al. (2025). Genetic diversity and population structure analysis of Pisum sativum var. abyssinicum genotypes from Northern Ethiopia using ISSR markers. Agrosystems, Geosciences & Environment, 8(1), e70151.

Hellwig, T., Abbo, S. & Ophir, R. (2022). Phylogeny and disparate selection signatures suggest two genetically independent domestication events in pea (Pisum L.). The Plant Journal, 110, 419–439.

Maxted, N. & Ambrose, M. (2001). Peas (Pisum L.). In: Plant Genetic Resources of Legumes in the Mediterranean, Kluwer, 181–190.

Riehl, S., Zeidi, M. & Conard, N.J. (2013). Emergence of agriculture in the foothills of the Zagros Mountains of Iran. Science, 341, 65–67.

Smýkal, P., Trněný, O., Brus, J., Hanáček, P., Rathore, A., Das Roma, R., Pechanec, V., Duchoslav, M., Bhattacharyya, D., Bariotakis, M., Pirintsos, S., Berger, J. & Toker, C. (2018). Genetic structure of wild pea (Pisum sativum subsp. elatius) populations in the northern part of the

Fertile Crescent reflects moderate cross-pollination and strong effect of geographic but not environmental distance. PLoS ONE, 13(3), e0194056.

Trněný, O., Brus, J., Hradilová, I., Rathore, A., Das, R.R., Kopecký, P., Coyne, C.J., Reeves, P., Richards, C. & Smýkal, P. (2018). Molecular evidence for two domestication events in the pea crop. Genes, 9(11), 535.

Weeden, N.F. (2018). Domestication of pea (Pisum sativum L.): The case of the Abyssinian pea. Frontiers in Plant Science, 9, 515.

Zohary, D. & Hopf, M. (2000). Domestication of Plants in the Old World, 3rd edn. Oxford University Press.

Chapter 42 — Flax (Linum usitatissimum): A Single Origin the Literature Corroborates Twice, and a Domestication That Was Never One Event

42.1 Admission, continuing Chapters 40–41's dual-purpose-crop thread

Flax completes, alongside pea (§41), the founder-crop pair this cycle had not yet reached from Zohary & Hopf's canonical eight-crop Southwest Asian founder package (einkorn and barley, Ch.2; chickpea and lentil, §2.8; pea, Ch.41): flax and bitter vetch. Flax is admitted here on the same footing already used for cotton (§22), Capsicum (§40) and pea (§41): the crop's dual identity, as both a fibre and an oilseed plant, invites the same genus/trait-level scrutiny those chapters gave multi-species or multi-purpose cases, rather than a single-line mention folded into Chapter 2's founder-crop package. Unlike pea, whose two named subspecies trace to two distinct wild gene pools (§41.2), flax's dispute is not over how many geographically independent domestications occurred, but over how many distinct domestication events — for oil, for fibre, for non-shattering capsules, for winter hardiness — sit behind one, genetically unanimous, single wild origin. This chapter tests what

the C, κ, D̄ triple and its resolvability predicate R(X) (§20.7.1–§20.7.2) say about a case that is doubly corroborated at C=1 but was demonstrably not domesticated in a single act.

42.2 A single wild progenitor, and a single geographic origin corroborated by two independent methods twenty years apart

Cultivated flax's wild progenitor is pale flax, Linum bienne Mill. (synonym L. usitatissimum subsp. angustifolium), a hypothesis first proposed by Heer (1872) and subsequently supported empirically by marker-based studies (Fu, Peterson, Diederichsen & Richards 2002; Fu & Allaby 2010). Two genetically independent studies, using different marker systems and separated by two decades, converge on a single domestication origin for the species. Allaby, Peterson, Merriwether & Fu (2005, Theoretical and Applied Genetics 112:58–65) sequenced 34 alleles of the 2.5 kb stearoyl-ACP desaturase (sad2) locus across 30 accessions of cultivated and pale flax; the resulting phylogeny supports a single domestication origin for extant cultivated flax and indicates that the earliest selection target was oil content rather than fibre. Fu (2025, Scientific Reports 15:8731) applied genotyping-by-sequencing to 93 Linum samples — 91 genetically diverse accessions from 32 countries, representing pale flax and four trait-defined domestication groups of cultivated flax (oilseed, fibre, winter, capsular-indehiscent) — generating 16,998 filtered SNPs across the 15 flax chromosomes; principal-component, neighbour-joining and Bayesian phylogenetic analyses all place every cultivated accession downstream of a single pale-flax-rooted lineage, with no genetic signal supporting an independent second domestication from a geographically separate wild population. Neither study is contradicted anywhere in the literature reviewed for this chapter: no source proposes a rival wild population, on a different continent or in a different part of L. bienne's range, as an independent second origin of cultivated flax.

On the two-independent-methods bar §2.2 set for einkorn, flax's C=1 is at least as well corroborated — arguably more so, given the 2025 study's genome-wide marker density against sad2's single-locus resolution.

42.3 Archaeobotanical corroboration, and why the location remains inherited rather than independently tested

Archaeobotanically, the earliest reported remains of pale flax come from Tell Abu Hureyra in northern Syria, dated 11,200–10,500 years BP (Hillman 1975, cited in Fu 2025), predating unambiguous evidence of cultivation and consistent with wild collection. The first archaeological indication of a cultivated form — enlarged seed size at Tell Ramad, Syria — is dated to roughly 9,000 years BP (van Zeist & Bakker-Heeres 1975), and twined flax-fibre fabrics recovered from Nahal Hemar Cave in the southern Levant carry an independent radiocarbon date of approximately 9,000 years BP (Schick 1988; Shamir & Rast-Eicher 2020), placing early fibre use alongside, not obviously after, the earliest cultivated-seed evidence. All of this sits within the same broad Fertile Crescent founder-crop corridor already established in this cycle for wheat, barley (Ch.2), chickpea and lentil (§2.8) — the same "core area" reading (Lev-Yadun, Gopher & Abbo 2000; §2.3) pea's own §41.3 flagged as an inherited, not independently tested, attribution.

The same caution applies here, for a related but distinct reason. Pale flax's wild range is unusually broad among this cycle's founder-crop progenitors — spanning Western Europe, the Mediterranean Basin, North Africa, South-West Asia, Iran and the Caucasus (Fu 2023) — and no source reviewed for this chapter reports an AFLP-, SNP-, or resequencing-based study that tests population structure across that full range and returns a single candidate wild population tied to a decimal-degree point, the way Heun et al. (1997) returned Karacadağ for einkorn (§2.2). The closest

comparable effort, sampling of Turkish L. bienne populations for phenotypic and ISSR-marker variation (Uysal et al. 2010, 2012), documents geographically structured variation within Turkey but was not designed to, and does not, test Turkey against the rest of the species' range as a domestication-origin hypothesis. Flax's Fertile-Crescent attribution is therefore reported here on the same footing as pea's subsp. sativum (§41.3): archaeobotanically anchored and consistent with the founder-package "core area" reading, but not independently resolved to a point by a study built to test the question.

42.4 The temporal question: one origin, several domestication events

§2.1 drew a distinction this cycle has returned to repeatedly — a geographic question (how many independent wild populations were domesticated?) and a temporal one (was domestication a single fast event or a protracted process?) — and flax answers the first cleanly (§42.2–42.3: C=1, unanimous) while answering the second in a way that is, on inspection, more structured than einkorn's own protracted-but-single-population case (§2.3). Fu, Diederichsen & Allaby (2012, Ecology and Evolution 2:139–152) and the same author's 2025 genome-wide study converge on a specific reading: cultivated flax descended from a single domestication of pale flax for oil use, followed by a sequence of further, genetically distinguishable selection events for capsular indehiscence, fibre quality and winter hardiness — not from three or four separately founded wild populations, but from repeated re-selection within the one already-domesticated oil lineage. Fu (2025)'s dated maximum-clade-credibility tree, rooted at an assumed 10,000 years BP for the initial oil domestication, places the split of indehiscent flax from the oil lineage at 7,117 years BP (SD 349), the divergence of the lineage that spread oil and fibre flax into Europe at 5,779 years BP (SD 205; 5,939 years BP, SD 305, when five

non-European accessions are excluded), and the node associated predominantly with winter-hardy flax at 5,104 years BP (SD 184); the earliest individually dated fibre-flax accession (a Czech landrace, sample f12) is placed at 4,245 years BP (SD 195). An independent demographic method (SMC++, run on four group pairs across all 15 chromosomes) returns compatible, though wider-ranging, estimates: oil flax splitting from pale flax 7,461 years BP (range 5,027–12,092), indehiscent flax departing from oil flax 7,093 years BP (range 4,500–9,483), fibre diverging from oil 5,407 years BP (range 2,327–8,607), and winter flax separating from oil 4,905 years BP (range 3,676–7,410). The author's own stated caveat is retained here rather than smoothed over: SMC++ estimates did not converge for many chromosomes and carry large standard deviations, and the assumed 10,000-year root itself sits several centuries before the earliest directly dated cultivated-seed evidence at Tell Ramad (§42.3) — a scaling assumption, not a directly measured date, exactly the kind of dependency §1.4 requires this cycle to disclose rather than present as settled.

This is a different structure from pea's C=2 (§41.2, two genetically independent domestications from two separate wild gene pools) and from rice's C=2/C=3 dispute (§4.2, competing geographic hypotheses). Flax's literature reports no rival wild-population hypothesis at any point in this sequence; every cited divergence is a split within the single already-domesticated lineage established at §42.2. The temporal richness here does not multiply C.

42.5 A real-coordinate check — illustrative only

Following the convention already used for the einkorn–chickpea core-area check (§2.8.4) and pea's own inter-regional check (§41.5), a great-circle distance is computed (code/Ch42_flax_distance_check.py) between Karacadağ, SE Turkey (37.67°N, 39.83°E) — the coordinate this cycle has used since

§2.2 for the einkorn wild-population locus, and reused at §2.8.4 as the founder-package "core area" anchor — and Tell Abu Hureyra, Raqqa Governorate, Syria (35.867°N, 38.400°E; 35°52′N, 38°24′E), flax's own earliest archaeobotanical anchor (§42.3). The computed distance is 237.5 km. Unlike pea's 2,688.2 km check between two only loosely comparable regional attributions (§41.5), this figure places flax's own earliest evidence markedly closer to the founder package's established core than pea's Ethiopian highland attribution was — consistent with, though not proof of, flax's conventional inclusion in the same tight Fertile Crescent nucleus already established for einkorn, chickpea, wheat and barley. As with every prior use of this convention, the figure is reported as illustrative only: Tell Abu Hureyra is an excavated archaeological site, not a genetically resolved wild-population locus, and no $\bar{D}$ or PI value is computed from this single pair.

42.6 Why PI=0 by the C=1 convention, and how this differs from einkorn's own route to the same floor

§20.7.2's second branch applies whenever C=1 and the single center is unanimously corroborated, with $\bar{D}$ set to 0 by convention regardless of whether that center's location has itself been resolved to a point — a branch that does not require R(X)=1, since $\bar{D}$ over a single point is trivially zero. Flax reaches PI=0 by exactly this branch: §42.2 established C=1 as doubly corroborated by independent genetic methods, and no rival wild-population hypothesis is reported anywhere in the literature reviewed. This is the same floor einkorn (§2.2) and chickpea (§2.8.1) reach, but by a structurally distinct route. Einkorn's C=1 is corroborated by a study built specifically to test population structure against the domestication question and return a point (Heun et al. 1997, independently confirmed by Kilian et al. 2007); flax's C=1 is corroborated by two studies that test the single-versus-multiple-

origin question directly and conclusively, but that were never designed to, and do not, return a decimal-degree wild-population locus (§42.3). Both routes satisfy §20.7.2's second branch, because that branch's criterion is unanimous corroboration of C=1, not point-resolution of the center — but the difference is disclosed here rather than left implicit, since collapsing "unanimously corroborated" and "independently point-resolved" into one description would overstate what the flax-specific literature has actually tested, in exactly the way §41.3 already cautioned against for pea's inherited attribution.

42.7 Placement in the master synthesis (Appendix A.3)

Flax is added to Appendix A.3 as a PI=0 case reached via §20.7.2's C=1-unanimous convention, with a branch label — "C=1, unanimous, two independent genetic methods; location regionally inherited, not independently point-tested" — that distinguishes it from einkorn's and chickpea's point-resolved routes to the same floor value, and from pea's and llama's ⊥ (not-computed) results, with which it should not be conflated despite the shared vocabulary of an "inherited" location attribution.

42.8 Synthesis note

Flax adds a case this cycle had not yet produced: a single, doubly-corroborated geographic origin that nonetheless required a temporal decomposition — one wild-to-domesticate transition followed by several dated, within-lineage re-selection events — before the crop's full domestication history could be reported honestly. That decomposition changes no PI value (§42.6): the index counts geographically independent domestication events, and flax has exactly one, however many trait-specific selection episodes followed it. What changes is only the discipline required to say so without either collapsing flax's protracted, multi-trait history into a

single date, or mistaking its several genetically dated internal splits for the kind of geographically independent second center pea (§41), rice (§4) and cotton (§22) each, in their own way, actually have.

References newly cited in Chapter 42

Allaby, R.G., Peterson, G.W., Merriwether, A. & Fu, Y.-B. (2005). Evidence of the domestication history of flax (Linum usitatissimum L.) from genetic diversity of the sad2 locus. Theoretical and Applied Genetics, 112(1), 58–65.

Fu, Y.-B. (2023). Pale flax (Linum bienne): an underexplored flax wild relative. In The Flax Genome, Compendium of Plant Genomes (eds. F.M. You & B. Fofana), pp. 37–53. Springer Cham.

Fu, Y.-B. (2025). Flax domestication processes as inferred from genome-wide SNP data. Scientific Reports, 15, 8731.

Fu, Y.-B. & Allaby, R.G. (2010). Phylogenetic network of Linum species as revealed by non-coding chloroplast DNA sequences. Genetic Resources and Crop Evolution, 57, 667–677.

Fu, Y.-B., Diederichsen, A. & Allaby, R.G. (2012). Locus-specific view of flax domestication history. Ecology and Evolution, 2(1), 139–152.

Fu, Y.-B., Peterson, G., Diederichsen, A. & Richards, K.W. (2002). RAPD analysis of genetic relationships of seven flax species in the genus Linum L. Genetic Resources and Crop Evolution, 49, 253–259.

Hillman, G. (1975). The plant remains from Tell Abu Hureyra: a preliminary report. Proceedings of the Prehistoric Society, 41, 70–73.

Schick, T. (1988). Nahal Hemar cave: cordage, basketry and fabrics. 'Atiqot (English Series), 18, 31–43.

Shamir, O. & Rast-Eicher, A. (2020). Continuity and discontinuity in Neolithic and Chalcolithic linen textile production in the southern Levant. In The Competition of Fibres: Early Textile Production in Western Asia, South-East and Central Europe (10,000–500 BC), Ancient Textile Series Vol. 32 (eds. W. Schier & S. Pollock), pp. 27–37. Oxbow Books.

Uysal, H., Fu, Y.-B., Kurt, O., Peterson, G.W., Diederichsen, A. & Kusters, P. (2010). Genetic diversity of cultivated flax (Linum usitatissimum L.) and its wild progenitor pale flax (Linum bienne Mill.) as revealed by ISSR markers. Genetic Resources and Crop Evolution, 57, 1109–1119.

Uysal, H., Kurt, O., Fu, Y.-B., Diederichsen, A. & Kusters, P. (2012). Variation in phenotypic characters of pale flax (Linum bienne Mill.) from Turkey. Genetic Resources and Crop Evolution, 59, 19–30.

van Zeist, W. & Bakker-Heeres, J.A.H. (1975). Evidence for linseed cultivation before 6000 BC. Journal of Archaeological Science, 2, 215–219.

Chapter 43 — The Other Domesticated Squashes: Cucurbita argyrosperma, C. moschata and C. maxima, and a Genus That Refuses to Give Up Its Fourth Wild Ancestor

43.1 Admission, continuing Chapter 22's and Chapter 41–42's intra-genus and dual-purpose threads

Cucurbita pepo was admitted to this cycle earlier, in the EAC (eastern agricultural complex) chapter, on the strength of its own dual domestication within a single species. This chapter completes the genus by admitting the three other domesticated Cucurbita taxa that reach commercial and archaeobotanical significance — C. argyrosperma (cushaw pumpkin, pipián squash), C. moschata

(butternut squash, calabaza) and C. maxima (buttercup and Hubbard squash) — on the same footing already used for cotton (§22): a genus in which the literature reports multiple, geographically independent domestication events, each meriting its own C, κ, D̄ evaluation rather than a single genus-level entry. Unlike cotton's four-continent spread, Cucurbita's independent domestications are compressed into a single hemisphere, which makes the genus a useful counter-example to any assumption that intra-generic polycentricity requires intercontinental distance.

The comparison anchor for the whole genus is Sanjur, Piperno, Andres & Wessel-Beaver (2002, Proceedings of the National Academy of Sciences 99:535–540), whose mitochondrial-gene phylogeny remains the only study to treat all domesticated and wild Cucurbita taxa within one analysis; it reports that the data support at least six independent domestication events from distinct wild ancestors across the genus. This chapter's three cases are three of those six; C. pepo's own two independent domestications (already treated in the EAC chapter) and C. ficifolia's more poorly resolved South American origin account for the remainder and are not re-derived here.

43.2 Cucurbita argyrosperma: a domestication tested against its own rival hypothesis, not merely proposed

Cultivated C. argyrosperma subsp. argyrosperma descends from the wild Mexican gourd C. argyrosperma subsp. sororia, a relationship first proposed on morphological and ecological grounds and subsequently supported by Sanjur et al.'s (2002) mitochondrial phylogeny. The decisive corroboration is genomic: Barrera-Redondo, Sánchez-de la Vega, Aguirre-Liguori, Castellanos-Morales, Gutiérrez-Guerrero, Aguirre-Dugua, Aguirre-Planter, Tenaillon, Lira-Saade & Eguiarte (2021, Horticulture Research 8:109) sequenced the first high-quality wild

Cucurbita genome (subsp. sororia) alongside genotyping-by-sequencing data for 192 wild, domesticated and feral individuals sampled across Mexico, yielding 12,813 filtered SNPs. Maximum-likelihood and ADMIXTURE analyses place every argyrosperma population in a single monophyletic clade, with the Jalisco and Guerrero populations occupying its basal branches and showing the closest genetic affinity to sororia populations from Jalisco specifically.

What distinguishes this case from flax's own C=1 (§42.2) is that the single-origin hypothesis was not merely returned by the data but explicitly tested against a named rival. The authors used Fastsimcoal2 to compare, by Akaike Information Criterion, a domestication-in-Jalisco model against a domestication-in-southern-Mexico model, each crossed with three gene-flow scenarios (continuous, secondary contact, none). The Jalisco-with-secondary-contact model won; the alternative region was explicitly discarded, not merely unmentioned. This is the same structure Heun et al. (1997) used for einkorn (§2.2) — a study built to adjudicate between named candidate origins, not simply to describe diversity — even though the resulting attribution here is a lowland sub-region of a Mexican state rather than a decimal-degree population locus.

Archaeobotanically, the earliest presumed record of argyrosperma is a set of phytoliths from Xihuatoxtla, Guerrero, dated to roughly 8,700 years BP (Piperno, Ranere, Holst, Iriarte & Dickau 2009, Proceedings of the National Academy of Sciences 106:5019–5024), co-occurring with early Zea mays evidence in the same Balsas River valley sequence. The authors of the genomic study are explicit that the taxonomic identity of these phytoliths is ambiguous — they cannot be assigned to argyrosperma with certainty against other Cucurbita taxa present in the region at the same date — so this date corroborates the general Balsas-basin setting rather than the

species-level attribution itself, a caveat this chapter retains rather than smooths over.

43.3 Cucurbita moschata: the domesticate whose wild ancestor no method has yet found

C. moschata is the genus's outstanding negative result, and it has stayed negative across three independent lines of evidence spanning more than two decades. Sanjur et al.'s (2002) mitochondrial survey concluded that the wild ancestor of C. moschata is still unknown, but that mtDNA data combined with other evidence suggest it will probably be found in the lowlands of northern South America — a probabilistic regional inference, not a resolved population. Kates, Soltis & Soltis (2017, Molecular Phylogenetics and Evolution 111:98–109) revisited the question with the most comprehensive nuclear phylogeny of the genus to date, 44 loci derived from introns of single-copy nuclear genes across wild and domesticated Cucurbita; their own stated conclusion is that expanded geographic sampling of key wild species is needed before the genetic origins of the crop taxa, moschata included, can be resolved. A subsequent cucurbit-wide review of powdery-mildew host relationships (2024, Journal of Plant Growth Regulation reviews literature, published as Horticultural Reviews / Taylor & Francis 2024) restates the same finding without qualification: the wild ancestor of C. moschata, domesticated in lowland northern South America, is still unknown.

Archaeobotanically, the strongest anchor is indirect: nonbitter C. moschata remains recovered in Panama and dated to approximately 9,200 years BP show that automatic selection for palatability, in Harlan's sense, had already occurred by that date (Piperno & Dillehay 2008, cited in Chomicki, Schaefer & Renner 2020, New Phytologist 226:1240–1255), which places domestication itself earlier still. This date is consistent with the lowland-northern-

South-America region flagged by the mitochondrial and nuclear studies alike, but consistency with a region is not the same as resolution to a wild population, and no source reviewed for this chapter narrows the candidate area further.

Because no study — mitochondrial, nuclear, or archaeobotanical — has returned a candidate wild population for C. moschata, this crop cannot be given a resolved center under this cycle's convention. It is marked ⊥ (not computed) at the C-count stage itself, on the same footing as pea's inter-regional relationship (§41) and llama's own unresolved case, rather than reaching PI=0 by the C=1-unanimous route flax and (§43.2) argyrosperma reach. The distinction matters: C=1 unanimous means every study agrees on one wild-population origin; ⊥ here means every study agrees a wild population has not yet been found at all. Collapsing the two into the same PI=0 floor would misrepresent what the moschata literature has actually established, and this chapter declines to do so.

43.4 Cucurbita maxima: a resolved wild ancestor, an unresolved point, and an archaeological record that sits somewhere else entirely

Cultivated C. maxima subsp. maxima descends from the free-living C. maxima subsp. andreana, a relationship supported independently by Sanjur et al.'s (2002) mitochondrial phylogeny — in which andreana groups with maxima and the wild species C. ecuadorensis in a well-supported clade — and by Kates et al.'s (2017) nuclear-locus phylogeny. This is a genuine two-independent-methods corroboration in the same sense flax's C=1 is (§42.2), separated by fifteen years and built on non-overlapping marker systems.

The region is conventionally given as north-central Argentina and Bolivia, following Nee's (1990, Economic Botany 44 supplement:56–68) synthesis and subsequent genetic work, but Sanjur et al. (2002)

are explicit that this attribution is not point-resolved: free-growing andreana populations described by Michael Nee from lowland central Bolivia share haplotypes with cultivated maxima, which the authors note may extend the candidate domestication zone into that region, while cautioning that historical information on the Bolivian populations is limited and that whether they represent a long-term wild presence or a naturalized escape from cultivation is not established. No source reviewed for this chapter reports a study built specifically to adjudicate between the Argentine and Bolivian sub-regions, in the way §43.2 showed for argyrosperma's Jalisco-versus-southern-Mexico test. C. maxima's C=1 is therefore reached by the same regionally-inherited route already flagged for flax (§42.3, §42.6): unanimous on a single wild lineage, not independently resolved to a point.

The archaeobotanical record adds a further complication rather than resolving it. The earliest secure evidence of cultivated maxima comes from the Peruvian coast, dated to approximately 4,000 years BP (Sauer 1993; Piperno & Stothert 2003, cited in Chomicki et al. 2020), where the crop appears never to have left the Neotropics in pre-Columbian times. This coastal Peruvian date sits at a considerable remove — geographically, from the Argentine-Bolivian andreana range the genetic data point to for the wild ancestor itself. Multidisciplinary archaeobotanical work in the Argentine Northwest (Lema 2011, Archaeological and Anthropological Sciences 3:113–139; Lema, Capparelli & Pochettino et al., subsequent volumes) has recovered maxima and andreana rind remains from sites such as Pampa Grande (dated 1,720±50 BP) that are far more recent than the Peruvian coastal record and cannot themselves push the domestication date earlier. In other words: the oldest cultivated remains and the genetically inferred wild-progenitor range are not in the same place, and no source reviewed here proposes an archaeological sequence that closes that gap. This

chapter reports the disjunction rather than resolving it by assumption.

43.5 Why three different PI outcomes from one genus, and what that says about the convention itself

§20.7.2's second branch sets D̄=0 by convention whenever C=1 and the single center is unanimously corroborated, independent of whether the center itself has been resolved to a point. Applied strictly to this chapter's three cases, the outcomes diverge in a way flax's own single case (§42) could only illustrate once:

C. argyrosperma reaches PI=0 by the strongest route available under this convention: C=1, corroborated by two independent genetic methods fifteen years apart, with the single-origin hypothesis explicitly tested against, and shown to outperform, a named rival region. This is functionally equivalent to einkorn's route (§2.2), even though the resolution achieved — a lowland sub-region of Jalisco and the adjoining Balsas basin, not a decimal-degree coordinate — is coarser than Karacadağ's.

C. maxima reaches PI=0 by the same convention, but via flax's weaker route: C=1 unanimous across two independent genetic methods, region given as Argentina/Bolivia, point unresolved, and — uniquely among this chapter's cases — an archaeobotanical record that sits at a documented geographic distance from the genetically inferred wild-progenitor range rather than simply failing to narrow it further.

C. moschata cannot be assigned a PI value at all. Three independent lines of evidence across more than two decades concur that no wild population has been identified, so the C-count itself is undetermined rather than unanimous. It is marked ⊥, not PI=0, and not silently omitted.

The result is a single genus producing all three of this cycle's principal epistemic categories — point-tested C=1, region-inherited C=1, and unresolved ⊥ — within three congeneric, similarly-aged domestication events. That range is itself the finding this section reports: R(X)'s resolvability predicate (§20.7.1) does not track taxonomic relatedness, crop importance, or even how long a question has been studied. It tracks only whether a specific study was built to answer it, and for one of Cucurbita's three other domesticates, no such study yet exists.

43.6 A real-coordinate check — illustrative only, and only where a coordinate exists to check

Following the convention used since §2.8.4 and reused at §41.5 and §42.5, a great-circle distance can only be computed between two resolved loci; this chapter has one such pair available. Barrera-Redondo et al. (2021) place C. argyrosperma's domestication in the lowlands of Jalisco and the Balsas basin, and the earliest associated archaeological date comes from Xihuatoxtla, Guerrero (the same Balsas River valley sequence; §43.2), so a within-chapter distance check of the kind performed for einkorn-against-core-area or flax-against-Tell-Abu-Hureyra would in this case measure a genetic attribution against an archaeological site inside the same drainage basin rather than two independently surveyed regions, and would therefore illustrate proximity that is already built into the genetic study's own geographic argument. Computing it would add a number without adding information, which §1.4's disclosure standard weighs against; no distance is computed in this section. For C. maxima, by contrast, a genuine two-region check — Argentine/Bolivian andreana range against the Peruvian coastal archaeological record — could be computed, but doing so would require assigning a single representative coordinate to two areas neither source resolves to a point, which would manufacture the

appearance of precision this chapter has just finished declining to claim in §43.4. Both omissions are disclosed here rather than left as silent gaps.

43.7 Placement in the master synthesis (Appendix A.3)

C. argyrosperma is added to Appendix A.3 as a PI=0 case reached via §20.7.2's C=1-unanimous convention, branch label "C=1, unanimous, two independent genetic methods, single-origin hypothesis explicitly tested against a named rival region (Fastsimcoal2/AIC); archaeological anchor taxonomically ambiguous." C. maxima is added as PI=0 via the same branch, but labelled "C=1, unanimous, two independent genetic methods; location regionally inherited (Argentina/Bolivia), not point-tested; archaeological record geographically disjoint from genetic attribution." C. moschata is added as ⊥ (not computed), labelled "wild progenitor unresolved across mtDNA (2002), 44-locus nuclear (2017) and subsequent review (2024); region only, not population, indicated." All three are cross-referenced to C. pepo's own two-domestication entry from the EAC chapter and to cotton's four-continent entry (§22) as this cycle's other cases of intra-generic or intra-specific polycentricity.

43.8 Synthesis note

This chapter closes the Cucurbita genus with three cases that resemble each other taxonomically far more than they resemble each other epistemically. Argyrosperma shows that a coarse geographic resolution — a lowland sub-region rather than a coordinate — can still be reached by a rigorously adjudicated test, and that R(X)'s bar is about method, not precision. Maxima shows that two independent genetic methods can agree unanimously on a wild lineage while leaving its exact range, and its relationship to the oldest cultivated remains, genuinely open. Moschata shows that

unanimity is not guaranteed merely because a question has been asked three times over two decades with three different technologies; sometimes the honest answer, restated in 2002, 2017 and 2024 alike, is that the wild ancestor has not been found. Reporting all three side by side, rather than defaulting to the genus's better-resolved cases, is the discipline this cycle has applied consistently since §1.4, and it is the reason this chapter assigns two PI=0 values and one ⊥ from a single genus rather than rounding the third case up to match the other two.

References newly cited in Chapter 43

Barrera-Redondo, J., Sánchez-de la Vega, G., Aguirre-Liguori, J.A., Castellanos-Morales, G., Gutiérrez-Guerrero, Y.T., Aguirre-Dugua, X., Aguirre-Planter, E., Tenaillon, M.I., Lira-Saade, R. & Eguiarte, L.E. (2021). The domestication of Cucurbita argyrosperma as revealed by the genome of its wild relative. Horticulture Research, 8, 109.

Chomicki, G., Schaefer, H. & Renner, S.S. (2020). Origin and domestication of Cucurbitaceae crops: insights from phylogenies, genomics and archaeology. New Phytologist, 226(5), 1240–1255.

Kates, H.R., Soltis, P.S. & Soltis, D.E. (2017). Evolutionary and domestication history of Cucurbita (pumpkin and squash) species inferred from 44 nuclear loci. Molecular Phylogenetics and Evolution, 111, 98–109.

Lema, V.S. (2011). The possible influence of post-harvest objectives on Cucurbita maxima ssp. maxima and ssp. andreana evolution under cultivation at the Argentinean Northwest: an archaeological example. Archaeological and Anthropological Sciences, 3(2), 113–139.

Nee, M. (1990). The domestication of Cucurbita (Cucurbitaceae). Economic Botany, 44(3, Supplement), 56–68.

Piperno, D.R., Ranere, A.J., Holst, I., Iriarte, J. & Dickau, R. (2009). Starch grain and phytolith evidence for early ninth millennium B.P. maize from the Central Balsas River Valley, Mexico. Proceedings of the National Academy of Sciences USA, 106(13), 5019–5024.

Sanjur, O.I., Piperno, D.R., Andres, T.C. & Wessel-Beaver, L. (2002). Phylogenetic relationships among domesticated and wild species of Cucurbita (Cucurbitaceae) inferred from a mitochondrial gene: implications for crop plant evolution and areas of origin. Proceedings of the National Academy of Sciences USA, 99(1), 535–540.

Sauer, J.D. (1993). Historical Geography of Crop Plants: A Select Roster. CRC Press.

Chapter 44 — Watermelon (Citrullus lanatus): A Progenitor Revised Twice in Six Years, and an Archaeological Anchor That Turned Out to Belong to a Different Species

44.1 Admission: a case where the disagreement is not live, but recently and repeatedly resolved

§20.7.1's resolvability predicate R(X) has so far been applied in this cycle to cases where a single study settled a single-versus-multiple-origin question (einkorn, §2.2; argyrosperma, §43.2) and to cases where the wild progenitor remains genuinely unresolved (C. moschata, §43.3). Watermelon is admitted here as a third pattern: a case where the correct wild-population attribution has been revised twice within seven years by three independent, methodologically escalating studies, each of which explicitly overturned the one before it rather than merely adding detail. Reporting this case honestly means reporting the sequence of corrections, not only the currently favoured endpoint — since a fourth correction cannot be

ruled out by this chapter, and the chapter's own epistemic posture toward its C=1 conclusion should reflect that.

44.2 The inherited hypothesis, and why it was a case of mistaken taxonomic identity rather than mistaken biology

For most of the twentieth century, the presumed wild ancestor of the dessert watermelon was the South African citron melon, then classified within the same broad C. lanatus complex as the cultivated crop. This was not a genetic hypothesis so much as an inherited taxonomic default: citron melon and watermelon had long been treated as conspecific or near-conspecific, so citron melon's wide distribution across southern Africa was read as evidence for a southern African origin of the crop as a whole.

44.3 First correction (2015): the type specimen was not the species everyone assumed it was

Chomicki & Renner (2015, New Phytologist 205:526–532) sequenced Linnaean type material together with modern and historical Citrullus collections across eleven plastid and nuclear gene regions. The result was not a refinement but a reclassification at the root: the type specimen of the name Citrullus lanatus, collected in South Africa in 1773, turned out not to represent the species now grown as watermelon at all, but a distinct species sister to C. ecirrhosus, a tendril-less South African endemic. Once the correct type was established, the true closest wild relative of the cultivated dessert watermelon resolved to a West African species — C. mucosospermus, the egusi melon, cultivated locally for its oil-rich seeds rather than its bitter flesh. The same study raised the genus from four recognized species to seven and stated explicitly that the South African citron melon had been independently domesticated as its own crop, not as watermelon's ancestor. This is a case in which the wrong wild population had been inherited for

decades not because the genetic signal was ambiguous, but because the reference specimen defining the crop's own scientific name had been misattributed — a source of error this cycle has not previously encountered in this form.

44.4 Second correction (2021): from West Africa to the Nile Valley, on genome-scale and iconographic evidence together

Renner, Wu, Pérez-Escobar, Silber, Fei & Chomicki (2021, Proceedings of the National Academy of Sciences 118:e2101486118) sequenced a chromosome-level genome of the Kordofan melon (C. lanatus subsp. cordophanus), a nonbitter, whitish-fleshed wild form collected from the Darfur region of Sudan, and compared it against resequenced accessions spanning the genus. The Kordofan melon, not the West African egusi melon, resolved as the closest relative of domesticated watermelon and its most likely direct progenitor — displacing the 2015 study's own West African attribution rather than merely adding a second candidate alongside it. The authors combined this genomic result with a re-reading of Egyptian tomb iconography: wall illustrations from the tomb of Chnumhotep at Saqqara (dated to approximately 4,450 years BP) and from a tomb at Meir (4,350–4,200 years BP) were reinterpreted as depicting nonbitter Citrullus fruit consistent with a Nile Valley, non-West-African setting for early cultivation. C. mucosospermus was retained in the genus's history not as the direct ancestor but as a contributor via introgression, per Pérez-Escobar et al. (2022, below).

44.5 Third correction (2022): the oldest seed ever assigned to the genus turns out not to belong to the domesticated lineage at all

Pérez-Escobar, Tusso, Przelomska, Wu, Ryan, Nesbitt, Silber, Preick, Fei, Hofreiter, Chomicki & Renner (2022, Molecular Biology and Evolution 39, msac168) sequenced ancient genomes from two

archaeological Citrullus seed lots: one from the Neolithic site of Uan Muhuggiag in the Libyan Sahara, radiocarbon-dated to 6,182–6,001 calibrated years BP and long treated in the literature as the oldest known watermelon remains on morphological grounds alone (Wasylikowa & van der Veen 2004), and a second, pharaonic-period Sudanese sample dated to roughly 3,300 years BP. The genomic result reverses the morphological identification for the older sample: the Libyan seeds do not belong to the lineage leading to today's sweet, red-fleshed watermelon at all, but to a genetically distinct, bitter-fleshed Citrullus population, evidently gathered and eaten for its seeds — some show tooth-cracking damage consistent with seed consumption — rather than cultivated for sweet flesh. The younger Sudanese seed, by contrast, carries nuclear DNA from both the bitter egusi-related lineage and the sweet watermelon lineage, indicating admixture between wild/seed-use forms and the domesticated dessert lineage by the second millennium BP. This finding means the archaeobotanical anchor this cycle would otherwise have used for watermelon's earliest secure date — the Libyan Neolithic seed — corroborates seed-focused human use of a Citrullus population in the Sahara during the African Humid Period, not the domestication of the dessert-watermelon lineage itself, and this chapter reports that distinction rather than collapsing it.

44.6 What the corroborated date range actually rests on

With the Libyan seed set aside as belonging to a different population, the earliest secure evidence specifically for the domesticated, sweet-fleshed lineage is iconographic rather than archaeobotanical: the Saqqara and Meir tomb paintings reviewed in Renner et al. (2021) place consumption of a nonbitter Citrullus fruit in the Nile Valley by approximately 4,360–4,450 years BP. A separately reported 3,560-year-old desiccated leaf recovered from a

mummy's sarcophagus in a Pharaonic tomb (Renner, Pérez-Escobar, Silber, Nesbitt, Preick, Hofreiter & Chomicki, 2019, bioRxiv 642785) yielded nuclear and plastid genomic data carrying the same diagnostic mutations found in modern cultivars at the LYCB lycopene-cycling locus and at the ClBt bitterness-regulating locus, directly confirming red-fleshed, nonbitter, domesticated watermelon in Egypt by that date; the same study independently identified white-fleshed, sweet Sudanese watermelons as the closest living relatives of the domesticated form, anticipating the Kordofan-melon attribution the 2021 genome paper would confirm two years later. Between the iconographic evidence at roughly 4,400 BP and the genomically confirmed leaf at roughly 3,560 BP, the chain of evidence for a domesticated dessert watermelon in the Nile Valley is continuous; before roughly 4,400 BP, no source reviewed for this chapter reports secure evidence specifically for the domesticated lineage, as distinct from wild or seed-use Citrullus populations more broadly.

44.7 Corroboration status: C=1, but resting on convergence rather than a single decisive test

Unlike argyrosperma's Fastsimcoal2/AIC test (§43.2), no single study in the watermelon literature was built to adjudicate the wild-population question by testing named rival hypotheses against each other in one model comparison. Instead, C=1 for the dessert-watermelon lineage rests on convergence across three methodologically distinct studies published within a single decade: type-material phylogenetics (Chomicki & Renner 2015), chromosome-level comparative genomics combined with iconography (Renner et al. 2021), and ancient-DNA population genomics (Pérez-Escobar et al. 2022), further corroborated by domestication-sweep analysis in a genus-wide super-pangenome (Wu et al. 2023, Plant Biotechnology Journal, PMC10502741). All

three genomic studies agree, as of the most recent (2023) survey, that the Kordofan melon of the Sudanese Nile Valley — not citron melon, and not egusi melon — is the closest living relative and most likely direct progenitor of the dessert watermelon. No source published after 2021 proposes a rival wild population for the dessert-watermelon lineage specifically. This is unanimity, but of a kind this cycle has not catalogued before: unanimity achieved by successive replacement of the field's own prior answer, twice, rather than by one study settling the question outright. §20.7.2's second branch applies on the same terms as before — C=1, unanimous, D̄=0 by convention — but this chapter records the instability of the count's own recent history in the branch label itself (§44.9), since a reader consulting only the 2021 or 2015 literature would reach a different, now-superseded, wild-population attribution.

44.8 The genus's other domesticates: citron melon and egusi melon as separate, not rival, cases

As §44.3 already disclosed, C. amarus (citron melon) was independently domesticated in southern Africa as its own crop — used historically and to the present for livestock fodder, preserves, and, in some southern African and Central Asian traditions, as a source of pectin — and is not a rival candidate for watermelon's ancestry so much as a second, separate domestication event within the same genus, structurally comparable to C. maxima and C. argyrosperma's separate status within Cucurbita (§43.8). C. mucosospermus (egusi melon) occupies a harder-to-classify middle position: it is cultivated as a distinct seed crop across West Africa, selected for large, soft-coated, oil-rich seeds rather than flesh, and genetic mapping work has identified a specific locus (WEG6.1, chromosome 6) controlling the seed-coat trait that distinguishes it from dessert watermelon — evidence of its own targeted selection

history — while Pérez-Escobar et al. (2022) show it has also contributed genetic material into the dessert-watermelon lineage via introgression. Whether egusi melon constitutes a third fully independent domestication event or a differently-selected population within a broader, partly reticulate West-to-Northeast African Citrullus domestication complex is not resolved by any source reviewed for this chapter, and this chapter does not adjudicate it. What can be stated without qualification is that Citrullus, like Cucurbita, is a genus in which more than one lineage has been brought under cultivation independently, and that the dessert watermelon's own now-converged C=1 should not be read as implying a genus-level C=1.

44.9 Placement in the master synthesis (Appendix A.3)

Dessert watermelon (C. lanatus, progenitor C. lanatus subsp. cordophanus) is added to Appendix A.3 as a PI=0 case reached via §20.7.2's C=1-unanimous convention, branch label "C=1, unanimous as of 2023, reached by successive replacement of two prior wild-population attributions (citron melon, pre-2015; egusi melon, 2015–2021) rather than by a single adjudicating test; earliest archaeobotanical candidate (Uan Muhuggiag, Libya, ~6,000 BP) reassigned by ancient DNA to a distinct, non-ancestral population; secure dated evidence for the domesticated lineage itself begins at ~4,400 BP (iconographic) and ~3,500 BP (genomically confirmed leaf)." Citron melon (C. amarus) is cross-referenced as a second, independent domestication within the same genus, on the same footing as C. maxima and C. argyrosperma's separate entries in Chapter 43; egusi melon (C. mucosospermus) is flagged as an unresolved intermediate case — a distinctly selected seed-crop population with documented introgression into the dessert-watermelon lineage — and is not assigned a PI value of its own.

44.10 Synthesis note

Watermelon closes this run of Cucurbitaceae chapters with a caution the cycle has not needed to state so directly before: unanimity in the current literature is not the same as stability across the literature's own history, and a C=1 reached by successive correction carries a different epistemic weight than a C=1 reached by one decisive test, even when both are reported identically as PI=0 under §20.7.2's convention. The 2022 ancient-DNA result is the clearest illustration available anywhere in this cycle of why archaeological age alone cannot stand in for population-level identity: the single oldest seed ever assigned to Citrullus, cited as the crop's earliest evidence in source after source for the better part of two decades, turned out on sequencing to belong to a different, non-ancestral lineage entirely. This cycle's no-invented-data discipline (§1.4) is usually tested by what the literature has not yet measured; watermelon tests it differently, by showing what the literature spent decades confidently measuring incorrectly, and how recently that was found out.

References newly cited in Chapter 44

Chomicki, G. & Renner, S.S. (2015). Watermelon origin solved with molecular phylogenetics including Linnaean material: another example of museomics. New Phytologist, 205(2), 526–532.

Pérez-Escobar, O.A., Tusso, S., Przelomska, N.A.S., Wu, S., Ryan, P., Nesbitt, M., Silber, M.V., Preick, M., Fei, Z., Hofreiter, M., Chomicki, G. & Renner, S.S. (2022). Genome sequencing of up to 6,000-year-old Citrullus seeds reveals use of a bitter-fleshed species prior to watermelon domestication. Molecular Biology and Evolution, 39(8), msac168.

Renner, S.S., Pérez-Escobar, O.A., Silber, M.V., Nesbitt, M., Preick, M., Hofreiter, M. & Chomicki, G. (2019). A 3500-year-old leaf from

a Pharaonic tomb reveals that New Kingdom Egyptians were cultivating domesticated watermelon. bioRxiv 642785 (preprint).

Renner, S.S., Sousa, A. & Chomicki, G. (2017). Chromosome numbers, Sudanese wild forms, and classification of the watermelon genus Citrullus, with 50 names allocated to seven biological species. Taxon, 66(6), 1393–1405.

Renner, S.S., Wu, S., Pérez-Escobar, O.A., Silber, M.V., Fei, Z. & Chomicki, G. (2021). A chromosome-level genome of a Kordofan melon illuminates the origin of domesticated watermelons. Proceedings of the National Academy of Sciences USA, 118(23), e2101486118.

Wasylikowa, K. & van der Veen, M. (2004). An archaeobotanical contribution to the history of watermelon, Citrullus lanatus (Thunb.) Matsum. et Nakai (syn. C. vulgaris Schrad.). Vegetation History and Archaeobotany, 13(4), 213–217.

Wolcott, K.A., Chomicki, G., Staedler, Y.M., Wasylikowa, K., Nesbitt, M., Schönenberger, J. & Renner, S.S. (2021). Three-dimensional X-ray-computed tomography of 3300- to 6000-year-old Citrullus seeds from Libya and Egypt compared to extant seeds throws doubts on species assignments. Plants, People, Planet, 3(6), 694–702.

Wu, S. et al. (2023). A Citrullus genus super-pangenome reveals extensive variations in wild and cultivated watermelons and sheds light on watermelon evolution and domestication. Plant Biotechnology Journal (advance online / PMC10502741).

Chapter 45 — Peach (Prunus persica): A Second Rosaceae Floor Case, and a Center Described Three Different Ways

45.1 Admission, on the same footing apple's own case opened

Peach is admitted on the same footing §33.1 opened for apple: a single, repeatedly and independently corroborated domestication centre, admitted not because its count is disputed — it is not — but because the case tests, a second time, whether this cycle's three-independent-study convention (§33.2) generalises past its first application, and because it surfaces a wrinkle apple's own chapter did not have to disclose: a centre whose existence and count are wholly uncontested, but whose own descriptive location shifts across the very sources that agree on it. Its closest relative in this cycle's own terms is therefore apple (Ch.33), the cycle's first Rosaceae case and the first to be reached by convergence across three independent studies rather than by a single decisive test.

45.2 Three independent whole-genome studies, one center

The draft peach reference genome, produced by the International Peach Genome Initiative, resequenced ten further *Prunus persica* accessions and reported a domestication bottleneck consistent with a single origin in China roughly 4,000–5,000 years ago (Verde et al. 2013, Nature Genetics). Cao et al. (2014, Genome Biology), resequencing 84 accessions independently, corroborated the same single-origin reading by a different method. Cao et al. (2019, Plant Biotechnology Journal), resequencing a substantially larger panel of 418 accessions, again reports that population-structure analysis classifies all wild lines into one clade at K=2, supporting the hypothesis that all currently grown domesticated and improved peaches originated from a single domestication event. Three independent whole-genome studies, spanning three different

sample sets and six years, converge on the same C=1 reading; no source reviewed for this chapter proposes a second, independently corroborated domestication centre anywhere in the cultivated lineage. Under the same convention already applied to apple (§33.2), three independently authored studies reaching the same C=1 verdict is treated as κ=1.0, unanimous — with a further distinction from apple: no single study reviewed here proposes a rival centre at all, not even an unreplicated one.

45.3 One center, described three different ways

Where apple's single open question concerned a candidate rival location (§33.4), peach's concerns something narrower: the same, uncontested centre is given markedly different regional descriptions across the literature this chapter reviewed, without any of the descriptions amounting to a rival centre. Archaeobotanical evidence anchors the crop's earliest secure remains at two Neolithic sites in Zhejiang province, in the lower Yangzi (Changjiang) river valley — Kuahuqiao (8,000–7,000 BP; approximately 30.14°N, 120.22°E) and Tianluoshan (7,000–6,500 BP, near present-day Yuyao, approximately 30.04°N, 121.15°E) — both showing two stone-size classes consistent with early selection already underway (Zheng, Crawford & Chen 2014, PLoS ONE). Population-genomic summaries of the same single event, by contrast, describe the centre in visibly different registers across independent papers: “native to the west of China” (Li et al. 2013); “the middle and lower Changjiang or Pearl River region of China” (Cao et al. 2016, as cited in Cao et al. 2019); and, in a 2025 chromosome-level genome paper for an unrelated blood-fleshed landrace, simply “originating in southwest China.” None of these phrasings — lower Yangzi/Zhejiang, west, middle-lower Changjiang-or-Pearl-River, and southwest — is presented by its own source as a rival to the others; none is defended against the

others; none carries a citation contesting a different one. This chapter reports the divergence rather than silently adopting the most precise of the four, since picking one would misrepresent how loosely the region is actually pinned down across the literature reviewed here, for a case whose C=1 status is not itself in any doubt.

45.4 A five-relative genus, and a wild ancestor still not directly identified

A second, distinct disclosure concerns the wild progenitor itself. Cultivated peach is known to be closely related to five wild taxa — *Prunus mira*, *P. davidiana*, *P. davidiana* var. *potaninii*, *P. kansuensis* and *P. ferganensis* — of which *P. davidiana* is reported as the most diverse, an outcrossing species with roughly three times the nucleotide diversity of domesticated peach (Verde et al. 2013). None of the five is reported, in any source reviewed here, as itself the direct wild ancestor of cultivated peach: the archaeological literature states plainly that peach-stone morphology through time is consistent with an as-yet-unidentified wild *P. persica* population as the true ancestor, distinct from all five named relatives (Zheng, Crawford & Chen 2014). This is a narrower gap than *C. moschata*'s (§43.3, wild progenitor unidentified at the species level across three separate methods over two decades): here the domestication event itself is unanimously corroborated as C=1 by three independent whole-genome studies, and only the identity of the specific ancestral wild population within a well-located region remains open. This chapter does not convert that open question into a location dispute, since no rival region is proposed by any source; it is disclosed as a distinct, narrower gap sitting inside an otherwise resolved C=1 case, rather than displacing it.

45.5 Applying §20.7's predicate: PI=0, by the same route as apple

C=1, unanimous across three independent whole-genome studies (Verde et al. 2013; Cao et al. 2014; Cao et al. 2019). κ=1.0, by the same three-independent-study convention §33.2 established for apple, with no rival corroborated centre proposed anywhere in the literature reviewed. By §20.7.2's C=1-unanimous branch, $PI(C,\kappa,\bar{D}) = C \times \kappa \times \bar{D} = 1 \times 1.0 \times 0 = 0$, independent of R(X), on exactly the same footing as apple, and requiring no new distance computation.

Crop/species (model)	C	κ	$\bar{D}$ (km)	PI	Branch (§20.7.2)
Peach (single-event model)	1 (no rival centre proposed, replicated or otherwise)	1.000	0	0	resolvable, unanimous

Peach reaches the same PI=0 floor as einkorn, rice (C=1 model), sunflower, horse, sheep, dromedary, donkey, potato and apple — reusing apple's own three-independent-study route rather than opening a new one, since the underlying evidentiary shape (three independent genomic studies, no disclosed rival at all) is the same, only cleaner: apple carried one disclosed, unreplicated rival claim (§33.4); peach, as reviewed here, carries none.

45.6 Synthesis note

Peach is added to Appendix A.2 as its twenty-third member, and to this cycle's Plantae total as its thirty-third species, the second

Rosaceae case after apple (Ch.33). Its own contribution to this cycle's method is narrower than most: not a new route to the PI=0 floor, but a demonstration that the floor can be reached with less residual disagreement than apple's own case carried, while still surfacing a genuinely new shape of disclosure — a center whose location is undisputed in count and unchallenged by any rival, yet described in four incompatible registers by sources that never engage with one another's phrasing. This chapter closes with the same caution apple's own synthesis note made explicit: three independent studies converging without any rival claim, however clean, licenses κ=1.0 under this cycle's own convention, not certainty beyond what that convention permits. A fourth study proposing a corroborated rival centre, or pinning the wild progenitor to one of the five named relatives or to a sixth, would require revision; nothing in this chapter forecloses that, and nothing in it anticipates the answer.

References newly cited in Chapter 45

Cao, K., Zheng, Z., Wang, L., Liu, X., Zhu, G., Fang, W., Cheng, S., Zeng, P., Chen, C., Wang, X., et al. (2014). Comparative population genomics reveals the domestication history of the peach, Prunus persica, and human influences on perennial fruit crops. Genome Biology, 15, 415.

Cao, K., Zhou, Z., Wang, Q., Guo, J., Zhao, P., Zhu, G., Fang, W., Chen, C., Wang, X., Wang, X., Tian, Z. & Wang, L. (2016). Genome-wide association study of 12 agronomic traits in peach. Nature Communications, 7, 13246.

Cao, K., Li, Y., Deng, C.H., Gardiner, S.E., Zhu, G., Fang, W., Chen, C., Wang, X. & Wang, L. (2019). Comparative population genomics identified genomic regions and candidate genes associated with

fruit domestication traits in peach. Plant Biotechnology Journal, 17(10), 1954–1970.

Li, X.-W., Meng, X.-Q., Jia, H.-J., Yu, M.-L., Ma, R.-J., Wang, L.-R., et al. (2013). Peach genetic resources: diversity, population structure and linkage disequilibrium. BMC Genetics, 14(1), 84.

The International Peach Genome Initiative, Verde, I., Abbott, A.G., Scalabrin, S., Jung, S., Shu, S., et al. (2013). The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. Nature Genetics, 45, 487–494.

Zheng, Y.-F., Crawford, G.W. & Chen, X.-G. (2014). Archaeological evidence for peach (Prunus persica) cultivation and domestication in China. PLoS ONE, 9(9), e106595.

Chapter 46 — Fig (Ficus carica): The Case §40.1 Ranked Last, and Why

46.1 Admission, closing the run §40.1 opened

Fig is admitted as the seventh and final case of the run §40.1 previewed when Capsicum opened this batch: peperoncino, pea, flax, the other domesticated squashes, watermelon, peach, and — ranked last in that preview, and for a stated reason — fig. §40.1 placed it there not because a case was lacking, but because the genomic literature supporting it was, in the chapter's own words at the time, less definitive than the others and needed checking before any commitment was made. This chapter is that check. It does not close on the same footing as its six predecessors in the run: pea, the other *Cucurbita* species, and watermelon reached either a disputed-location R(X)=0 reading or a unanimous C=1 floor; peperoncino, flax, and peach reached similarly disclosed but computed positions. Fig closes differently — not because less evidence exists than for

those cases, but because the evidence that does exist, reviewed here for the first time in this cycle, is split between an archaeological claim unresolved for nearly two decades and a genomic reading published only months before this chapter was written, and no source reviewed here reconciles the two.

46.2 The archaeobotanical claim, and the dispute that has followed it since 2006

The dating previously assumed for fig domestication — described by *Kislev, Hartmann & Bar-Yosef (2006)* themselves as "generally accepted" at roughly 6,500 years ago in the Near East — was directly challenged by that same paper's own central finding: nine carbonized fig fruits and hundreds of individual drupelets recovered from Gilgal I, an early Neolithic village in the lower Jordan Valley some 13 km north of Jericho, in deposits dated to 11,400–11,200 years before present. The fruits were parthenocarpic — lacking viable embryos — and Kislev et al. read this trait as evidence that the Gilgal I trees had been propagated from intentionally planted cuttings, proposing fig as the first domesticated plant of the Neolithic Revolution, roughly a thousand years before the earliest corroborated cereal domestications already covered in this cycle (Ch.2).

Lev-Yadun, Ne'eman, Abbo & Flaishman (2006), commenting in the same journal later that year, disputed the inference rather than the find itself: parthenocarpic fig trees are known to arise spontaneously within wild populations and to persist and spread without human intervention, so that carbonized parthenocarpic fruit at a Neolithic site does not, on its own, distinguish a cultivated tree from a wild parthenocarpic mutant that Neolithic foragers simply gathered from. Kislev, Hartmann & Bar-Yosef (2006), responding in the same issue, maintained their original reading. This cycle's own no-invented-data, disclosed-disagreement discipline (§1.4) does not adjudicate between them: no source

reviewed for this chapter reports a subsequent, independent test — genetic, isotopic, or otherwise — that has settled which of the two readings the Gilgal I material actually supports, and none is supplied here to close the gap.

46.3 A 2025–2026 population-genomic study proposes a diffuse, multi-regional model

Independently of the Gilgal I dispute, and addressing a different question, *Khadari, Kakenov, Achtak, Charafi, Chalak, Santoni, Kjellberg & Cornille* genotyped 949 fig accessions — cultivated and spontaneous individuals of *Ficus carica sensu stricto*, together with its close relatives *F. carica* subsp. *rupestris* and *F. colchica* — sampled from 48 sites across 14 Mediterranean and Near Eastern countries, genotyped at 14 microsatellite markers. The study was posted to bioRxiv in September 2025 and subsequently accepted for publication in *Horticulture Research* (2026). Bayesian clustering resolved three major gene pools within *F. carica sensu stricto* itself — Moroccan-Algerian, Northern Mediterranean, and Levantine — with cultivated and spontaneous trees genetically indistinguishable from one another within each region. On the strength of this local genetic continuity, and the absence of the large-scale west-to-east diffusion signature the same authors report for olive, they conclude that fig domestication "likely occurred independently in at least two Mediterranean regions" — the Levant, and a western/central area — proposing a diffuse, regionally repeated model of domestication in place of the single-Levantine-origin-then-diffusion hypothesis the field had previously carried over from olive and grapevine by analogy, rather than tested directly for fig itself.

46.4 What this reading does, and does not, establish under this cycle’s convention

Two features of the 2025–2026 study keep it from entering this cycle's PI computation, on the same disclosed-limits footing §1.4

has applied throughout. First, it is a single study: no second, independently authored population-genomic analysis has yet engaged with its multi-regional reading, in either direction, in the literature reviewed for this chapter. This cycle has repeatedly withheld κ from single, structurally unreplicated proposals even when they are the most recent and most comprehensive treatment a case has received (§29.3's alpaca caveat is the closest precedent); the same restraint applies here, for a question — whether C=1 or C≥2 — more consequential than any single κ value, since it is the count the rest of the index's formal apparatus (§20.7) presupposes as already settled before D̄ or κ can be assigned at all. Second, and independently of replication: the study itself reports its three gene pools as regions, not as point-level candidate origins. No coordinate is given for the Levant cluster or the Moroccan-Algerian cluster at the resolution this cycle's D̄ computations elsewhere require (e.g. §22.5's cotton centres, §9.5's common-bean centres) — so that even a second, corroborating study would not by itself supply what a PI computation needs; a further, point-resolving study would still be required. Fig therefore fails the resolvability predicate R(X) at two independent stages at once: the C-count stage, where the traditional C=1 assumption and the newly proposed C≥2 reading are each single-source and mutually unreconciled; and, conditionally, the location stage, where neither reading, if accepted, currently offers a point coordinate to compute a distance from.

46.5 Why no distance value is reported, unlike this cycle's other ⊥ cases

Every other member of Appendix A.3 reports some distance figure, however qualified — maize's disputed-location span, cotton's three-of-four illustrative subset, even llama's single center still anchors one end of a comparison. Fig reports none, for a reason distinct from any of them: this chapter is not choosing between rival point coordinates the literature has proposed and left unresolved (maize, Bactrian camel), and it is not missing a coordinate for an

otherwise agreed center (chicken, turkey, cotton, llama). It is missing agreement on the count itself, at the same stage *C. moschata* (Ch.43, §43.3) was left unresolved, but by a structurally different route: *C. moschata*'s gap is a twenty-year absence of any candidate wild population under any model; fig's gap is a freshly contested reading, where the newer of the two proposals is the one this chapter finds more directly evidenced by population-level sampling, but where "more directly evidenced" is not this cycle's own standard for computation — replication and point-level resolution are, and neither is yet available.

46.6 Placement in the master synthesis (Appendix A.3)

Fig is added to Appendix A.3 as a thirteenth member, on a ninth distinct ground within that section's own running tally of reasons (§43.7's note last counted eight): a proposed C≥2 reading — Khadari et al.'s diffuse, multi-regional model — that is both unreplicated by any second study and, on its own terms, reported at regional rather than point-level resolution, sitting alongside a traditional C=1 assumption that this chapter finds was itself never independently corroborated by a whole-genome or population-genomic study in the literature reviewed here. No PI value is computed, and none is estimated in its place.

46.7 Synthesis note

Fig closes the run §40.1 opened, and does so as the run's only member to reach neither a resolvable PI value nor the PI=0 floor — an outcome consistent with §40.1's own preview, which ranked it last of seven candidates precisely because its literature was, at the time, judged not yet ready to commit to a number. Reviewed properly, this turns out not to be a case of thin evidence but of two separate bodies of evidence that do not speak to each other: a nineteen-year-old archaeological dispute about a single site's mode of use, and a months-old genomic study about the crop's overall

population structure, addressing different questions on different timescales, with no source reviewed here attempting to reconcile them. §1.4's no-invented-data discipline was written for exactly this outcome — not to force a synthesis the literature has not yet produced, but to disclose, as precisely as the sources allow, that it has not yet been produced. A future independent population-genomic or whole-genome study, corroborating or refuting Khadari et al.'s regional structure and resolving it to point-level candidate origins, would allow this chapter to be revised into a computed case; nothing above anticipates which reading such a study would support.

References newly cited in Chapter 46

Khadari, B., Kakenov, S., Achtak, H., Charafi, J., Chalak, L., Santoni, S., Kjellberg, F. & Cornille, A. (2025/2026). Diffuse and regionally structured domestication of the common fig (Ficus carica L.) in the Mediterranean Basin. Posted to bioRxiv September 2025; published in Horticulture Research, 2026, uhag113.

Kislev, M.E., Hartmann, A. & Bar-Yosef, O. (2006). Early domesticated fig in the Jordan Valley. Science, 312(5778), 1372–1374.

Kislev, M.E., Hartmann, A. & Bar-Yosef, O. (2006). Response to Comment on "Early Domesticated Fig in the Jordan Valley". Science, 314(5806), 1683.

Lev-Yadun, S., Ne'eman, G., Abbo, S. & Flaishman, M.A. (2006). Comment on "Early Domesticated Fig in the Jordan Valley". Science, 314(5806), 1683.

Chapter 47 — Sweet Potato (Ipomoea batatas): A Case Outside the Index on Two Independent Grounds

47.1 Admission, opened after the cycle's own stated closure

The volume's own closing pages, following Chapter 46, describe the run beginning with Capsicum (§40.1) as having reached its last case in fig, and describe agriculture's arc, taken with the earlier ceramics, metallurgy, horse, and wheel volumes, as closing the Network Horizon cycle's founder-effect programme. This chapter does not reopen that claim so much as qualify it: fig was the last case previewed in §40.1's own run, not the last case this cycle could in principle examine, and a case meeting this cycle's own admission bar — a live, source-documented dispute this cycle's no-invented-data discipline (§1.4) is built to disclose rather than adjudicate — was raised for consideration after that closure was written. Sweet potato (Ipomoea batatas) is admitted here on that basis: as a supplementary case, reached after the cycle's stated closing point, held to the same evidentiary standard as every other chapter, and disclosed as arriving in that order rather than folded silently into the run it follows.

Sweet potato is, on first look, an unlikely candidate for a late addition: it is one of the world's most extensively sequenced staple crops, and thirteen years of molecular work already exist for it at the point this chapter is written. What that thirteen years of work has produced, however, is not a converging answer but a still-open, still-shifting dispute over what founded the cultivated lineage at all — and, layered on top of it, a second and entirely separate dispute over how the crop crossed the Pacific once domestication, however it happened, was complete. Both are documented below. Neither is resolved here.

47.2 The origin-mechanism dispute, thirteen years and counting

Roullier, Duputié, Wennekes, Benoit, Fernández Bringas, Rossel, Tay, McKey & Lebot (2013), working from chloroplast and nuclear ITS sequences together with nuclear microsatellites across a broad sample of cultivated sweet potato and its wild diploid and polyploid relatives, reported no support for an allopolyploid origin involving Ipomoea trifida and I. triloba together, the hypothesis standing in the literature at the time. Their own data instead supported an autopolyploid origin from the same lineage that gave rise to I. trifida — but from at least two distinct autopolyploidization events in differentiated wild populations, one read as Central American and one as South American in origin, with later secondary contact and introgression between the two. On this reading, sweet potato's own founding event is not singular: it is, at least, two, from one wild species.

Muñoz-Rodríguez, Carruthers, Wood, Williams, Weitemier, Kronmiller, Ellis, Anglin, Longway, Harris, Rausher, Kelly, Liston & Scotland (2018), working from far denser nuclear and chloroplast phylogenies generated five years later, again supported an autopolyploid origin with I. trifida as sole progenitor — but read their own, larger dataset as consistent with a single origin, explained by chloroplast capture (I. trifida acting first as progenitor, then again as a later introgression partner) rather than by Roullier et al.'s two independent founding events. The two papers agree on the broad mechanism — autopolyploidy, I. trifida as progenitor — and disagree on the count that follows from it, one event or at least two, from data of different scale, five years apart, with no source reviewed here reconciling the two counts directly.

Gao, Soriano, Cao, Yang & Lu (2020), analysing 811 conserved single-copy genes, rejected both terms of that agreement at once: their own reading proposes sweet potato as a segmental allopolyploid carrying three partially differentiated subgenomes,

traced not to I. trifida alone but to I. trifida, I. tenuissima, and I. littoralis together — explicitly framing hexaploid sweet potato as neither a true autopolyploid nor a true allopolyploid in the classical two-way sense either the 2013 or the 2018 paper had assumed.

Muñoz-Rodríguez, Wells, Wood, Carruthers, Anglin, Jarret & Scotland (2022) then described a new species, Ipomoea aequatoriensis, a wild autotetraploid from coastal Ecuador identified by morphological, phylogenetic, and genomic analysis as sweet potato's closest known tetraploid relative — proposing it, alongside the already-established diploid I. trifida, as the two direct parents of an allopolyploid origin, and explicitly framing this as a revision of the autopolyploid readings both the 2013 and 2018 papers had converged on.

Yan, Li, Wang, Wang, Moeinzadeh, Quispe-Huamanquispe, Fan, Fang, Wang, Nie, Wang, Tanaka, Heider, Kreuze, Gheysen, Wang, Vingron, Bock & Yang (2024), using a newly developed haplotype-based phylogenetic method across sweet potato's two constituent subgenomes, accepted I. aequatoriensis as a genome donor but reassigned its role: on their reading, I. aequatoriensis supplied the diploid-side subgenome, while a separate wild tetraploid population, I. batatas 4x, not I. aequatoriensis, supplied the tetraploid-side subgenome — the reverse of the pairing Muñoz-Rodríguez et al. (2022) had proposed two years earlier, and, on the count of contributing taxa and their assigned roles, a third distinct allopolyploid model in four years.

Wu, Sun, Zhao, Hamilton, Mollinari, De Siqueira Gesteira, Kitavi, Yan, Wang, Yang, Yencho, Buell & Fei (2025), reporting the first haplotype-resolved, chromosome-level genome assembly of a sweet potato cultivar, found ancestry from I. aequatoriensis contributing a substantial share of the genome, consistent with a donor role rather than a distant outgroup — but reported the remaining, I. batatas 4x-like portion of the genome as still not

traceable to any specific, currently sampled wild population, describing that donor as not yet identified in the wild. Their own reading revives Gao et al.'s (2020) "segmental allopolyploid" framing, on updated species assignments, but explicitly leaves one of the genome's own contributing lineages without a named source population at the most technically advanced reading this dispute has yet received.

47.3 Why the count predicate itself is not well-formed

§20.7.1's predicate for assigning a center count C presupposes a single, genetically bounded domestication event with an agreed wild progenitor lineage, over which candidate centers can then be proposed and counted or contested — the situation this cycle's A.4 group (dog, sorghum, lentil, tea, soybean; §12.4, §25.4, §2.8.2, §35.3, §36.6) already reports for cases where the wild lineage itself is settled and only the center count within it is disputed. Sweet potato's own literature does not reach that starting point. Across the six studies reviewed in §47.2, the wild taxa proposed as contributing to the cultivated hexaploid genome range from one (I. trifida alone, autopolyploid) to two, under at least three non-equivalent pairings (I. trifida + I. triloba, rejected by Roullier et al. 2013; I. aequatoriensis + I. trifida, Muñoz-Rodríguez et al. 2022; I. aequatoriensis + I. batatas 4x, Yan et al. 2024 and, on updated assignment, Wu et al. 2025), to three (I. trifida + I. tenuissima + I. littoralis, Gao et al. 2020). This is not a disputed count of centers within one agreed progenitor lineage, of the kind A.4 already reports; it is a disagreement over how many wild species, and which ones, founded the cultivated lineage at all — the same structural problem this cycle's Appendix A.5 already reports for banana, where admixture across several named taxa compounds into one mosaic cultivar genome before any C can be assigned (§27.4–§27.5). Sweet potato belongs beside banana in A.5, not beside dog or sorghum in A.4, on the same ground: §20.7.1's predicate

presupposes a single proposed center set with a genetically bounded referent, and no reading reviewed here supplies one that the rest of the reviewed literature agrees to.

47.4 A dispute that is not layered but rival

Banana's own A.5 entry describes a sequence of hybridization events that compounds, cumulatively, into one genome (§27.5): the studies documenting it do not so much contradict one another as accumulate. Sweet potato's literature does not accumulate in the same way. Roullier et al. (2013) and Muñoz-Rodríguez et al. (2018) agree on mechanism and disagree on count; Gao et al. (2020) rejects the mechanism both papers share; Muñoz-Rodríguez et al. (2022) and Yan et al. (2024) agree on a two-taxon allopolyploid frame and disagree on which taxon played which role, a reversal rather than a refinement; and Wu et al. (2025), the most technically direct reading available at the time this chapter was written, both supports part of the 2024 assignment and leaves one contributing lineage's source population formally unidentified. No two of the six studies reviewed in §47.2 report the same set of contributing taxa in the same roles. This does not change the classification reached in §47.3 — sweet potato remains ⊥ at the same stage banana does, the count predicate's own object undefined — but it is reported here as a distinct feature of the case: unlike banana, where each new study has tended to add to an accepted sequence, sweet potato's thirteen-year record is one of successive, largely non-cumulative revision, with the most recent (2025) reading still returning an unresolved lineage rather than a closing one.

47.5 A second, independent dispute: human transport or natural dispersal to Polynesia

Separately from the question of how the crop was first founded, a second, long-running dispute concerns how it later reached Polynesia, thousands of kilometres and, on any reading, a

substantial span of time removed from wherever and however domestication itself occurred. Roullier, Benoit, McKey & Lebot (2013), testing what they term the "tripartite hypothesis" against modern and herbarium chloroplast and nuclear microsatellite data, reported strong support for a prehistoric, human-mediated transfer of sweet potato from the Peru–Ecuador region into Polynesia, later followed by two separate, historically documented European-era introductions from Mexico and the Caribbean; their reading is reinforced, though not directly tested, by the documented lexical resemblance between Polynesian terms for the crop (kumara and its cognates) and Quechua-family terms for the same plant.

Muñoz-Rodríguez et al. (2018), in the same paper already discussed for the origin-mechanism dispute in §47.2, read their own phylogenetic placement of a 1769 Cook-voyage herbarium specimen from Polynesia as evidence against the tripartite hypothesis: the Polynesian lineage's split from its closest American relatives, on their molecular-clock estimate, considerably predates any documented human presence in the Pacific, which they take as evidence for natural, pre-human long-distance dispersal — by birds, wind, or ocean currents — rather than for a Polynesian voyaging return from South America. This should be recorded precisely, and not conflated with a stronger claim the source itself does not make: the divergence-time estimate is a lineage-split age, not a directly dated arrival on any specific island, and the same paper's own, separately stated estimate for the age of the sweet potato lineage as a whole is older still; the natural-dispersal reading rests on treating the lineage split as a reasonable proxy for the timing of arrival, an inferential step the paper itself presents as interpretation rather than as a second, independently dated line of evidence.

Ioannidis, Blanco-Portillo, Sandoval, Hagelberg, Miquel-Poblete, Moreno-Mayar, Rodríguez-Rodríguez, Quinto-Cortés, Auckland,

Parks, Robson, Hill, Avila-Arcos, Sockell, Homburger, Wojcik, Barnes, Herrera, Berríos, Acuña, Llop, Eng, Huntsman, Burchard, Gignoux, Cifuentes, Verdugo, Moraga, Mentzer, Bustamante & Moreno-Estrada (2020) do not analyse sweet potato at all: working from genome-wide human data across 807 individuals from seventeen Polynesian island populations and fifteen Pacific-coast Native American groups, they report conclusive evidence for a single prehistoric contact event in eastern Polynesia, prior to the settlement of Rapa Nui, with a Native American population most closely related to present-day Colombian groups, dated to approximately 1200 CE. This establishes that pre-Columbian, transoceanic human contact of some kind did occur; it is cited in the tripartite-hypothesis literature as circumstantial support for the plausibility of human-mediated plant transport specifically, but it is human genetic evidence, not sweet-potato genetic evidence, and this chapter does not treat it as resolving the plant-dispersal question on its own.

No source reviewed here reconciles Roullier et al.'s (2013) human-transport reading with Muñoz-Rodríguez et al.'s (2018) natural-dispersal reading; both remain current in the literature at the time this chapter was written, addressing the same transfer event from data of different kinds — population genetics of the crop itself, in both cases, plus, for the human-contact question specifically, population genetics of the people who might have carried it.

47.6 Why the two disputes do not combine into a single ⊥ reason

Fig (Ch.46, §46.4) reached ⊥ at two stages of the same predicate at once — the C-count stage and, conditionally, the location stage — because both disputes concerned the same domestication event under §20.7's own sequential model. Sweet potato's second dispute is not a further stage of the same predicate: it concerns a documented transfer, long after domestication however it occurred,

of an already-domesticated crop across the Pacific, a question §20.7.1's predicate was never built to address at all, prior stage or otherwise. Whichever origin-mechanism reading in §47.2–§47.4 eventually prevails, the Polynesia dispersal question in §47.5 would remain exactly as open as it is reported here; and whichever way the Polynesia question is eventually settled, it would resolve nothing about which, or how many, wild taxa founded the cultivated hexaploid lineage. The two disputes are reported together in this chapter because they attach to the same species and because both meet this cycle's own bar for disclosure (§1.4), not because they are one another's stages.

47.7 Placement in the master synthesis (Appendix A.5)

Sweet potato is added to Appendix A.5 as a sixth member, alongside banana, yeast, honey bee, koji, and vanilla, on the same ground already stated for banana in §47.3: §20.7.1's predicate presupposes a single proposed center set with a genetically bounded referent, which the reviewed literature does not supply for a wild-progenitor count ranging from one to three species across six studies published between 2013 and 2025. No PI value is computed, and none is estimated in its place. The Polynesia dispersal dispute (§47.5) is recorded in this chapter for completeness and is not separately tabulated in Appendix A, on the logic stated in §47.6: it is not a reason internal to §20.7.1's predicate, so it does not add a distinct row or a distinct ground within that appendix's own running tally.

47.8 Synthesis note

Sweet potato is not admitted here to contradict the closure the pages following Chapter 46 already state; it is admitted as a supplementary case, reached after that closure, held to the same bar every other chapter in this cycle has been held to, and disclosed in that order rather than smoothed into the run that precedes it. What

thirteen years of increasingly detailed molecular work has produced for this species is not a converging answer but a widening one: the number of candidate contributing wild taxa proposed across the six studies reviewed here has not settled toward one reading, and the most technically advanced of them, published in 2025, still returns a lineage without a fully identified source. §1.4's no-invented-data discipline was written for exactly this outcome — not to force a synthesis this literature has not produced, but to record, as precisely as the sources allow, that it has not been produced, and to record separately, rather than fold together, the second and unrelated dispute over how the crop later crossed the Pacific. A future study identifying the wild population Wu et al. (2025) report as still undiscovered, or reconciling any two of the six origin-mechanism readings reviewed in §47.2, would allow this chapter to be revised; nothing above anticipates which reading such a study would support.

References newly cited in Chapter 47

Gao, M., Soriano, S.F., Cao, Q., Yang, X. & Lu, G. (2020). Hexaploid sweetpotato (Ipomoea batatas (L.) Lam.) may not be a true type to either auto- or allopolyploid. PLoS ONE, 15(3), e0229624.

Ioannidis, A.G., Blanco-Portillo, J., Sandoval, K., Hagelberg, E., Miquel-Poblete, J.F., Moreno-Mayar, J.V., Rodríguez-Rodríguez, J.E., Quinto-Cortés, C.D., Auckland, K., Parks, T., Robson, K., Hill, A.V.S., Avila-Arcos, M.C., Sockell, A., Homburger, J.R., Wojcik, G.L., Barnes, K.C., Herrera, L., Berríos, S., Acuña, M., Llop, E., Eng, C., Huntsman, S., Burchard, E.G., Gignoux, C.R., Cifuentes, L., Verdugo, R.A., Moraga, M., Mentzer, A.J., Bustamante, C.D. & Moreno-Estrada, A. (2020). Native American gene flow into Polynesia predating Easter Island settlement. Nature, 583(7817), 572–577.

Muñoz-Rodríguez, P., Carruthers, T., Wood, J.R.I., Williams, B.R.M., Weitemier, K., Kronmiller, B., Ellis, D., Anglin, N.L., Longway, L., Harris, S.A., Rausher, M.D., Kelly, S., Liston, A. & Scotland, R.W. (2018). Reconciling conflicting phylogenies in the origin of sweet potato and dispersal to Polynesia. Current Biology, 28(8), 1246–1256.

Muñoz-Rodríguez, P., Wells, T., Wood, J.R.I., Carruthers, T., Anglin, N.L., Jarret, R.L. & Scotland, R.W. (2022). Discovery and characterization of sweetpotato's closest tetraploid relative. New Phytologist, 234(4), 1185–1194.

Roullier, C., Benoit, L., McKey, D.B. & Lebot, V. (2013). Historical collections reveal patterns of diffusion of sweet potato in Oceania obscured by modern plant movements and recombination. Proceedings of the National Academy of Sciences, 110(6), 2205–2210.

Roullier, C., Duputié, A., Wennekes, P., Benoit, L., Fernández Bringas, V.M., Rossel, G., Tay, D., McKey, D. & Lebot, V. (2013). Disentangling the origins of cultivated sweet potato (Ipomoea batatas (L.) Lam.). PLoS ONE, 8(5), e62707.

Wu, S., Sun, H., Zhao, X., Hamilton, J.P., Mollinari, M., De Siqueira Gesteira, G., Kitavi, M., Yan, M., Wang, H., Yang, J., Yencho, G.C., Buell, C.R. & Fei, Z. (2025). Phased chromosome-level assembly provides insight into the genome architecture of hexaploid sweetpotato. Nature Plants, 11, 1951–1959.

Yan, M., Li, M., Wang, Y., Wang, X., Moeinzadeh, M.-H., Quispe-Huamanquispe, D.G., Fan, W., Fang, Y., Wang, Y., Nie, H., Wang, Z., Tanaka, A., Heider, B., Kreuze, J.F., Gheysen, G., Wang, H., Vingron, M., Bock, R. & Yang, J. (2024). Haplotype-based phylogenetic analysis and population genomics uncover the origin and domestication of sweetpotato. Molecular Plant, 17(2), 277–296.

Chapter 48 — Reindeer (Rangifer tarandus): The Boundary Honey Bee Lacked, Measured but Not Located

48.1 Admission, continuing the cycle's supplementary practice

Sweet potato (Ch.47) was admitted after this cycle's own stated closure, on the ground that a case meeting the cycle's admission bar had been raised after that closure was written. Reindeer (Rangifer tarandus) is admitted here on the same basis and by the same route: not as a reopening of that closure, but as a second supplementary case, reached still later, held to the same evidentiary standard as every chapter before it. It is admitted for a reason distinct from sweet potato's own: not a predicate that fails to find a well-formed object to count (§47.3), but a predicate that finds an object — a measurable genetic boundary between wild and domestic populations, the first this cycle has been able to report a number for since honey bee's chapter reported the absence of one (§31.4) — and still returns ⊥, for reasons compounding across three independent grounds documented below.

48.2 The two-pole model: archaeology and the first genetic evidence

Archaeological evidence for reindeer domestication is itself unsettled on dating grounds this chapter does not attempt to resolve. In Arctic Siberia, harness fittings recovered from Ust'-Polui, Tiutei-Sale I, and Iarte VI on the Yamal Peninsula, interpreted by comparison with contemporary Nenets sled-training equipment, have been dated to approximately 2,000 years before present (Losey et al., 2020). In Fennoscandia, the earliest direct evidence of draught use — sledge fittings, and a shift in settlement pattern away from major waterbodies — is conventionally placed in the Late Iron Age, around 800–900 CE, with earlier and more contested material (lidded wooden coffins shaped like sledges,

dated 1510–1130 BCE) not treated here as settled evidence of domestication itself.

Genetic evidence for where domestication happened is more securely established, and points to two geographically separated origins rather than one. Røed et al. (2008), analysing mitochondrial sequences and nuclear microsatellites across wild and domestic herds throughout Eurasia, found two mitochondrial haplotype clusters (II and Ib) present in 89% of domestic reindeer sampled in Norway and Finland and essentially absent from central and eastern Russian herds, together with a clustering analysis assigning Russian and Fennoscandian herds to statistically distinct groups. The authors read this as evidence that Sámi domestication in Fennoscandia proceeded independently of domestication among indigenous cultures in western Russia — a two-pole model, not a one-pole model with later diffusion.

48.3 A boundary this cycle can, for the first time in this group, actually measure

Every other case grouped so far in Appendix A.3 or A.5 on grounds of a genetic-boundary problem — honey bee foremost among them (§31.4) — reaches ⊥ or is excluded from the index's domain because no source reports a usable differentiation statistic at all. Reindeer's literature does not have that problem. Weldenegodguad et al. (2020), sequencing a de novo reindeer genome together with 23 additional individuals, report a genome-wide fixation index (FST) of 0.039786 between the two main geographic groups their data resolve — Fennoscandian versus Russian–Alaskan. Wu et al. (2024), resequencing 32 genomes from Canada, Norway, Siberia, and China, report a mean FST of 0.08 between wild and domestic populations specifically, and set that figure directly against other domesticates measured the same way in their own cited literature: dog versus wolf, FST = 0.223 (Axelsson et al., 2013); taurine versus zebu cattle, FST = 0.215 (Porto-Neto et al., 2014); Asiatic mouflon

versus sheep landraces and improved breeds, FST = 0.125 and 0.132 respectively (Li et al., 2020). On this comparison, reindeer's wild–domestic boundary is real, reported, and the weakest of the five. Kharzinova et al. (2018), genotyping 135 animals across the Nenets Autonomous District, Murmansk region, western Taymyr, and Yakutia with the BovineHD BeadChip, report pairwise FST values between domestic breed pairs as low as 0.018 and between wild subpopulations as low as 0.004, with domestic–wild comparisons generally higher but never approaching dog/wolf's or cattle's own reported figures. No case reviewed elsewhere in this cycle for a boundary problem has a reported number to set against these; reindeer is the first.

48.4 Sex-biased erosion, not absence, of the boundary

The boundary reindeer's literature measures is not stable in the way a floor-case boundary is. Anderson, Kvie, Davydov & Røed (2017), studying wild and domestic Rangifer in Northeastern Zabaĭkal'e, Russia (documented at approximately 57°N), report strong genetic differentiation between the two forms alongside a documented indigenous tradition of deliberate, controlled interbreeding — herders exchanging or importing wild males to renew domestic bloodlines. Mitochondrial haplotype sharing between the wild and domestic gene pools was found to be low, which the authors read as evidence that gene flow across the boundary is overwhelmingly male-mediated: domestic herds absorb wild paternal lineages at a measurable rate while their maternal lineages remain comparatively stable. This is the structural inverse of honey bee's problem: where honey bee's chapter found no boundary to erode because none was ever reported as established (§31.4), reindeer's literature reports an established boundary being continuously, deliberately, and asymmetrically eroded from one side only — a third condition this cycle has not yet catalogued under either heading.

48.5 A complication no other case in this cycle has: one pole's own evidence undermined after the fact, and its own wild source still unidentified

Røed, Bjørklund & Olsen (2018), working from ancient and modern mitochondrial sequences from Fennoscandia, report that the maternal gene pool of Scandinavian domestic reindeer underwent a major genetic replacement during the sixteenth and seventeenth centuries, concurrent with the transition to full pastoralism, with significant loss of native haplotypes and introduction of non-native ones. This bears directly on §48.2: the two mitochondrial haplotype clusters (II and Ib) that Røed et al. (2008) used to argue for an independent Fennoscandian pole are themselves, on the 2018 paper's own later and more temporally resolved reading, partly a post-medieval introduction rather than an unbroken signal from the original domestication event the 2008 paper's argument requires. No source reviewed here reconciles the two readings directly; the 2018 paper does not withdraw the two-pole model, but it does show that the specific genetic evidence supporting one of its two poles is not the continuous record it was read as in 2008.

A second and independent problem attaches to the same pole. Pokharel, Weldenegodguad et al. (2023), reporting the largest population-genomic dataset for reindeer assembled to date (58 individuals, a new reference assembly), state plainly that their whole-genome sequencing data of Russian geographic populations — Nenets and Eveny domestic reindeer among them — do not reveal a candidate population whose ancestry could account for the Fennoscandian domestic lineage; the ancestral wild source of Fennoscandian domestic reindeer, on this reading, remains unidentified even in the most technically advanced dataset available at the time this chapter was written. The Russian/Siberian pole carries no equivalent problem in the same source: its own genetic affinities (to Finnish wild forest reindeer, to a domestic

population from the Zabaįkal region) are reported, even where their causes are not fully settled. The asymmetry — one of two proposed centers with an unidentified wild source, the other without — is structurally distinct from C. moschata's chapter (Ch.43, §43.7), where no candidate wild population is reported for any center; reindeer's problem sits at only one of its two poles, not both.

48.6 Further proposed poles the genetic data has never tested

The two-pole genetic model is not the only model reindeer's own literature has proposed. Røed, Kvie, Losey et al. (2020), reviewing earlier ethnographic and archaeological literature, record polycentric hypotheses dating to the early twentieth century locating additional, independent origins of reindeer husbandry in the Sayan and Baikal regions of southern Siberia (Hatt, 1919; Wiklund, 1918; Maksimov, 1928), and more recent proposals locating further independent origins on the Yamal Peninsula (Fedorova, 2000) and in the Polar Ural Mountains (Golovnëv, 1993). None of these four additional candidate centers has been directly tested against the genomic clustering reported in §48.2–§48.3, which resolves populations at the scale of 'Fennoscandia' and 'Russia/Alaska' broadly rather than at the scale of these named sub-regions. The count question this cycle's A.4 group (dog, sorghum, lentil, tea, soybean) already reports for cases with an agreed wild lineage and a disputed number of centers within it is, for reindeer, unresolved at a finer grain than even the genetic two-pole literature has reached: C could be as low as two, on the genomic evidence directly cited here, or as high as five or six, on ethnohistoric proposals no genomic dataset reviewed in this chapter has yet evaluated.

48.7 No point-level coordinate for either genetically corroborated pole

§20.7.1's resolvability predicate requires each proposed center to be a reported point — a latitude/longitude pair tied to a named site or surveyed location — not a named region. Guinea pig (§37.5), turkey (§21.5), and soybean (§36.5) each supplied an illustrative great-circle distance because their own cited literature named specific archaeological sites or cities as anchors for otherwise-broad centers. No source reviewed in this chapter offers an equivalent anchor for reindeer's two genetically corroborated poles: 'Fennoscandia' spans Norwegian, Swedish, and Finnish reindeer-herding territory at the scale of a subcontinent, and the 'Russian/Alaskan' cluster in Pokharel et al. (2023) itself spans sampling sites from Arkhangelsk to Sakha to Alaska, thousands of kilometres apart, treated as one genetic pole rather than one place. This chapter therefore follows the rule this cycle's own appendix already applied to koji, cacao, and date palm rather than the rule it applied to guinea pig, turkey, and soybean (Appendix C, closing note to Chapters 32–35): a case named only as a region, with no anchor point reported anywhere in the reviewed literature, is left out of the distance calculation entirely rather than assigned a coordinate this cycle did not find in a source.

48.8 Applying §20.7's predicate: R(X)=0, on a compound and new ground

Neither proposed center clears §20.7.1's point-resolvability bar ($r_i = 0$ for both), so $R(X) = 0$ regardless of which reading of C in §48.6 is adopted, and §20.7.2's partial function returns $\perp$ on its third branch. The reason is not a single one of this cycle's nine existing A.3 grounds. It is not chicken's reason (no candidate center reaches point resolution, independent of count) alone, because reindeer's count is itself independently disputed across a wider range than chicken's ever was. It is not soybean's or guinea pig's count-dispute reason alone, because reindeer's boundary, unlike theirs, is directly

measured (§48.3) rather than absent or taxonomically prior to measurement. It is not honey bee's or C. moschata's reason, because reindeer's boundary exists and one pole's wild source, while unidentified, is not unidentified for both poles as C. moschata's is for its only one. What is new is the combination: a measured, asymmetrically eroding boundary (§48.3–§48.4), attached to two centers neither of which is point-resolved (§48.7), one of which has its own founding evidence partly undercut by a later, more temporally resolved study and its own wild source still unidentified in the best available data (§48.5), with the count itself open at a coarser grain than the genetic literature has tested (§48.6). No other case in this cycle combines a reported differentiation statistic with an unresolved count and an internally contested evidentiary basis for one of its own centers.

48.9 Placement in Appendix A.3, a tenth distinct ground

Reindeer is added to Appendix A.3 as a fourteenth row and a tenth distinct ground, after maize, Bactrian camel, chicken, turkey, cotton, broomcorn millet, cat, llama, guinea pig, capsicum, pea, C. moschata, and fig. No PI value is computed for reindeer, and none is estimated in its place, consistent with §1.4. No total previously reported for this appendix changes as a result of a row that did not exist before; reindeer's own arithmetic is stated fresh here.

48.10 Synthesis note

Reindeer was raised, in the discussion leading to this chapter, as a candidate for a genuinely new form of irresolvability rather than a further instance of one already catalogued — honey bee's boundary problem was the closest existing precedent, and the two cases turned out, on the sources' own terms, not to be the same. Honey bee's chapter reported an absence: no source establishes a genetic boundary between managed and wild populations for most of the species' management history. Reindeer's literature reports the

opposite starting point — a boundary that is measured, quantified, and set explicitly against other domesticates in the cited sources themselves (§48.3) — and still fails to produce a PI, for reasons that have nothing to do with whether a boundary exists and everything to do with where its two proposed centers are, how many there may really be, and whether one center's own founding evidence has survived scrutiny it received only after the two-pole model was already established. §1.4's discipline was written to report exactly this kind of outcome without smoothing it into a shape this cycle's existing categories already had room for. A future study resolving Pokharel et al.'s (2023) unidentified Fennoscandian wild source, or testing the Sayan-Baikal, Yamal, and Polar Ural proposals reviewed in §48.6 against genomic data, would allow this chapter to be revised; nothing above anticipates which reading such a study would support.

References newly cited in Chapter 48

Anderson, D.G., Kvie, K.S., Davydov, V.N. & Røed, K.H. (2017). Maintaining genetic integrity of coexisting wild and domestic populations: Genetic differentiation between wild and domestic Rangifer with long traditions of intentional interbreeding. Ecology and Evolution, 7, 6790–6802.

Kharzinova, V.R., Dotsev, A.V., Deniskova, T.E., Solovieva, A.D., Fedorov, V.I., Layshev, K.A., Romanenko, T.M., Okhlopkov, I.M., Wimmers, K., Reyer, H., Brem, G. & Zinovieva, N.A. (2018). Genetic diversity and population structure of domestic and wild reindeer (Rangifer tarandus L. 1758): A novel approach using BovineHD BeadChip. PLOS ONE, 13(11), e0207944.

Losey, R.J. et al. (2020). Domestication as Enskilment: Harnessing Reindeer in Arctic Siberia. Journal of Archaeological Method and Theory, published online May 12, 2020.

Pokharel, K., Weldenegodguad, M., Dudeck, S., Honkatukia, M., Lindeberg, H., Mazzullo, N., Paasivaara, A., Peippo, J., Soppela, P., Stammler, F. & Kantanen, J. (2023). Whole-genome sequencing provides novel insights into the evolutionary history and genetic adaptation of reindeer populations in northern Eurasia. Scientific Reports, 13, 23019.

Røed, K.H., Flagstad, Ø., Nieminen, M., Holand, Ø., Dwyer, M.J., Røv, N. & Vilà, C. (2008). Genetic analyses reveal independent domestication origins of Eurasian reindeer. Proceedings of the Royal Society B: Biological Sciences, 275, 1849–1855.

Røed, K.H., Bjørklund, I. & Olsen, B.J. (2018). From wild to domestic reindeer – Genetic evidence of a non-native origin of reindeer pastoralism in northern Fennoscandia. Journal of Archaeological Science: Reports, 19, 279–286.

Røed, K.H., Kvie, K.S., Losey, R.J. et al. (2020). Temporal and structural genetic variation in reindeer (Rangifer tarandus) associated with the pastoral transition in Northwestern Siberia. Ecology and Evolution, published online 2020.

Weldenegodguad, M. et al. (2020). Genome sequence and comparative analysis of reindeer (Rangifer tarandus) in northern Eurasia. Scientific Reports, 10, 8980.

Wu, B., Ren, Q., Yan, X., Zhao, F., Qin, T., Xin, P., Cui, X., Wang, K., Du, R., Røed, K.H., Côté, S.D., Yannic, G., Li, Z. & Qiu, Q. (2024). Resequencing of reindeer genomes provides clues to their docile habits. Evolution Letters, 8, 494–504.

Chapter 49 — Quinoa (Chenopodium quinoa): A Sixth Member of the Disputed-Count Group, on a Different Evidentiary Footing

49.1 Admission, continuing the cycle's supplementary practice

Sweet potato (Ch.47) and reindeer (Ch.48) were both admitted after this cycle's own stated closure, each on the ground that a case meeting the cycle's admission bar had been raised after that closure was written. Quinoa (Chenopodium quinoa) is admitted here on the same basis, as a third supplementary case, held to the same evidentiary standard as every chapter before it. It is admitted for a reason distinct from both of its predecessors: not an unresolved count of contributing wild taxa (§47.3), and not a measured boundary attached to unlocated centers (§48.7–§48.8), but a live disagreement about how many domestication events, not which or how many wild species, produced the crop's two principal cultivated forms — a dispute that sits inside a single agreed wild-progenitor lineage, and belongs beside dog, sorghum, lentil, tea, and soybean in this cycle's Appendix A.4, on evidence of a different kind from any of the five.

49.2 The progenitor is agreed; the event count is not

Quinoa's cultivated lines fall into two broad groups: a highland (Andean altiplano, Peru and Bolivia) group and a lowland or coastal group, centred on Chile. Jarvis, Ho, Lightfoot, Schmöckel, Li, Borm, Ohyanagi, Mineta, Michell, Saber, Kharbatia, Rupper, Sharp, Dally, Boughton, Woo, Gao, Schijlen, Guo, Momin, Negrão, Al-Babili, Gehring, Roessner, Jung, Murphy, Arold, Gojobori, van der Linden, van Loo, Jellen, Maughan & Tester (2013/2017), reporting the first chromosome-scale quinoa reference genome together with resequencing of a wild-relative panel, found the wild diploid Chenopodium hircinum to be the closest wild relative of the

cultivated tetraploid across all sampled accessions — a point no source reviewed in this chapter disputes. What the same paper's own data left open was the count: a single wild-caught C. hircinum accession (BYU 566, from Chile) placed at the phylogenetic base of the coastal cultivated ecotype specifically, rather than at the base of both ecotypes together, which the authors read as consistent with two independent domestication events — one highland, one coastal — rather than the single event, highland-first, coastal-later reading the literature had previously assumed.

49.3 Two later, independent panels place the same diagnostic accession differently

Zou, Chen, Xiao, Liu, Zhou, Diao, Sun, Yang, Grover, Wang, Rushton, Bao, Yang, Wang, Ye, Lin, Yang, Bennetzen & Xu et al. (2017), assembling an independent high-quality quinoa reference genome from a different accession, placed the same BYU 566 sample at the base of both the lowland and the highland cultivated clades together, rather than at the base of the coastal clade alone — a direct disagreement with Jarvis et al.'s own placement of the identical diagnostic accession, from an independently generated dataset. Patiranage, Kebede, Alqudah, Kassahun, Simon, Curti, Delfini, Rojas, Barros, Cai, Coituz, Franco, Espinoza, Yactayo, Adhikari, Bhargava, Gómez-Pando, Bertero, Fuentes, Bertero, Emrani & Schmid et al. (2022), sequencing whole genomes from 310 accessions — an order of magnitude more than the sixteen quinoa lines and two wild accessions Jarvis et al. worked from — likewise found BYU 566 basal to both cultivated clades, and state directly that their own, larger dataset does not follow the two-independent-events reading of Jarvis et al. (2017) for that reason. The disagreement is not, therefore, between one team's early hypothesis and everyone else's later confirmation of it: it is between three independently assembled datasets, two of which place a shared diagnostic wild accession one way and one of which places it

another, with the two more recent and more heavily sampled readings agreeing with each other against the earlier one.

49.4 A fourth, maternally inherited line of evidence

Maughan, Chaney, Lightfoot, Cox, Tester, Jellen & Jarvis (2019), reporting the first complete mitochondrial genome assembled for the genus Chenopodium together with a chloroplast genome from the same quinoa accession (PI 614886), examined the highland/coastal division through an evidentiary channel none of the nuclear-genome studies above draws on: maternally inherited organellar DNA, which tracks the female parental lineage directly rather than being reconstructed from a nuclear phylogeny shaped by both parents. Phylogenetic networks built from mitochondrial and chloroplast variants across the sampled Chenopodium panel supported two conclusions: that an A-genome diploid served as the maternal, cytoplasm-donating parent in quinoa's ancestral tetraploidization event, and — bearing directly on the dispute at issue in this chapter — that highland and coastal quinoa were independently domesticated, each from its own maternal source. This is not a fourth vote in the same nuclear-genome debate reviewed in §49.2–§49.3; it is a different marker class returning the same two-event conclusion Jarvis et al. (2017) drew from nuclear data before Zou et al. (2017) and Patiranage et al. (2022) read the same nuclear locus differently. Maughan et al. (2019) do not resolve the disagreement over the placement of BYU 566 in the nuclear trees, and their own sampling is centred on a different accession (PI 614886); the organellar result stands alongside the nuclear datasets as a fourth line of evidence bearing on the count, not as an adjudication between them.

49.5 A single-origin reading, and the alternative it proposes but does not test

Mizuno, Toyoshima, Fujita, Fukuda, Kobayashi, Ueno, Tanaka, Tanaka, Nishihara, Mizukoshi, Yasui & Fujita (2020), genotyping 136 newly generated inbred lines by genotyping-by-sequencing together with existing whole-genome sequencing data, resolved three genetic subpopulations (northern highland, southern highland, lowland) and found the highest nucleotide diversity in the highland groups, read as consistent with a single domestication event near Lake Titicaca followed by later spread to the lowland. The same paper is explicit that its own single-origin reading leaves open how the lowland population came to differ so sharply from its nearer, southern-highland relatives, and floats — without testing — the possibility that lowland quinoa's distinctiveness reflects later crossing with wild C. hircinum in the Chilean lowland itself, a mechanism that would leave a single founding event but a compound later history, rather than two founding events as such.

49.6 Three scenarios where the field itself does not choose one

Patiranage et al. (2022), having found their own data inconsistent with Jarvis et al.'s specific two-event reading, do not conclude in favour of a single event either. They report three explicitly unresolved alternative readings of their own FST value (0.36 between highland and lowland) and associated linkage-disequilibrium and diversity statistics: two independent domestication events with a substantial bottleneck on the lowland population; a single domestication with strong subsequent population growth specific to the lowland; or strong adaptive selection acting on the lowland population after a single domestication event. The paper states plainly that distinguishing among the three would require sequencing a larger, more representative panel of the wild outgroup species (C. berlandieri,

C. hircinum, C. pallidicaule, C. suecicum) than any study reviewed here has yet assembled, and does not itself choose among them.

49.7 Why this is a disputed count, not a disputed location or an unbounded lineage

Unlike sweet potato, whose wild-taxon identity is itself disputed across a range of one to three candidate species (§47.3), quinoa's wild progenitor is undisputed across every study reviewed in this chapter: Chenopodium hircinum. Unlike banana, koji, or sweet potato in Appendix A.5, no source here proposes a sequence of accumulating hybridization events across several named taxa; the disagreement concerns a single lineage and a single count, C=1 versus C=2, precisely the shape of problem this cycle's A.4 group already catalogues for dog, sorghum, lentil, tea, and soybean. What distinguishes quinoa's version of that dispute is its evidentiary basis. Dog's C=1-versus-2 disagreement (Bergström et al. 2020 versus Frantz et al. 2016) turns on competing interpretations of substantially overlapping ancient-DNA datasets by partly overlapping research groups. Quinoa's dispute instead turns on the placement, by three independently generated genomic datasets published across nine years (2017, 2017, 2020, 2022), of one diagnostic wild accession — the same physical sample, BYU 566 — at the base of one cultivated clade in the earliest reading and at the base of both clades in every reading since, without any of the four papers reviewed here directly reconciling the discrepancy in placement of that single accession.

49.8 No coordinate dispute; κ is left unassigned, following A.4's established rule

As with dog, sorghum, lentil, tea, and soybean, no distance or coordinate computation is offered here. §20.7.1's predicate requires a resolved C before a corroboration count κ, and through it a Polycentricity Index, can be assigned; no reading reviewed in this

chapter commands sufficient consensus to fix C for quinoa. Following the rule already applied to the other five members of this appendix group, κ is left unassigned and PI is not computed.

49.9 Placement in Appendix A.4 as a sixth member

Quinoa is added to Appendix A.4 as a sixth member, alongside dog, sorghum, lentil, tea, and soybean, on the same structural ground already stated for that group: a disputed center count within an agreed wild-progenitor lineage, rather than a disputed location or an unbounded founding event. No PI value is computed, and none is estimated in its place, consistent with §1.4.

49.10 Synthesis note

Quinoa is not admitted here to reopen the closure the pages following Chapter 46 already state; it is admitted, like sweet potato and reindeer before it in this same supplementary run, as a case meeting the cycle's own admission bar after that closure was written. What nine years of increasingly well-resourced sequencing has produced for this species is not a converging count but an oscillating one: a single wild accession has anchored two different placements, the earlier one unreplicated by either later, larger dataset, and the most recent, best-resourced reading available declines to choose among three of its own proposed explanations for the pattern it finds. This is a distinct form of instability from dog's live disagreement between overlapping research teams, or from the coarser markers elsewhere in this cycle that simply failed to detect a signal later technology found (§50.3–§50.4): here, successive high-resolution datasets keep returning to the same unresolved question about the same physical specimen. A future study sequencing a larger and more representative wild-outgroup panel, of the kind Patiranage et al. (2022) themselves call for, would allow this chapter to be revised; nothing above anticipates which of the three proposed readings such a study would support.

References newly cited in Chapter 49

Jarvis, D.E., Ho, Y.S., Lightfoot, D.J., Schmöckel, S.M., Li, B., Borm, T.J.A., Ohyanagi, H., Mineta, K., Michell, C.T., Saber, N., Kharbatia, N.M., Rupper, R.R., Sharp, A.R., Dally, N., Boughton, B.A., Woo, Y.H., Gao, G., Schijlen, E.G.W.M., Guo, X., Momin, A.A., Negrão, S., Al-Babili, S., Gehring, C., Roessner, U., Jung, C., Murphy, K., Arold, S.T., Gojobori, T., van der Linden, C.G., van Loo, E.N., Jellen, E.N., Maughan, P.J. & Tester, M. (2017). The genome of Chenopodium quinoa. Nature, 542, 307–312.

Maughan, P.J., Chaney, L., Lightfoot, D.J., Cox, B.J., Tester, M., Jellen, E.N. & Jarvis, D.E. (2019). Mitochondrial and chloroplast genomes provide insights into the evolutionary origins of quinoa (Chenopodium quinoa Willd.). Scientific Reports, 9, 185.

Mizuno, N., Toyoshima, M., Fujita, M., Fukuda, S., Kobayashi, Y., Ueno, M., Tanaka, K., Tanaka, T., Nishihara, E., Mizukoshi, H., Yasui, Y. & Fujita, Y. (2020). The genotype-dependent phenotypic landscape of quinoa in salt tolerance and key growth traits. DNA Research, 27(4), dsaa022.

Patiranage, D.S.R., Rey, E., Emrani, N., Wellman, G., Schmid, K., Jarvis, D.E., Rey, E. & Maughan, P.J. et al. (2022). Genome-wide association study in quinoa reveals selection pattern typical for crops with a short breeding history. eLife, 11, e66873.

Zou, C., Chen, A., Xiao, L., Muller, H.M., Ache, P., Haberer, G., Zhang, M., Jia, W., Deng, P., Huang, R., Fahlgren, N., Ilut, D.C., Chow, J., Bilinski, P., Katz, E., Denolf, P., Bakker, E.-J., Schranz, M.E., Mockler, T.C., Bergelson, J., Nagler, J.E., Schilling, M. & Zhang, J. (2017). A high-quality genome assembly of quinoa provides insights into the molecular basis of salt bladder-based salinity tolerance and the exceptional nutritional value. Cell Research, 27, 1327–1340.

Chapter 50 — Helmeted Guinea Fowl (Numida meleagris): A Location Dispute Resolved, and a Chronology That Was Not

50.1 Admission, continuing the cycle's supplementary practice

Sweet potato (Ch.47), reindeer (Ch.48), and quinoa (Ch.49) were each admitted after this cycle's own stated closure, on the ground that a case meeting the cycle's admission bar had been raised after that closure was written. Helmeted guinea fowl (Numida meleagris) is admitted here as a fourth supplementary case, on a footing distinct from all three: not an unresolved wild-taxon count (§47.3), not a measured boundary attached to unlocated centers (§48.7–§48.8), and not a disputed event count within an agreed lineage (§49.7), but a case in which the most recent genomic study appears to resolve a century-old regional dispute in favour of one candidate area over its rivals, and still fails §20.7.1's point-resolvability bar on the same ground as chicken and turkey — while adding a chronological conflict none of this cycle's other cases has reported.

50.2 Three hypotheses, from three kinds of evidence, over more than a century

Darwin (1883), in the second edition of The Variation of Animals and Plants under Domestication, proposed that domestic guinea fowl descended from wild stock in East Africa. Blench & MacDonald, editing The Origins and Development of African Livestock: Archaeology, Genetics, Linguistics and Ethnography (2000), assembled archaeological, linguistic, and ethnographic evidence pointing instead to a West African domestication. Andah, Okpoko, Shaw & Sinclair, editing The Archaeology of Africa: Food, Metals and Towns (2014), reviewing artistic and osteological material, proposed a third reading: dual, independent origins less

than 2,000 years before present (YBP), in both West Africa (Mali) and East Africa (Sudan). As Shen, Peng, Adeola, Kui, Duan, Miao, Eltayeb, Lichoti, Otecko, Strillacci, Gorla, Bagnato, Charles, Sanke, Dawuda, Okeyoyin, Musina, Njoroge, Agwanda, Kusza, Nanaei, Pedar, Xu, Du, Nneji, Murphy, Wang, Esmailizadeh, Dong, Ommeh & Zhang (2021) note in introducing their own genomic study, this dual-origin dating is itself younger than Egyptian hieroglyphic depictions of the bird dated to roughly 2400 BC, and younger still than the bird's documented introduction into Greece around 500 BC — though neither of those earlier records indicates whether the depicted birds were wild or domesticated.

50.3 Earlier marker systems found no structure to locate a center with

Adeola, Ommeh, Murphy, Wu, Peng & Zhang (2015), sequencing the mitochondrial D-loop of Nigerian domestic guinea fowl, and Murunga, Kennedy, Imboma, Malaki, Kariuki, Ndiema, Obanda, Agwanda, Lichoti & Ommeh (2018), doing the same for Kenyan domestic populations, both reported an absence of detectable genetic structuring among African domestic guinea fowl populations. Kayang, Youssao, Inoue, Naazie, Abe, Ito & Inoue-Murayama (2010) and Botchway, Adenyo, Kayang, Hayano & Inoue-Murayama (2013), using microsatellite markers, reported the same pattern. All four studies read this absence of structure as evidence for a comparatively recent domestication followed by rapid, continent-wide dispersal — not as evidence for any one candidate region over another. At this technological resolution, the dispute among Darwin's, Blench & MacDonald's, and Andah et al.'s hypotheses was not adjudicated; it could not be, because the marker systems available found no geographic signal at all to adjudicate with.

50.4 Whole-genome data recovers a signal the markers could not

Vignal, Boitard, Thébault, Dayo, Yapi-Gnaore, Youssao Abdou Karim, Berthouly-Salazar, Pálinkás-Bodzsár, Guémené, Thibaud-Nissen, Warren, Tixier-Boichard & Rognon (2019), assembling the first guinea fowl reference genome and pool-sequencing whole genomes from twelve populations across Africa and Europe — including wild birds from Burkina Faso (West Africa) and South Africa — reported that the wild population from Burkina Faso showed a closer genetic relationship to domestic populations than the wild population from South Africa did. Shen et al. (2021), assembling an improved reference genome and sequencing 129 individual whole genomes — 89 domestic, 34 wild, and 6 wild relatives, from Africa, Asia, and Europe — found by phylogeny, PCA, and ADMIXTURE that wild guinea fowl from Nigeria (West Africa) were consistently closer to domestic populations than wild guinea fowl from Kenya or Sudan (East Africa), and state this result rejects Darwin's East African hypothesis directly. Demographic modelling (momi2) in the same study inferred a single split between wild and domestic lineages at approximately 5,452 years before present (95% bootstrap interval 9,916–2,548), with a later divergence between Nigerian and Sudanese domestic lineages at approximately 1,261 YBP.

50.5 A chronology the genomic resolution does not itself address

The dual-origin hypothesis that Shen et al.'s genomic evidence is read as superseding (Andah et al. 2014) is dated to under 2,000 YBP. The same paper's own inferred wild–domestic split, on which its West African, single-origin conclusion rests, is dated to approximately 5,452 YBP — three to four millennia earlier. Shen et al. (2021) offer their result as resolving the geographic dispute (West Africa over East Africa, and over a dual origin), not the temporal one, and no passage in the paper reconciles why a split this old would leave the earliest cited archaeological husbandry

evidence — the Malian and Sudanese material Andah et al. (2014) review, dated under 2,000 YBP — as the earliest available trace of an event the genomic data place millennia before it. Nor does any source reviewed here establish whether the ~5,452 YBP split itself marks domestication, or an earlier population separation that a domestication event, evidenced only much later archaeologically, subsequently made use of. This is a distinct question from the geographic one, and it remains open in the literature reviewed for this chapter.

50.6 Why this still does not reach a computable C

Despite genomic convergence on West Africa, and more specifically on Nigeria, as the region most closely related to domestic guinea fowl, no source reviewed in this chapter names a specific archaeological site, settlement, or surveyed coordinate for the founding event itself. "Nigeria," "Burkina Faso," and "West Africa" are country- and region-scale labels, the same grain of resolution this cycle already reports for chicken (§20.6) and turkey (§21.5–§21.6): a best-supported single candidate region without a point-level anchor. §20.7.1's resolvability predicate requires a reported point — a surveyed location or named site — not a national or subcontinental label, and no reading reviewed here supplies one.

50.7 A second complication: reversal, not mere refinement, of the underlying signal

Guinea fowl's version of this problem differs from chicken's and turkey's in one respect worth recording separately. In those two cases, successive studies have refined estimates without reversing the basic shape of the evidence available. In guinea fowl's literature, the shift is more abrupt: mitochondrial and microsatellite markers (2010–2018) found no detectable population structure at all among African domestic guinea fowl, a finding those studies' own authors read as evidence of rapid post-domestication dispersal erasing any

geographic signal; whole-genome sequencing (2019, 2021) then recovered a clear structure distinguishing a Nigerian wild-affiliated cluster from Kenyan and Sudanese wild populations. This is not two datasets disagreeing about where the same signal points, as with the single diagnostic wild accession in quinoa's literature (§49.3); it is a lower-resolution technology reporting no signal where a higher-resolution technology later found one.

50.8 Applying §20.7's predicate: R(X)=0, sharing chicken's and turkey's ground, compounded

Because the best-supported candidate center — West Africa, and within it Nigeria — is not reported at point resolution ($r_i=0$), $R(X)=0$ under §20.7.1, and §20.7.2 returns $\perp$, following the same branch already applied to chicken and turkey. What guinea fowl adds is not a new branch but two compounding features neither of those two cases carries: an unreconciled, multi-millennial gap between the genomic split date and the surviving archaeological husbandry-evidence date for the same event (§50.5), and a reversal, rather than a refinement, of the underlying structural signal as marker technology improved (§50.7). Guinea fowl is, with donkey (Ch.23), one of only two species this cycle's own sources describe as domesticated within Africa (Shen et al. 2021, citing Gifford-Gonzalez & Hanotte 2011).

50.9 Placement in Appendix A.3

Guinea fowl is added to Appendix A.3 as a fifteenth row, sharing chicken's and turkey's no-point-resolution ground, with the compounding features of §50.5 and §50.7 recorded as this case's own distinguishing detail rather than as a new numbered ground. No PI value is computed, and none is estimated in its place, consistent with §1.4.

50.10 Synthesis note

Guinea fowl was raised, in the discussion leading to this chapter, as a candidate worth checking rather than assuming: a species whose domestication genetics looked, on first inspection, too thin a literature to support a genuine case. The check found the opposite — a sequence of studies running from 2010 microsatellite work through a 2021 population-genomic study of 129 whole genomes, resolving a geographic dispute that had stood, in some form, since Darwin. What it could not find, in any source reviewed, was a reconciliation between that resolution's own chronology and the archaeological record the resolution is read against, nor an account of why decades of marker-based work found no structure at all before whole-genome sequencing recovered one clearly. §1.4's no-invented-data discipline was written for exactly this kind of outcome: to report a genuine, well-evidenced resolution on one axis of a dispute without manufacturing a resolution on the other axis the sources do not supply. A future study dating the archaeological material at Ust'-Polui-scale precision in West Africa, or testing whether the ~5,452 YBP split itself corresponds to domestication or precedes it, would allow this chapter to be revised; nothing above anticipates which reading such a study would support.

References newly cited in Chapter 50

Adeola, A.C., Ommeh, S.C., Murphy, R.W., Wu, S.-F., Peng, M.-S. & Zhang, Y.-P. (2015). Mitochondrial DNA variation of Nigerian domestic helmeted guinea fowl. Animal Genetics, 46(5), 576–579.

An, H., Qi, X., Gaynor, M.L., Hao, Y., Gebken, S.C., Mabry, M.E., McAlvay, A.C., Teakle, G.R., Conant, G.C., Barker, M.S., Fu, T., Yi, B. & Pires, J.C. (2019). Transcriptome and organellar sequencing highlights the complex origin and diversification of allotetraploid Brassica napus. Nature Communications 10, 2878.

Andah, B., Okpoko, A., Shaw, T. & Sinclair, P. (Eds.) (2014). The Archaeology of Africa: Food, Metals and Towns. London: Routledge.

Blench, R. & MacDonald, K.C. (Eds.) (2000). The Origins and Development of African Livestock: Archaeology, Genetics, Linguistics and Ethnography. London: UCL Press.

Botchway, P.K., Adenyo, C., Kayang, B.B., Hayano, A. & Inoue-Murayama, M. (2013). Development of 31 polymorphic microsatellite markers for guinea fowl (Numida meleagris) using next-generation sequencing technology. Conservation Genetics Resources, 5, 1163–1165.

Daniels, J. & Roach, B.T. (1987). Taxonomy and evolution. In Heinz, D.J. (ed.), Sugarcane Improvement Through Breeding, Vol. 11, pp. 7–84. Amsterdam: Elsevier.

Darwin, C. (1883). The Variation of Animals and Plants under Domestication (2nd ed.). London: John Murray.

Kayang, B.B., Youssao, I., Inoue, E., Naazie, A., Abe, H., Ito, S. & Inoue-Murayama, M. (2010). Genetic diversity of Helmeted Guineafowl (Numida meleagris) based on microsatellite analysis. Journal of Poultry Science, 47, 120–124.

Murunga, P., Kennedy, G.M., Imboma, T., Malaki, P., Kariuki, D., Ndiema, E., Obanda, V., Agwanda, B., Lichoti, J.K. & Ommeh, S.C. (2018). Mitochondrial DNA D-loop diversity of the helmeted guinea fowls in Kenya and its implications on HSP70 gene functional polymorphism. BioMed Research International, 2018, 7314038.

Shen, Q.-K., Peng, M.-S., Adeola, A.C., Kui, L., Duan, S., Miao, Y.-W., Eltayeb, N.M., Lichoti, J.K., Otecko, N.O., Strillacci, M.G., Gorla, E., Bagnato, A., Charles, O.S., Sanke, O.J., Dawuda, P.M., Okeyoyin, A.O., Musina, J., Njoroge, P., Agwanda, B., Kusza, S., Nanaei, H.A.,

Pedar, R., Xu, M.-M., Du, Y., Nneji, L.M., Murphy, R.W., Wang, M.-S., Esmailizadeh, A., Dong, Y., Ommeh, S.C. & Zhang, Y.-P. (2021). Genomic analyses unveil helmeted guinea fowl (Numida meleagris) domestication in West Africa. Genome Biology and Evolution, 13(6), evab090.

Vignal, A., Boitard, S., Thébault, N., Dayo, G.-K., Yapi-Gnaore, V., Youssao Abdou Karim, I., Berthouly-Salazar, C., Pálinkás-Bodzsár, N., Guémené, D., Thibaud-Nissen, F., Warren, W.C., Tixier-Boichard, M. & Rognon, X. (2019). A guinea fowl genome assembly provides new evidence on evolution following domestication and selection in galliformes. Molecular Ecology Resources, 19, 997–1014.

Chapter 51 — European Rabbit (Oryctolagus cuniculus): A Location Without Dispute, and a Date Three Methods Cannot Agree On

51.1 Admission, continuing the cycle's supplementary practice

Sweet potato (Ch.47), reindeer (Ch.48), quinoa (Ch.49), and helmeted guinea fowl (Ch.50) were each admitted after this cycle's own stated closure, on the ground that a case meeting the cycle's admission bar had been raised after that closure was written. European rabbit (Oryctolagus cuniculus) is admitted here as a fifth supplementary case, on a footing distinct from all four: not an unresolved wild-taxon count (§47.3), not a measured boundary attached to unlocated centers (§48.7–§48.8), not a disputed event count within an agreed lineage (§49.7), and not a resolved location paired with an unreconciled chronology and a reversed structural signal (§50.5, §50.7), but a case in which three independent genomic studies agree on a single source population, at the same regional grain already catalogued for chicken, turkey, and guinea fowl — while the source literature itself states, in terms no other case in this

cycle uses, that the traditional single-event date built on top of that agreed location is not merely disputed but demonstrably built on a documented citation error, and that no method available — genetic, archaeological, or textual — converges on a replacement date.

51.2 Three independent genomic studies, one location

Carneiro, Afonso, Geraldes, Garreau, Bolet, Boucher, Tircazes, Queney, Nachman & Ferrand (2011), resequencing sixteen autosomal and X-linked loci across wild and domestic rabbits, found domestic rabbits nested within O. c. cuniculus populations from France rather than from the Iberian Peninsula, and read the pattern as consistent with a single origin of domestication in wild populations from France. Carneiro, Rubin, Di Palma, Albert, Alföldi, Martinez Barrio, Pielberg, Rafati, Sayyab, Turner-Maier, Younis, Afonso, Aken, Alves, Barrell, Bolet, Boucher, Burbano, Campos, Chang, Duranthon, Fontanesi, Garreau, Heiman, Johnson, Mage, Peng, Queney, Rogel-Gaillard, Ruffier, Searle, Villafuerte, Xiong, Young, Forsberg-Nilsson, Good, Lander, Ferrand, Lindblad-Toh & Andersson (2014), assembling a reference genome and resequencing domestic breeds against wild rabbits sampled at fourteen localities across the Iberian Peninsula and southern France, confirmed the same source population and reported that the wild ancestor was, at the time of domestication, confined to the Iberian Peninsula and southern France. Alves, Carneiro, Afonso et al. (2015), genotyping forty-five microsatellites across 471 individuals from sixteen breeds and thirteen wild localities, reported the same French-population signal and estimated a founding domestic population of fewer than 1,200 individuals. No source reviewed in this chapter proposes a second, rival domestication center for O. c. cuniculus; Long, Qiu, Zeng, Tang & Zhang (2003), sequencing mitochondrial control-region variation in Chinese domestic rabbits, and Xie, Song, Wang, Di, Li, Wang, Yang, Qiao, Wang, Li, Xie, Xie, Liu, Ning, Tang, Li, Wu, Zhang, Wang &

Fan (2024), sequencing 142 whole genomes and twenty-five further NCBI accessions across six Chinese indigenous breeds, both report that Chinese domestic rabbits descend from this same European source population via later introduction and trade, not from an independent Asian domestication; Xie et al. (2024) place that introduction at approximately 800–1,500 years before present, arriving first on China's southeast coast before spreading inland.

51.3 The cost of the bottleneck: diversity loss and breed structure

Alves, Carneiro, Afonso et al. (2015)'s same microsatellite survey quantifies what the founding event in §51.2 cost the lineage genetically, a figure no other case in this cycle's A.3 group reports alongside its location result. Averaged across the sixteen surveyed breeds, domestication and subsequent breed formation together are estimated to have removed approximately one-fifth of the genetic diversity present in the ancestral wild population, with a mean F_ST of 22% now separating breeds from one another despite the short time elapsed since breed diversification. The same study found no structure beyond this breed-level signal — no deeper geographic sub-structuring within the domestic lineage — a pattern its authors read as the joint product of a single, recent geographic origin (§51.2) and a non-bifurcating history of breed formation, in which most breeds were themselves derived from repeated crosses between two or more earlier breeds rather than from independent regional lines. This is a measurement of the bottleneck's genetic magnitude, not of its date or its location; it neither sharpens §51.2's already-resolved geography nor bears on the chronological dispute addressed from §51.5 onward, and is reported here as a distinct, independently corroborated quantity rather than folded into either.

51.4 Not a point-level coordinate, on the same ground already catalogued for chicken, turkey, and guinea fowl

Despite this three-study convergence, no source reviewed here names a surveyed site, settlement, or point coordinate for the founding population. "Southern France," "the Iberian Peninsula and southwest France," and "wild populations from France" are region-scale labels, the same grain of resolution this cycle already reports for chicken (§20.6), turkey (§21.5–§21.6), and guinea fowl (§50.6): a best-supported, essentially unanimous single candidate region without a site-level anchor. §20.7.1's resolvability predicate requires a reported point, and no reading reviewed here supplies one.

51.5 The inherited single-event narrative, and how it collapsed

The literature prior to 2018 assumed domestication proceeded from a single, dateable event: monks in southern France, around AD 600, prompted by a papal ruling attributed to Pope Gregory the Great that fetal rabbits (laurices) did not count as meat and could be eaten during Lent. Irving-Pease, Frantz, Sykes, Callou & Larson (2018), tracing this claim back through its citation chain, found no such ruling in the historical record, and identified the likely source of the confusion as a conflation of Pope Gregory the Great with Gregory of Tours, whose own writings mention a layperson, Roccolenus, eating young rabbits during Lent — a passing anecdote about one man's diet, not a papal edict directed at an institution. No source reviewed in this chapter defends the AD 600 date on independent grounds once this attribution is set aside.

51.6 Three methods, three incommensurate readings

Irving-Pease et al. (2018) tested the AD 600 date against genetic, archaeological, and textual evidence and found the three methods do not converge. The genetic molecular-clock estimate, based on divergence between wild and domestic rabbit genomes, returned a

date of approximately 15,000 years before present — a figure the authors read not as a domestication date but as the signature of a Pleistocene population split driven by glacial-period range contraction, predating domestication of any species. The archaeological record shows osteological differentiation between wild and domestic skeletal morphology becoming detectable only more than 2,000 years after the earliest Roman-period rabbit-keeping, placing the morphological threshold many centuries after both the Roman evidence and the traditional AD 600 date. The textual record itself begins earlier still: Varro's De Re Rustica (1st century BC), cited by Irving-Pease et al. (2018), describes keeping rabbits alongside hares in a leporarium on the Iberian Peninsula under Roman management, centuries before the monastic narrative's proposed starting point. No two of the three methods agree on an order of magnitude, let alone a date.

51.7 A fourth line, older than any of the three: Palaeolithic association and Roman husbandry

Larson, senior author of Irving-Pease et al. (2018) and director of Oxford's Palaeogenomics & Bio-Archaeology Research Network, summarising the same study for the University of Oxford, sets out a fourth line of evidence not fully separated from the textual record in §51.6: archaeological deposits show rabbits already hunted by humans in the Palaeolithic, in the same Iberian Peninsula and southwest France region §51.2's genomic studies later identify as the domestic lineage's wild source, tens of thousands of years before any proposed domestication date. The Roman evidence in the same account is husbandry rather than hunting — the first documented use of hutches — later still than the Palaeolithic material but earlier than the monastic narrative by centuries, consistent with Varro's leporarium (§51.6). Taken together, hunting, husbandry, and the eventual genetically-bounded domestic lineage form a continuum spanning tens of thousands of

years in the same region, not a sequence of unrelated events; this is the empirical basis for Irving-Pease's own conclusion, addressed directly in §51.9, that no single date is the right unit of analysis for this case.

51.8 Why the genetic reading cannot itself be sharpened

Irving-Pease et al. (2018) report that four published rabbit mutation-rate estimates vary by up to 45% (1.62×10^{-9} to 2.35×10^{-9}), and state that this uncertainty alone is sufficient to prevent the molecular-clock estimate from being converted into a calendar date precise enough to test against either the archaeological or textual readings. This is not a single anomalous result awaiting replication, of the kind this cycle has recorded elsewhere (e.g., apple's unreplicated Iranian candidate, §33.5); it is a stated property of the method itself, at the mutation-rate inputs currently available.

51.9 A distinguishing feature: the predicate's location is resolved, but its event is not

Every prior ⊥ case in this cycle's A.3 group fails §20.7.1's predicate either because the best-supported center is not reported at point resolution (chicken, turkey, llama, guinea fowl) or because the location itself is disputed among rival candidates (maize, Bactrian camel, broomcorn millet). Rabbit fails on the first of these grounds — §51.4 — but the source literature adds a complication none of those cases carries: it is not merely that a point coordinate is missing, but that the authors of the paper most directly bearing on chronology state explicitly that domestication is better understood as a continuum than as an event, and that "any story…predicated on an event is unlikely to be accurate" (Irving-Pease, quoted in the University of Oxford's own report on the paper). This is a claim about the object of §20.7.1's predicate itself — whether a single dateable founding event is the right unit of analysis — made by the source study, not inferred by this cycle's own synthesis.

51.10 Applying §20.7's predicate: R(X)=0, sharing chicken's, turkey's, and guinea fowl's ground, with a distinct compounding feature

Because the best-supported candidate center — the O. c. cuniculus range of the Iberian Peninsula and southern France — is not reported at point resolution (r_i=0), R(X)=0 under §20.7.1, and §20.7.2 returns ⊥, following the same branch already applied to chicken, turkey, and guinea fowl. What rabbit adds is not a new branch but a compounding feature distinct from guinea fowl's own (§50.5, §50.7): guinea fowl's chapter reported an unreconciled gap between two dates and a reversal of a structural signal across marker technologies; rabbit's own source literature reports three methods that fail to agree even in order of magnitude for a single, geographically uncontested case, a fourth, older line of evidence extending the same continuum further still (§51.7), and a documented citation error at the root of the narrative that had previously been used to paper over that disagreement. No PI value is computed, and none is estimated in its place, consistent with §1.4.

51.11 Placement in Appendix A.3 as a sixteenth row

Rabbit is added to Appendix A.3 as a sixteenth row, sharing chicken's, turkey's, and guinea fowl's no-point-resolution ground, with the compounding features of §51.5–§51.10 recorded as this case's own distinguishing detail rather than as a new numbered ground. No PI value is computed, and none is estimated in its place, consistent with §1.4.

51.12 Synthesis note

Rabbit was raised as a candidate on the strength of an unusually clean location result — three independently generated genomic datasets, spanning 2011 to 2015, agreeing on a single source population without a rival ever having been seriously proposed in the literature reviewed, and a fourth, 2024 study extending that same agreement to the Chinese diaspora population. What the

check found, once the traditional AD 600 narrative was traced to its root, was not a second location dispute but a demonstration, by the authors most responsible for testing it, that no method currently available — genetic, archaeological, or textual, including the Palaeolithic and Roman evidence that extends the record further back still (§51.7) — assigns this well-located case a date the other methods can confirm, and that the version of the story used for decades to reconcile them rests on a documented mix-up between two different men named Gregory. §1.4's no-invented-data discipline was written for exactly this kind of outcome: to report a genuinely resolved geography without manufacturing a resolved chronology the sources themselves say cannot yet be produced. A future study resolving the rabbit mutation-rate discrepancy, or dating osteological change in newly excavated Iberian or French assemblages with a precision this chapter's sources do not yet have, would allow this chapter to be revised; nothing above anticipates which reading such a study would support.

References newly cited in Chapter 51

Alves, J.M., Carneiro, M., Afonso, S. et al. (2015). Levels and patterns of genetic diversity and population structure in domestic rabbits. PLoS ONE, 10(12), e0144687.

Carneiro, M., Afonso, S., Geraldes, A., Garreau, H., Bolet, G., Boucher, S., Tircazes, A., Queney, G., Nachman, M.W. & Ferrand, N. (2011). The genetic structure of domestic rabbits. Molecular Biology and Evolution, 28(6), 1801–1816.

Carneiro, M., Rubin, C.-J., Di Palma, F., Albert, F.W., Alföldi, J., Martinez Barrio, A., Pielberg, G., Rafati, N., Sayyab, S., Turner-Maier, J., Younis, S., Afonso, S., Aken, B., Alves, J.M., Barrell, D., Bolet, G., Boucher, S., Burbano, H.A., Campos, R., Chang, J.L., Duranthon, V., Fontanesi, L., Garreau, H., Heiman, D., Johnson, J., Mage, R.G., Peng, Z., Queney, G., Rogel-Gaillard, C., Ruffier, M.,

Searle, S., Villafuerte, R., Xiong, A., Young, S., Forsberg-Nilsson, K., Good, J.M., Lander, E.S., Ferrand, N., Lindblad-Toh, K. & Andersson, L. (2014). Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. Science, 345(6200), 1074–1079.

Irving-Pease, E.K., Frantz, L.A.F., Sykes, N., Callou, C. & Larson, G. (2018). Rabbits and the Specious Origins of Domestication. Trends in Ecology & Evolution, 33(3), 149–152.

Long, J.-R., Qiu, X.-P., Zeng, F.-T., Tang, L.-M. & Zhang, Y.-P. (2003). Origin of rabbit (Oryctolagus cuniculus) in China: evidence from mitochondrial DNA control region sequence analysis. Animal Genetics, 34(2), 82–87.

Xie, K., Song, Z., Wang, Y., Di, Y., Li, W., Wang, Y.B., Yang, A., Qiao, X., Wang, B., Li, M., Xie, X.P., Xie, X.H., Liu, L., Ning, C., Tang, H., Li, X.Y., Wu, X., Zhang, Q., Wang, D. & Fan, X. (2024). Whole-genome resequencing revealed the origin and domestication of Chinese domestic rabbits. bioRxiv 2024.03.26.586758 (preprint; peer-reviewed publication status not confirmed in this cycle's search, disclosed as such at first citation, §51.2).

Chapter 52 — Tomato (Solanum lycopersicum): A Staged Domestication Across Two Continents, and a Location Dispute the Two-Step Model Resolves by Reassignment

52.1 Admission, continuing the cycle's supplementary practice as a sixth case

Sweet potato (Ch.47), reindeer (Ch.48), quinoa (Ch.49), helmeted guinea fowl (Ch.50), and European rabbit (Ch.51) were each admitted after this cycle's own stated closure, each on a footing distinct from the others already catalogued. Tomato (Solanum lycopersicum) is admitted here as a sixth supplementary case, on a footing distinct from all five: not an unresolved wild-taxon count

(§47.3), not a measured boundary attached to unlocated centers (§48.7–§48.8), not a disputed event count within an agreed lineage (§49.7), and not a resolved location paired with an unreconciled chronology (§50.5, §50.7, §51.9), but a single, staged domestication process running through two named intermediate forms across two continents — in which an older dispute over where domestication happened is not adjudicated but resolved by reassigning each of the two rival locations to a different stage of one lineage.

52.2 Three named forms, one lineage: SP, SLC, and SLL

The cultivated tomato's own literature distinguishes three named groups along a single evolutionary line, not two rival species: the fully wild, small-fruited Solanum pimpinellifolium (SP), native to coastal and mid-elevation Ecuador and Peru; an intermediate group, S. lycopersicum var. cerasiforme (SLC), of mixed wild, semi-domesticated, and feral status, with a broad range extending from the Andean region of Ecuador and northern Peru north through Central America into Mexico; and the fully domesticated S. lycopersicum var. lycopersicum (SLL), the cultivated tomato of commerce. Rick & Holle (1990) first proposed SLC as the evolutionary intermediate between SP and SLL on the basis of allozyme variation, a reading later carried forward by genome-scale work.

52.3 The two-step model and its two independent lines of support

Blanca et al. (2012), genotyping SNP markers and morphological traits across a broad tomato collection, and Blanca et al. (2015), sequencing whole genomes of SP, SLC, and SLL accessions, both propose a two-step domestication process: a first step in South America, in which SP was brought under initial human selection to produce SLC in the Andean region of southern Ecuador and northern Peru; and a second step in Mesoamerica, in which SLC — having migrated north as a semi-domesticated or weedy form —

was further selected into the large-fruited SLL. Lin et al. (2014), resequencing 360 tomato accessions, and Razifard et al. (2020), applying population-genomic methods focused specifically on the intermediate stages, both report results consistent with this same two-step sequence, identifying Mexican SLC populations as genetically closest to SLL and reporting the lowest population differentiation ($F_{es} = 0.21$) between SLC-Mexico and SLL of any SLC subgroup surveyed.

52.4 An older single-locus dispute, and how the two-step model resolves rather than adjudicates it

Before the two-step model was established, the literature disputed a simpler question: was tomato domesticated in Mesoamerica, or in Ecuador and northern Peru, near SP's own center of origin? Sim et al.'s earlier Mesoamerican reading and a rival South American reading were, in effect, two candidate answers to a single-location question of the same shape this cycle has met before — maize's Balsas-versus-Jalisco dispute (§6.3–§6.4) and Bactrian camel's HI-versus-HII dispute (§19.5–§19.6) are both disputes of this kind, over which of two named locations hosts one single center. Tomato's own literature (Blanca et al., 2015) resolves this differently from either of those two precedents: rather than one location being tested and preferred over the other, or the dispute being left open and reported as a location-uncertainty distance, both locations are retained — each assigned to a different stage of one continuous lineage. Ecuador and northern Peru host the SP-to-SLC transition; Mesoamerica hosts the SLC-to-SLL transition. Neither side of the older dispute was wrong; each was answering a different half of a single question that had not yet been split in two.

52.5 A documented complication the two-step model itself discloses: trait loss and reconvergence

Razifard et al. (2020) add a finding with no precedent elsewhere in this cycle. Their population-genomic reconstruction indicates that several traits conventionally treated as diagnostic of full domestication — changes in fruit weight and shape associated with loci including fw2.2, fw3.2, lc, and ovate — first arose in the South American SLC population, prior to its northward migration, but were subsequently lost or diminished as SLC spread toward Mesoamerica, and were then reselected, convergently, once SLC reached Mesoamerica and gave rise to SLL. This is not a simple funnel in which each stage adds to the last: it is a lineage that gained domestication-associated traits, partially lost them in transit, and reacquired them independently at the far end of its own range. No other single-lineage, staged case in this cycle — including coffee's own sequential wild-origin/domestication-pathway model (§39.4, §39.7) — reports this particular pattern of gain, loss, and reconvergence within one continuous process.

52.6 A real-coordinate check — illustrative only

Loja, Ecuador (approximately 3.99°S, 79.20°W), a locality within the SP/early-SLC range repeatedly surveyed in the cited literature, and Puebla, Mexico (approximately 19.04°N, 98.20°W), a representative point within the central Mexican highlands where SLC-to-SLL improvement is placed, sit approximately 3,300 km apart on a great-circle path. As with coffee's own wild-origin/domestication-pathway anchors and flax's regionally inherited center, this distance is reported as an illustrative geographic span between two named stages of one lineage, not as a Polycentricity Index D̄: the two points are not rival, independently corroborated centers for one event, so §2.7's index is not built to weight the distance between them.

52.7 Why this reaches the C=1 floor via coffee's own route, with two disclosed wrinkles

No source reviewed in this chapter proposes a second, independently corroborated domestication center for tomato standing outside the SP→SLC→SLL lineage itself; C=1 under §2.7's definition, and κ=1.0 follows the same convention already applied to coffee's single, doubly-corroborated lineage. This extends coffee's own seventh route to the C=1 floor (§39.4, §39.7: a wild-origin region and a domestication-pathway region reported as sequential stages of one lineage, rather than rival centers) rather than establishing a new one. Tomato discloses two features neither coffee nor any earlier member of this route carries: an older single-location dispute resolved by reassigning each candidate to a different stage rather than by testing one against the other (§52.4), and a documented episode of trait loss and convergent reacquisition partway through the staged process (§52.5). Both are reported as this route's own further variation, not as grounds for a different outcome.

52.8 Placement in Appendix A.2 as a tenth route

Tomato is added to Appendix A.2 as a tenth route to the C=1 floor, extending coffee's sequential-stage logic (itself the group's seventh route) with the two disclosed features of §52.4–§52.5, in the same spirit that peach (Ch.45) extended apple's own three-independent-study route without registering as a wholly new one. No PI value beyond 0 is computed or estimated in its place, consistent with §1.4.

52.9 Synthesis note

Tomato was raised as a candidate on the strength of an unusually well-resolved staged lineage: two named intermediate forms, four independent genomic studies converging on their sequence, and a documented reassignment of an older single-location dispute rather than its outright resolution. What the check found, once the

two-step model was examined closely, was not a cleaner version of coffee's own case but a structurally related one with its own complication: the very traits that mark "domestication" were not acquired once and kept, but gained, partially lost, and independently reacquired across two continents. §1.4's no-invented-data discipline is served here by reporting that complication in full rather than smoothing it into a simpler staged-funnel narrative the sources themselves do not support. A future study resolving whether the reselected Mesoamerican alleles are identical by descent to their South American predecessors, rather than independently derived, would sharpen §52.5's own finding; nothing above anticipates which reading such a study would support.

References newly cited in Chapter 52

Blanca, J., Cañizares, J., Cordero, L., Pascual, L., Diez, M.J. & Nuez, F. (2012). Variation revealed by SNP genotyping and morphology provides insight into the origin of the tomato. PLoS ONE, 7(10), e48198.

Blanca, J., Montero-Pau, J., Sauvage, C. et al. (2015). Genomic variation in tomato, from wild ancestors to contemporary breeding accessions. BMC Genomics, 16, 257.

Lin, T., Zhu, G., Zhang, J. et al. (2014). Genomic analyses provide insights into the history of tomato breeding. Nature Genetics, 46, 1220–1226.

Razifard, H. et al. (2020). Genomic Evidence for Complex Domestication History of the Cultivated Tomato in Latin America. Molecular Biology and Evolution, 37(4), 1118–1132.

Rick, C.M. & Holle, M. (1990). Andean Solanum lycopersicum var. cerasiforme: genetic variation and its evolutionary significance. Economic Botany, 44(3 Supplement), 69–78.

Chapter 53 — Citrus (Citrus spp.): A Second Mosaic Genome, and a Genus Redefined by Its Own Hybrids

53.1 Admission, continuing the cycle's supplementary practice as a seventh case

Citrus (Citrus spp.) is admitted here as a seventh supplementary case, and as this cycle's second case — after banana (Ch.27) — whose own literature reports a domestication process the C, κ, D̄ triple was not built to describe: not a discrete choice among candidate centers for one event, but a sequence of hybridizations across several named ancestral taxa contributing to a single mosaic genome in most cultivated forms.

53.2 Three true ancestral species, and a rapid Himalayan radiation

Wu, Terol, Ibanez et al. (2018), sequencing the genomes of 58 Citrus and related accessions, resolved the genus's confusing taxonomic history into three true ancestral species, each represented today by essentially unadmixed accessions: the citron (Citrus medica), the pummelo (Citrus maxima), and the mandarin (Citrus reticulata). Gonzalez-Ibeas et al. (2021), building on the same phylogeny, report that ancestral citrus originated in the Himalayan foothills and diversified through a rapid radiation during the late Miocene, giving rise to these and the genus's other wild species, though no source reviewed here identifies a selective mechanism behind that radiation's speed.

53.3 The familiar fruits as hybrids of the three ancestors

Wu et al. (2018) report that the great majority of commercially important citrus — sweet orange, sour orange, grapefruit, lemon, and most limes — are not further wild species but hybrids among citron, pummelo, and mandarin, or hybrids of those hybrids. Sweet orange derives from a pummelo×mandarin cross; sour orange derives from a similar but independent pummelo×mandarin cross;

lemon derives from a citron×sour-orange cross, and so carries pummelo and mandarin ancestry at one remove. Wu, Prochnik, Jenkins et al. (2014), sequencing diverse mandarin, pummelo, and orange genomes directly, report an extensive network of relatedness among mandarins and sweet oranges, with the majority of sequenced mandarin accessions carrying detectable pummelo admixture — a pattern the authors read as evidence that pummelo introgression contributed to the selection of more palatable mandarin fruit, not merely as neutral background mixture.

53.4 A further wrinkle since 2018: wild mandarin diversity and apomixis

Wu et al. (2021), extending the 2018 survey to a wider collection of East Asian citrus, report the discovery of a previously unsequenced wild species, Citrus ryukyuensis, native to the Ryukyu Islands, together with a further wild mainland Asian mandarin population, and trace how the capacity for apomictic (asexual, seed-borne) reproduction in mandarins has shaped their own diversification independently of the admixture history described in §53.3. This does not revise the three-ancestor model itself, but adds a documented layer of within-mandarin structure that the 2018 survey's own sampling had not yet captured.

53.5 Why no C is assigned

Following the same ground already established for banana (§27.4–§27.5), §20.7.1's resolvability predicate presupposes a single proposed center set for one domestication event; citrus's own literature instead reports a documented sequence of hybridization events among three named ancestral species, contributing to a single mosaic genome in most cultivated forms, rather than a discrete choice among rival centers for one event. No C is assigned, and no PI is computed or estimated in its place, consistent with §1.4. Citrus is this cycle's second case reaching this outcome, on the same

ground as banana rather than a newly distinguished one; unlike banana's own genus, however, citrus's three ancestral parents are, on the evidence reviewed here, still each individually locatable to a broad region (Himalayan foothills radiation, §53.2), a detail banana's own more diffuse hybridization history does not supply in the same form.

53.6 Placement in Appendix A.5 as a seventh member

Citrus is added to Appendix A.5 as a seventh member, alongside banana, yeast, honey bee, koji, vanilla, and sweet potato, each excluded from the index's domain for its own distinct reason. Citrus's own reason is banana's: admixture across named taxa compounds into one genome before any single C can be assigned.

53.7 Synthesis note

Citrus was raised as a candidate because its own genomic literature, like banana's, describes a domestication history the Polycentricity Index was never built to count — not a dispute over where or how many times a single event occurred, but a reticulate history in which the "event" itself is a repeated hybridization among a small number of true ancestors. What the check found was a case cleaner than banana's in one respect (three named, individually resolvable ancestral species rather than a diffuse hybrid swarm) and, since 2018, a case still actively being revised as further wild diversity within those ancestors is documented (§53.4). §1.4's discipline is served here by reporting a well-evidenced mosaic history honestly as outside the index's domain, rather than forcing an artificial single C onto a genus whose own researchers describe it as a network.

References newly cited in Chapter 53

Wu, G.A., Terol, J., Ibanez, V. et al. (2018). Genomics of the origin and evolution of Citrus. Nature, 554(7692), 311–316.

Wu, G.A., Prochnik, S., Jenkins, J. et al. (2014). Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. Nature Biotechnology, 32, 656–662.

Wu, G.A. et al. (2021). Diversification of mandarin citrus by hybrid speciation and apomixis. Nature Communications.

Gonzalez-Ibeas, D. et al. (2021). Shaping the biology of citrus: I. Genomic determinants of evolution. The Plant Genome, 14(3), e20104.

Chapter 54 — Fava Bean (Vicia faba): A Wild Progenitor Proposed from a Single Extinct Assemblage, and Never Confirmed From a Living Population

54.1 Admission, continuing the cycle's supplementary practice as an eighth case, on a new ground within Appendix A.3

Fava bean (Vicia faba) is admitted here as an eighth supplementary case, and as a new, seventeenth row within Appendix A.3's ⊥ group, on a ground distinct from every case already catalogued there. Chicken, turkey, cotton, cat, llama, guinea pig, pea, guinea fowl, and rabbit each fail §20.7.1's predicate because a best-supported center is not reported at point resolution, or because rival regions remain unresolved; C. moschata fails it further back still, because no candidate wild population has ever been reported by any method. Fava bean's own literature reports something distinct from both: a candidate wild progenitor has been proposed, from a single archaeobotanical assemblage, but that candidate is itself extinct — no living population exists against which any genetic method could test or corroborate the proposal.

54.2 A founder crop with no living wild relative

Fava bean is among the founder crops of the Neolithic Near East, yet, uniquely among this cycle's cereal and legume founder-crop cases (einkorn, barley, chickpea, lentil, pea, flax), no wild population of Vicia faba, and no other Vicia species cross-compatible with it, has ever been found alive. Jayakodi et al. (2023), reporting a chromosome-scale assembly of the faba genome, state plainly that despite the crop's global importance, no extant wild progenitor has been found, while noting that several related species native to the same region — Vicia narbonensis, Vicia palaestina, and Vicia kalakhensis — offer some hope of a genetic connection not yet demonstrated. Multiple independent sources spanning nearly four decades of research converge on the same statement in the same terms: the wild ancestor is unknown, and crosses between V. faba and its nearest congeners have not produced fertile offspring.

54.3 The domestication event: Lower Galilee, approximately 10,200 years before present

Caracuta et al. (2015), reporting charred faba bean remains from three adjacent Neolithic sites in the Lower Galilee region of the southern Levant, date the earliest intensive farming of the crop to approximately 10,200 cal BP, on the basis of biometric measurement, radiocarbon dating, and stable carbon isotope analysis of the archaeological remains, cross-checked against experiments on modern material. The large quantity of beans recovered indicates production at a scale the authors read as achievable only by planting selected, non-dormant seed stock, and they further suggest, from the same evidence, that domestication-relevant selection of non-dormant plants may have begun as early as the eleventh millennium cal BP — earlier than the date at which intensive farming itself is directly attested. Kislev (1985), reporting an earlier find of Neolithic horsebean (the crop's other common

name) at Yiftah'el in the same Lower Galilee region, provided the first named site associated with this early cultivation.

54.4 A proposed but unconfirmed extinct progenitor: el-Wad, Mount Carmel

Caracuta et al. (2016), reporting wild-morphology faba bean seeds recovered from the Natufian layers of el-Wad Terrace on Mount Carmel, provide what the authors describe as the first, and so far only, physical remains of the crop's proposed wild ancestor. X-ray CT scan analysis of these seeds supplied the first biometric measurements of the species prior to domestication, distinguishing them from the larger, domesticated morphology seen at the Lower Galilee sites of §54.3. The authors date these Natufian wild-type seeds to approximately 14,000 years before present — nearly three millennia before the earliest directly dated domestication evidence — and read their presence at el-Wad as consistent with a wild population that grew nearby, in the Lower Galilee itself, where farming of the crop is later attested. No comparable find, before or since, is reported anywhere in the literature reviewed for this chapter.

54.5 A real-coordinate check — illustrative only

El-Wad Terrace, on Mount Carmel (approximately 32.67°N, 34.97°E), and Yiftah'el, in the Lower Galilee (approximately 32.75°N, 35.17°E), sit approximately 20–30 km apart — consistent with Caracuta et al.'s (2016) own description of a wild population growing "nearby." As with every other illustrative check in this cycle, this is a real point-to-point distance between two named sites, not a claim about the two species' or populations' full ranges, and not a Polycentricity Index D̄: fava bean's C-count is not resolved at all (§54.6–§54.7), so no PI computation applies here in the first place.

54.6 Why a proposed extinct progenitor cannot be genetically corroborated — a new, distinct ⊥ ground

Every corroborated C=1 or C=2 case elsewhere in this cycle rests on at least one genetic method — population genomics of living cultivars and wild relatives, ancient DNA, or both — confirming or bounding a proposed wild source. Fava bean's own literature cannot supply this for its own proposed progenitor, for a structural reason distinct from C. moschata's (§43.7): C. moschata's wild ancestor has never been proposed by any method, genetic or morphological, across three independent studies spanning more than twenty years. Fava bean's wild ancestor has been proposed — once, from a single Natufian assemblage, on morphometric and biometric grounds — but the proposed population is extinct, leaving no living descendant lineage against which any genetic test could be run. Jayakodi et al.'s (2023) 2023 genome paper, published seven years after Caracuta et al.'s (2016) find, still states that no extant wild progenitor has been found, without citing the el-Wad material as resolving the question — not because the two claims conflict (an extinct wild population and the absence of a living one are compatible statements), but because an archaeobotanical identification of an extinct population is not, and cannot become, the kind of genetically corroborated result this cycle's C-count elsewhere requires.

54.7 Applying §20.7's predicate: ⊥, on a ground distinct from every case in Appendix A.3's existing list

No source reviewed here reports a genetically corroborated wild population for Vicia faba, living or extinct; the sole candidate (§54.4) is morphometric and archaeological, not genetic, and cannot in principle be upgraded to a genetic result without a living population to sequence. §20.7.1's predicate is not met, and §20.7.2 returns ⊥. This is reported as a new, distinct ground within the ⊥ group: not a missing point coordinate for an otherwise-

corroborated center (chicken, turkey, guinea fowl, rabbit), not rival unresolved regions (cat, cotton), and not simply the absence of any candidate at all (C. moschata), but a single proposed candidate that is structurally unconfirmable by the evidentiary standard this cycle applies everywhere else. No PI value is computed, and none is estimated in its place, consistent with §1.4.

54.8 Placement in Appendix A.3 as a seventeenth row

Fava bean is added to Appendix A.3 as a seventeenth row, on the distinct ground set out in §54.6–§54.7, alongside chicken, turkey, cotton, broomcorn millet, cat, llama, guinea pig, capsicum, pea, C. moschata, fig, reindeer, guinea fowl, and European rabbit.

54.9 Synthesis note

Fava bean was raised as a candidate because it offers this cycle a case genuinely different from C. moschata's own no-candidate-at-all result: a wild ancestor has been proposed, and proposed on real physical evidence, but that evidence can never be extended into the kind of genetic corroboration every other resolved case in this cycle rests on, because the proposed population no longer exists to be sequenced. §1.4's no-invented-data discipline is served here by reporting exactly what the sources say — a domestication date near 10,200 cal BP, a proposed wild ancestor dated nearly three millennia earlier at a site a few tens of kilometers away, and a 2023 genome paper that still describes the ancestor as unfound — without resolving the tension between an archaeological identification and a genomic silence that only a currently nonexistent living population could ever settle. Should a close wild relative (V. narbonensis, V. palaestina, or V. kalakhensis) ever be shown by genomic evidence to be the crop's true wild source, this chapter's own ⊥ result would need to be revised; nothing above anticipates that outcome.

References newly cited in Chapter 54

Caracuta, V. et al. (2015). The onset of faba bean farming in the Southern Levant. Scientific Reports, 5, 14370.

Caracuta, V., Weinstein-Evron, M., Kaufman, D., Yeshurun, R., Silvent, J. & Boaretto, E. (2016). 14,000-year-old seeds indicate the Levantine origin of the lost progenitor of faba bean. Scientific Reports, 6, 37399.

Maughan, P.J., Chaney, L., Lightfoot, D.J., Cox, B.J., Tester, M., Jellen, E.N. & Jarvis, D.E. (2019). Mitochondrial and chloroplast genomes provide insights into the evolutionary origins of quinoa (Chenopodium quinoa Willd.). Scientific Reports, 9, 185.

Jayakodi, M. et al. (2023). The giant diploid faba genome unlocks variation in a global protein crop. Nature (published online 8 March 2023).

Kislev, M.E. (1985). Early Neolithic horsebean from Yiftah'el, Israel. Science, 228(4698), 319–320.

Chapter 55 — Goose (Anser anser domesticus and Anser cygnoides domesticus): Two Domestications, and a Resolvability Split Turkey's Own Branch Anticipated

55.1 Admission, continuing the cycle's supplementary practice as a ninth case

Goose (Anser anser domesticus, derived from the wild greylag goose, and Anser cygnoides domesticus, derived from the wild swan goose) is admitted here as a ninth supplementary case, and as a new, eighteenth row within Appendix A.3's ⊥ group. Structurally it is the closest match this cycle has produced to turkey's own case (Ch.21, §21.6): two independently corroborated domestication events, from two different wild species, of which only one carries a reported point-level coordinate. What goose adds is a

compounding feature turkey's own pair did not carry: each pole's own dating evidence disagrees internally with itself, and the two disagreements run in opposite directions. At the resolved pole, the archaeological date is older than the genomic date; at the unresolved pole, the genomic date is older than any archaeological or iconographic anchor. Both are reported below exactly as the cited sources state them, without adjudicating between archaeology and genomics at either pole, consistent with §1.4.

55.2 Two wild progenitors, independently corroborated across four evidentiary lines

That domestic geese descend from two distinct wild species, not one, has been corroborated independently and repeatedly since the late 1960s: karyotype comparison (Bhatnagar, 1968) found the chromosomes of Chinese domestic and wild swan geese identical to one another and distinct from European domestic and wild greylag geese; mitochondrial restriction-fragment and D-loop studies (Shi et al., 1998, 2006; Li et al., 2011) reached the same two-cluster split using unrelated markers and unrelated sample sets; and Wen et al. (2023), reporting whole-genome resequencing of 74 individuals spanning 14 domestic breeds and both wild species, recovered the identical split in PCA, ADMIXTURE, and maximum-likelihood phylogenies built independently from genome-wide SNPs and from mitochondrial data alone. Every domestic Chinese breed but one, and every European breed, sorts cleanly with its own proposed wild ancestor across all four methods. This is C=2 by the same doubly-corroborated, independent-lineage standard already applied to cattle (Ch.13), water buffalo (Ch.14), and turkey (Ch.21) — two real domestication events in two real species, not two centers within a single species.

55.3 The Chinese pole: Tianluoshan, and a disclosed archaeology–genomics gap

Eda et al. (2022), reporting histological, oxygen- and nitrogen-stable-isotope, and morphological analysis of goose bones excavated at Tianluoshan — a rice-cultivation village of the Hemudu culture in the lower Yangtze River valley, Yuyao, Zhejiang (approximately 30.05°N, 121.15°E) — identify a locally bred goose population maintained across several generations without the introduction of migratory wild individuals, plausibly fed on cultivated paddy rice alongside the human occupants. The authors read this as an early stage of domestication, and date it to approximately 7,000 years before present, which they report as the oldest secure poultry-domestication evidence of any species reviewed in their own comparative discussion, older than the earliest secure evidence for domestic chickens, ducks, or turkeys. This is a genuine point-level coordinate, tied to a named, excavated site, exactly as §20.7.1 requires. Independently, Wen et al. (2023), using whole-genome demographic inference (SMC++ and ∂a∂i, best-fit isolation-with-migration model), estimate the split between Chinese domestic geese and wild swan geese at approximately 3,499 years before present (95% CI ± 120 years) — roughly 3,500 years younger than Tianluoshan's own archaeological date. Wen et al. disclose the discrepancy themselves, rather than resolving it, noting explicitly that the Tianluoshan study did not extract ancient DNA, so the archaeological and genomic lines cannot yet be cross-validated against a single sample set. This chapter reports both dates as given, without preferring one over the other.

55.4 The European pole: a continental range, a prey pathway, and no proposed point

The wild greylag goose's own breeding range runs across northern and central Europe and Asia, wintering in southern Europe and North Africa — a continental distribution, not a locality. No source

reviewed here — not Wen et al. (2023), not Heikkinen et al. (2020), not the review literature on poultry domestication more broadly — proposes a single excavated site, or any other point-level coordinate, as the origin of the European lineage. The domestication process itself is described in the ancient-DNA literature on European goose remains as following a 'prey pathway': geese first hunted, then progressively brought under looser and looser herd management, a gradual process without a single founding event tied to one place. The earliest material association reviewed here is iconographic rather than archaeozoological: Egyptian Old Kingdom tomb paintings, dated by Zeuner (1963, cited in Wen et al., 2023) to 2686–1991 BC, depict birds resembling domestic-type geese. This is evidence of use and possession at a much later date, in a specific place, not evidence of where or when the wild greylag was first managed; the two are not the same claim, and this chapter does not conflate them. A further complication works against even treating Egypt as an approximate stand-in: the domestic goose's own pink-billed morphology tracks the eastern greylag subspecies, A. a. rubrirostris, whose breeding range runs through Romania, Turkey, and southern Russia into northeastern China, rather than the western nominate subspecies A. a. anser that breeds in Iceland and northern and central Europe. Wen et al.'s own genomic estimate for this split, approximately 7,552 years before present, is thousands of years older than the Egyptian iconographic evidence, and is itself the older of this chapter's two domestication-date estimates — the reverse of the Chinese pole's own pattern, where the archaeological date is the older one.

55.5 A further complication: the Yili goose, and why 'European' does not mean 'in Europe'

Wen et al. (2023) report that one Chinese breed, the Yili goose, raised in Xinjiang in China's far northwest, is not descended from

the wild swan goose like every other Chinese breed reviewed, but from the wild greylag goose — clustering with European domestic breeds and the wild greylag reference sample across PCA, ADMIXTURE, and both genome-wide and mitochondrial phylogenies, a result already reported by Li et al. (2011) from mitochondrial data alone. This is not read here as a third domestication center: no source proposes an independent Xinjiang origin for Yili geese, and the same genomic and phylogenetic evidence that separates Yili from the swan-goose lineage places it inside the same greylag-derived lineage as the European breeds, most plausibly by translocation and subsequent local breeding rather than a second, independent founding event. It is reported here because it shows that the greylag-derived lineage's own present-day range is not confined to the continent its conventional name implies, echoing a pattern already disclosed for Bactrian camel's genomic range (§19.4) and cotton's four-species geography (§22.4). Wen et al. additionally document substantial post-domestication gene flow from Chinese (swan-goose-derived) breeds into Yili individuals, detected by TreeMix and D-statistics and concentrated in part at the IGF-1 locus, plausibly affecting Yili body size. This is a separate, later process from either founding event and is not folded into this chapter's C-count, following the same discipline already applied to llama and alpaca's post-conquest hybridization (§29.6) and to dog's own wild–domestic gene flow (§12.4).

55.6 A real-coordinate check — illustrative and partial only

Computed via great-circle distance (code/Ch55_goose_distance_check.py, same haversine convention and mean Earth radius, 6,371.0088 km, used throughout this cycle): Tianluoshan (approximately 30.05°N, 121.15°E) and Meidum, Egypt (approximately 29.39°N, 31.15°E) — the site of the Old Kingdom tomb paintings cited in §55.4 — are 8,425.7 km apart. This

figure carries the same caveat §21.5 attached to turkey's own illustrative span, in a stronger form: Meidum is not even a candidate origin point for the greylag lineage, only the location of the earliest secure iconographic association reviewed here, many millennia after Wen et al.'s own genomic date for the split itself. Reporting this distance as anything more than an illustrative span between one real, corroborated center and one real, differently-motivated site would manufacture a European center where the cited sources supply none.

55.7 Applying §20.7's predicate: turkey's own branch, with a new compounding feature

Let X = {x_China, x_Europe}. x_China is a reported point (Tianluoshan; Eda et al., 2022), so r_China = 1. x_Europe has no reported point in any source reviewed here (Wen et al., 2023; Heikkinen et al., 2020; Zeuner, 1963), so r_Europe = 0. By §20.7.1, R(X) = 0, since R(X)=1 requires r_i=1 for every i. By §20.7.2's partial-function definition, PI(C,κ,D̄) = ⊥: C=1 is false (two independent, doubly corroborated events), and R(X)=1 is false, so neither the resolvable branch nor the C=1-unanimous branch applies.

This is the second case on turkey's own branch — two doubly corroborated centers, resolvability split unevenly between them — rather than a new branch of its own. What goose adds is a feature no prior case on this branch carries: at both poles, the source literature's own archaeological and genomic dating disagree with each other, and the direction of disagreement is reversed between the two poles. Neither disagreement is adjudicated here; both are disclosed exactly as reported (§55.3, §55.4).

55.8 Placement in Appendix A.3 as an eighteenth row

Goose is added to Appendix A.3 as an eighteenth row, on turkey's own resolvability-split ground (§55.7), alongside chicken, turkey, cotton, broomcorn millet, cat, llama, guinea pig, capsicum, pea, C.

moschata, fig, reindeer, guinea fowl, European rabbit, and fava bean.

55.9 Synthesis note

Goose was raised as a candidate because it offered this cycle a second instance of a structure only turkey had previously supplied — two independently corroborated domestications of two different wild species, one resolvable to a point, one not — against a fully independent evidentiary record: avian rather than mammalian, East Asian and West Eurasian rather than Mesoamerican and North American, and resting on whole-genome demographic inference rather than ancient-DNA phylogeography. §1.4's discipline is served here by reporting both of the record's own internal tensions rather than resolving either: Tianluoshan's archaeological date of approximately 7,000 BP sits alongside Wen et al.'s own genomic estimate of approximately 3,499 BP for the same lineage, a gap the source paper discloses but cannot yet close for want of ancient DNA from the site itself; and the European lineage's genomic date of approximately 7,552 BP sits several millennia before the earliest iconographic evidence anyone reviewed here has proposed, with no point-level coordinate offered for the intervening record at all. Should either gap close — ancient DNA recovered from Tianluoshan itself, or a proposed excavated site for the greylag lineage's own founding population — this chapter's report of two internally disputed dates would need to be revised; nothing above anticipates that outcome.

References newly cited in Chapter 55

Bhatnagar, M.K. (1968). Mitotic chromosomes of white Chinese geese. Journal of Heredity, 59(3), 191–195.

Eda, M., Itahashi, Y., Kikuchi, H., Sun, G., Hsu, K.H., Gakuhari, T. et al. (2022). Multiple lines of evidence of early goose domestication in a 7,000-y-old rice cultivation village in the lower Yangtze River,

China. Proceedings of the National Academy of Sciences, 119(12), e2117064119.

Heikkinen, M.E., Ruokonen, M., White, T.A., Alexander, M.M., Gunduz, I., Dobney, K.M. et al. (2020). Long-term reciprocal gene flow in wild and domestic geese reveals complex domestication history. G3, 10(9), 3061–3070.

Li, H.F., Zhu, W.Q., Chen, K.W.H.Y., Xu, W.J. & Song, W. (2011). Two maternal origins of Chinese domestic goose. Poultry Science, 90(12), 2705–2710.

Shi, X.W., Zeng, F.T., Qiu, X.P. & Zhang, Y.P. (1998). Mitochondrial DNA polymorphism and origin differentiation in major Chinese goose breeds. Journal of Genetics, 25(6), 499–507.

Shi, X.W., Wang, J.W., Zeng, F.T. & Qiu, X.P. (2006). Mitochondrial DNA cleavage patterns distinguish independent origin of Chinese domestic geese and Western domestic geese. Biochemical Genetics, 44(5–6), 237–245.

Wen, J., Li, H., Wang, H., Yu, J., Zhu, T., Zhang, J., Li, X., Jiang, Z., Ning, Z. & Qu, L. (2023). Origins, timing and introgression of domestic geese revealed by whole genome data. Journal of Animal Science and Biotechnology, 14, 26.

Chapter 56 — Yam (Dioscorea spp.): Three Independent Domestications, and the Cycle's First Case Where Every Center Fails to Resolve

56.1 Admission, continuing the cycle's supplementary practice as a tenth case

Yam (Dioscorea spp.) is admitted here as a tenth supplementary case, and as a new, nineteenth row within Appendix A.3's ⊥ group. It departs structurally from every case catalogued there so far. Chicken (Ch.20) reached ⊥ with a single best-supported center that

itself never resolves to a point. Turkey (Ch.21), cotton (Ch.22), and goose (Ch.55) reached ⊥ with two or more independently corroborated centers, of which at least one resolves. Yam supplies this cycle's first case with more than one independently corroborated center — three, unanimously reported across the review literature — of which none resolves to a point. §20.7's predicate returns R(X)=0 identically whether one center fails to resolve or all three do, and this chapter does not propose a new formal branch; what follows is a qualitative record the taxonomy in §20.8's synthesis tables has not yet had occasion to carry.

56.2 Three independent domestications, unanimously reported

That yam was domesticated independently at least three times, once on each of three continents, is reported without dispute in the review literature assembled here: in West and Central Africa (Dioscorea rotundata, and the closely related triploid D. cayenensis), in Asia and the Pacific (Dioscorea alata), and in tropical South America (Dioscorea trifida) (Sugihara et al., 2021; Scarcelli et al., 2019). This is C=3 on the same doubly-or-better-corroborated, independent-lineage standard already applied to cotton's four species (Ch.22) and Capsicum's five (Ch.40): three separate wild source pools, three separate cultivated species, three separate continents, with no source reviewed here treating any two of the three as a single event.

56.3 The African pole: a region, and a live dispute over the wild progenitor's own identity

D. rotundata's own wild source has itself been read two incompatible ways by genomic studies published a year apart. Scarcelli et al. (2019), sequencing cultivated D. rotundata alongside its two closest wild relatives, report that cultivated yam was domesticated from a single forest species, Dioscorea praehensilis, and infer that the expansion of African yam agriculture began in

the Niger River basin. Sugihara et al. (2020), sequencing 336 further Guinea yam accessions, do not support this: their results indicate a hybrid origin, from crosses between the savannah species Dioscorea abyssinica and the same forest species D. praehensilis, with the abyssinica parent's contribution concentrated on the sex chromosome. The two studies agree that D. praehensilis contributed to D. rotundata's genome; they disagree about whether it did so alone. Neither reading offers a point-level coordinate in any case: the Niger River basin is named as a region, not a site, and yam remains, unlike cereal grains, are not durable in most African depositional environments, so no archaeobotanical anchor comparable to Tianluoshan's goose bones (§55.3) or the Fertile Crescent's charred grain assemblages (§2.3) has been reported for this pole in any source reviewed here.

56.4 The Asian-Pacific pole: an unlocated center, and a second gene pool the traditional count does not recognize

D. alata's own center of origin is described in the review literature reviewed here as unknown at any resolution finer than a region: the greatest phenotypic variability is reported from southern Southeast Asia and Melanesia, read as the probable center of origin, and no wild population of D. alata has ever been identified in nature. A further complication the traditional three-continent count does not itself register: Sharif et al. (2020), genotyping 600 accessions spanning four continents, report an early divergence between a mainland Southeast Asian gene pool and a Pacific gene pool, with continuous migration between them, and read this as evidence for two independent domestication origins within what the traditional literature reports as a single Asian pole. Neither of these two sub-origins is assigned a point-level coordinate by Sharif et al. or by any other source reviewed here. The nearest thing to a point anywhere in this pole's record is archaeological rather than genomic: Fullagar et al. (2006), reporting starch-grain and use-wear evidence from

stone tools excavated at Kuk Swamp, in the Upper Wahgi Valley of Papua New Guinea's Western Highlands (approximately 5.78°S, 144.33°E), identify yam processing from Phase 2 onward, roughly 6,950–6,440 cal BP. This is not treated here as a resolved center for either D. alata sub-origin: Fullagar et al.'s own identification is to genus level only (Dioscorea sp.), not to species, and no source reviewed here claims Kuk Swamp as the founding site of either the mainland or the Pacific gene pool rather than one early node within a much broader highland and lowland New Guinea record.

56.5 The South American pole: the least-studied of the three

D. trifida is the least genomically studied of the three poles. Bousalem et al. (2010, cited in Sugihara et al., 2021), using AFLP markers, distinguish a cultivated, autotetraploid form from a wild, diploid form found in French Guiana, and report a region where the diploid form predominates, without narrowing that region to a site. The crop's own cultivated range is reported, across the sources reviewed here, as the border zone spanning Brazil, Guyana, Suriname, and French Guiana — again a region, not a point — and Sugihara et al. (2021) name D. trifida's own whole-genome duplication, alongside D. rotundata's West African hybridization and D. alata's global dispersal, as one of three domestication processes their own review treats as still incompletely resolved. No source reviewed here proposes coordinates for this pole at all, point-level or otherwise more specific than the four-territory border region.

56.6 Why no illustrative real-coordinate check is reported here

Every real-coordinate check elsewhere in this cycle, illustrative or otherwise, has needed at least one named point to anchor it — turkey's Oaxaca findspot (§21.5), goose's Tianluoshan site (§55.6), or fig's own decision to report none at all (§46.5) when even that was unavailable. Yam's three poles supply not even one: the African

pole offers a named river basin, the Asian-Pacific pole offers a named archaeological site whose own crop identification stops at genus level, and the South American pole offers a four-territory border region. Reporting a distance between any two of these would manufacture a precision none of the cited sources claims for any of them. Consistent with §46.5's own precedent, no real-coordinate check is computed for this chapter.

56.7 Applying §20.7's predicate: a new instantiation, with every center unresolved

Let X = {x_Africa, x_AsiaPacific, x_SouthAmerica}. No source reviewed here reports a point-level coordinate for any of the three, so r_Africa = r_AsiaPacific = r_SouthAmerica = 0. By §20.7.1, R(X) = 0, since R(X)=1 requires r_i=1 for every i. By §20.7.2's partial-function definition, PI(C,κ,D̄) = ⊥: C=1 is false (three independent events are corroborated, unanimously), and R(X)=1 is false, so neither the resolvable branch nor the C=1-unanimous branch applies.

This is not a new branch of the equation, which already covers this outcome, but it is a new instantiation within the ⊥ group's own qualitative record: every prior multi-center case on turkey's branch (turkey itself, cotton, goose) carried at least one resolved center among several; chicken's own branch carried a single center that never resolved. Yam is this cycle's first case with three or more independently corroborated centers, none of which resolves. Two further compounding features distinguish it still further from either branch: the African pole's own wild source is disputed between two published models of unequal parentage (§56.3), and the Asian-Pacific pole conceals, within what the traditional count reports as one center, a second, independently founded gene pool no source has yet assigned coordinates of its own (§56.4).

56.8 Placement in Appendix A.3 as a nineteenth row

Yam is added to Appendix A.3 as a nineteenth row, on the compound ground set out in §56.3–§56.7, alongside chicken, turkey, cotton, broomcorn millet, cat, llama, guinea pig, capsicum, pea, C. moschata, fig, reindeer, guinea fowl, European rabbit, fava bean, and goose.

56.9 Synthesis note

Yam was raised as a candidate because the review literature converges, more completely than for any other case in this cycle, on a bare unanimous count — three independent domestications, three continents, three species — while converging on almost nothing else. Not one of the three poles offers a named, excavated, or surveyed point comparable to einkorn's core area, Tianluoshan's goose bones, or even turkey's own Oaxaca findspot; the closest approach, Kuk Swamp, identifies its own yam remains no further than genus level. §1.4's discipline is served here by reporting the unanimous count plainly, and by reporting each pole's own regional-only resolution, its own internal disputes (the African progenitor's contested parentage; the Asian-Pacific pole's undisclosed second gene pool), and its own evidentiary gap (South America's near-total absence of genomic study) without manufacturing a coordinate, a distance, or a resolution none of the cited sources supplies. Should a point-level find comparable to Tianluoshan's ever be reported for any of the three poles, or should Sharif et al.'s two Asian-Pacific gene pools ever be assigned separate coordinates, this chapter's zero-resolved count would need revision; nothing above anticipates that outcome.

References newly cited in Chapter 56

Fullagar, R., Field, J., Denham, T. & Lentfer, C. (2006). Early and mid Holocene tool-use and processing of taro (Colocasia esculenta) and yam (Dioscorea sp.) and other plants at Kuk Swamp in the

Highlands of Papua New Guinea. Journal of Archaeological Science, 33, 595–614.

Scarcelli, N., Cubry, P., Akakpo, R., Thuillet, A.-C., Obidiegwu, J., Baco, M.N., Otoo, E., Sonké, B., Dansi, A., Djedatin, G., Mariac, C. et al. (2019). Yam genomics supports West Africa as a major cradle of crop domestication. Science Advances, 5(5), eaaw1947.

Sharif, B.M. et al. (2020). Genome-wide genotyping elucidates the geographical diversification and dispersal of the polyploid and clonally propagated yam (Dioscorea alata). Annals of Botany, 126(6), 1029.

Sugihara, Y., Darkwa, K., Yaegashi, H., Natsume, S., Shimizu, M. et al. (2020). Genome analyses reveal the hybrid origin of the staple crop white Guinea yam (Dioscorea rotundata). Proceedings of the National Academy of Sciences, 117(50), 31987–31992.

Sugihara, Y., Kudoh, A., Oli, M.T., Takagi, H., Natsume, S., Shimizu, M., Abe, A., Asiedu, R., Asfaw, A., Adebola, P. & Terauchi, R. (2021). Population genomics of yams: evolution and domestication of Dioscorea species. In P. Rajora (Ed.), Population Genomics: Crop Plants (pp. 1–28). Springer, Cham.

Chapter 57 — Avocado (Persea americana): Three Independent Domestications, and the Cycle's First Case Where Every Center Resolves

57.1 Admission, continuing the cycle's supplementary practice as an eleventh case

Avocado (Persea americana) is admitted here as an eleventh supplementary case, and as a new, tenth row within Appendix A.1's list of resolvable cases with a non-zero Polycentricity Index — the first three-center case this cycle has been able to place there, rather than in Appendix A.3 alongside yam (Ch.56), cotton (Ch.22),

or Capsicum (Ch.40). Avocado's three botanical races — Mexican, Guatemalan, and Lowland (formerly "West Indian," a name recent genomic work treats as inaccurate and no longer uses) — were long suspected of separate origins on morphological grounds alone; whole-genome resequencing has since converged on the same reading.

57.2 Three botanical races, genomically confirmed as three independent domestication events

Solares, Morales-Cruz et al. (2023) sequenced a reference genome from the Gwen cultivar and resequenced 30 P. americana accessions spanning all three races, plus outgroups. Admixture mapping, principal component analysis, and a maximum-likelihood phylogeny independently converge on three well-supported, reciprocally monophyletic clades corresponding to the Mexican, Guatemalan, and Lowland races, with two putatively wild accessions from Chiapas intercalating the Lowland and Guatemalan clades in a pattern the authors read as reinforcing separate domestication of those two groups specifically. The paper states its population-genomic results as consistent with three separate domestication events. A further, disclosed correction in the same paper is worth noting for calibration rather than for the index itself: the dominant Hass cultivar, long read as a roughly even Guatemalan–Mexican hybrid by earlier marker-based studies, resolves in this whole-genome analysis as predominantly Guatemalan in origin.

57.3 Two very different divergence times, read as wild-lineage splits predating domestication

The same study's coalescent-based demographic inference (MSMC2) places the split between the Mexican lineage and the other two at approximately 1.3 million years ago, while the Lowland and Guatemalan lineages diverge from each other far

more recently, at approximately 44,000 years ago — both figures far older than any plausible domestication date for a perennial tree crop, and read by the authors as divergence among wild progenitor populations rather than as a domestication-era event. This roughly thirty-fold asymmetry between the two split times is disclosed here as reported, not smoothed into a single figure.

57.4 A prior, independent SNP dataset corroborating the same three-way structure

The three-race structure is not a single-paper finding. Talavera, Soorni, Bombarely, Matas & Hormaza (2019) genotyped 71 accessions against a draft Hass reference using 7,108 SNP markers and recovered the same three-way clustering (Mexican, Guatemalan, West Indian/Lowland), plus a distinct Guatemalan × Mexican hybrid group, four years before Solares et al.'s whole-genome resequencing. The two studies used different reference assemblies, different marker sets, and different statistical methods — PCA and STRUCTURE against a de novo SNP panel, versus admixture, PCA, TreeMix, and maximum-likelihood phylogeny against a long-read reference genome — and converge on the same partition, the same doubly-corroborated-by-independent-method standard already applied to flax (Ch.42, §42.6) and to C. maxima (Ch.43, §43.7).

57.5 An archaeological anchor at El Gigante Rockshelter, and a naming/geography wrinkle

VanDerwarker, Thakar, Hirth, Domic et al. (2025) report a directly radiocarbon-dated sequence of avocado seed and rind remains from El Gigante Rockshelter in western Honduras spanning roughly the last 11,000 years, with selection for larger, thicker-rinded fruit detectable by 7,565–7,265 cal. B.P. and reaching its clearest expression by 2,250–2,080 cal. B.P. The excavated seed morphology is described as consistent with P. americana var.

guatemalensis — but the same paper is explicit that this variety's own development is congruent with genetic data for a highland zone spanning both Guatemala and Honduras, not Guatemala alone: the race name inherited from earlier taxonomy does not coincide with a national or even a single-country boundary. This is disclosed here as a naming wrinkle, not folded into a fourth center: no source reviewed in this chapter treats Honduras as an independent domestication locus distinct from the Guatemalan race.

57.6 A real-coordinate check — illustrative only, anchored to disclosed accession localities

As with every real-coordinate check in this cycle, the three points used here are not asserted as the literal find-spots of each race's original wild population, which the cited genomic studies do not report at that resolution; they are real, disclosed collection localities for named accessions in Solares et al.'s (2023) own sample table, used illustratively. For the Guatemalan race: Antigua, Guatemala (14.5586°N, 90.7295°W), the budwood-collection site recorded for the Linda, Nabal, and Nimlioh cultivars (1914–1917). For the Lowland race: Hunucmá, Yucatán, Mexico (21.0333°N, 89.8667°W), the origin recorded for accession 263-C, scored in that table as 100% Lowland with no admixture. For the Mexican race: Atlixco, Puebla, Mexico (18.9083°N, 98.4342°W), the 1911 budwood-collection site recorded for Fuerte, a Guatemalan × Mexican hybrid whose Mexican ancestry predominates and whose collection locality sits within the Mexican race's own highland range. Great-circle distances computed from these three points: Atlixco–Antigua 952.1 km, Atlixco–Hunucmá 925.9 km, Antigua–Hunucmá 725.7 km; $\bar{D}$ = 867.9 km.

57.7 Applying §20.7's predicate: R(X)=1, this cycle's first three-center resolution

Let X = {x_Mexican, x_Guatemalan, x_Lowland}. Each of the three clears the resolvability bar via a disclosed real coordinate (§57.6), so R(X)=1 holds on all three conjuncts simultaneously — the same predicate that failed on all three of yam's centers (§56.7) now succeeds on all three of avocado's, despite an identical C=3. Because all three domestication events are treated by the cited genomic literature as fully and independently corroborated by the same dataset, rather than as a fractional or introgressed secondary contribution, κ=1.000, the value already assigned to pig, water buffalo, cattle, and squash in Appendix A.1. PI = C × κ × $\bar{D}$ = 3 × 1.000 × 867.9 ≈ 2,604.

57.8 Placement in Appendix A.1 as a tenth entry, and the contrast with yam made explicit

Avocado is added to Appendix A.1 as a tenth entry, ranked seventh of the ten by PI value — immediately behind barley (3,384) and ahead of the rice C=2 model (704), between the group's five-member upper cluster (pig through squash, 4,565–13,050) and its lower two entries (grapevine, goat). Its significance for this appendix is structural rather than positional: it is this cycle's first C=3 case to resolve on all three centers, standing as the direct counterpart to yam (Ch.56) that this cycle's own earlier working notes anticipated — identical center count, opposite resolvability outcome, and a reminder that C alone predicts neither R(X) nor PI.

57.9 Synthesis note

Avocado was raised as a candidate specifically because its literature converges as cleanly as any three-center case reviewed in this cycle, and because that convergence had not previously been tested against this cycle's own resolvability predicate. It clears that test on every count the surrounding chapters have used to fail comparable

cases elsewhere — SNP corroboration by two independent methods (§57.4), an archaeological anchor consistent with, though not identical in scope to, the genomic reading (§57.5), and disclosed real coordinates sufficient to compute rather than withhold a Polycentricity Index (§57.6–§57.7). Its most interesting result may be the least numerical one: a case can share yam's exact center count and still land at the opposite end of this cycle's central distinction.

References newly cited in Chapter 57

Solares, E., Morales-Cruz, A., Figueroa Balderas, R., Focht, E., Ashworth, V.E.T.M., Wyant, S., Minio, A., Cantu, D., Arpaia, M.L. & Gaut, B.S. (2023). Insights into the domestication of avocado and potential genetic contributors to heterodichogamy. G3 Genes|Genomes|Genetics 13(2), jkac323.

Talavera, A., Soorni, A., Bombarely, A., Matas, A.J. & Hormaza, J.I. (2019). Genome-Wide SNP discovery and genomic characterization in avocado (Persea americana Mill.). Scientific Reports 9, 20137.

VanDerwarker, A.M., Thakar, H.B., Hirth, K., Domic, A.I., Harper, T.K., George, R.J., Johnson, E.S., Newhall, V., Scheffler, T.E., McCool, W.C., Wann, K., Gaut, B.S., Kistler, L. & Kennett, D.J. (2025). Early evidence of avocado domestication from El Gigante Rockshelter, Honduras. Proceedings of the National Academy of Sciences 122(10), e2417072122.

Chapter 58 — Common Carp (Cyprinus carpio): This Cycle's First Osteichthyes, and a Historical Rival Hypothesis Resolved by Single-Origin Genomics

58.1 Admission, continuing the cycle's supplementary practice as a twelfth case, and this cycle's first bony fish

Common carp (Cyprinus carpio) is admitted here as a twelfth supplementary case, and as a new, twenty-fifth row within

Appendix A.2's list of resolvable cases at the PI=0 floor. It is also this cycle's first case drawn from Pisces/Osteichthyes — a taxonomic first in the same sense that yeast (Ch.30, Fungi) and honey bee (Ch.31, Insecta) were each first members of their own kingdom or class, though carp's own outcome, unlike either of theirs, places it squarely inside the index's domain rather than in Appendix A.5.

58.2 A single origin, dispersing into two geographically and genetically distinct subspecies

Xu, Zhang, Wang et al. (2014) sequenced a draft genome of domesticated C. carpio (strain Songpu) and resequenced 33 representative accessions from a worldwide collection. Their result is stated directly: genome resequencing demonstrates a single origin for C. carpio, structured into two subspecies, C. carpio haematopterus (East Asian) and C. carpio carpio (Ponto-Caspian/European). The two subspecies form two distinct genomic groups, consistent with their separate geographic ranges and separate husbandry histories, but traceable, on this reading, to one wild-origin event rather than two.

58.3 An older historical/cultural hypothesis: an independent domestication in China

Balon (1995), reviewing paleogeographical, morphological, ecological, linguistic, archaeological, and historical evidence, situates the wild ancestor's own range in the Black, Caspian, and Aral Sea drainages, with a natural dispersal east into Siberia and China and west to the Danube. The same review credits Roman aquaculture with the earliest documented culture of carp collected from the Danube, continued through medieval monastic “piscinae” — but ancient Chinese pond-culture traditions, textually attested well before the Roman record, had long been treated in the ichthyological literature as a candidate for an independently arrived-at husbandry practice on the eastern population, rather

than as an eastward transplant of an already-domesticated western stock. On a purely cultural-historical reading, this leaves open whether Chinese carp husbandry represents a second, independent center rather than an extension of the same one.

58.4 Why the dispute is resolved rather than left open

Xu et al.'s (2014) resequencing directly addresses the genetic version of this question, not merely the cultural-historical one Balon's review raises: a single wild origin, with the Ponto-Caspian and East Asian subspecies representing two later-diverging branches of one lineage rather than two independently domesticated wild populations. This is the same kind of resolution already applied to date palm's African diversity (Ch.35, §35.6, read as introgression rather than a second center) and to citrus's older two-center reading (Ch.53, §53.4, superseded by a single mosaic-genome model) — an older account proposing a second independent center, superseded by a single coherent genomic dataset that reads the same pattern as one origin with later structure. Carp differs from both precedents in the character of the superseded claim: date palm's and citrus's earlier readings were themselves partly genetic or morphological; Balon's rival account here rests on textual and archaeological husbandry-tradition evidence, predating any genomic test of the question by two decades — the oldest-dated rival hypothesis this cycle has recorded being overtaken by genomic evidence.

58.5 Applying §20.7's predicate: R(X)=1, C=1, a new route to the floor

With a single corroborated wild origin (§58.2) and no second population independently supported by the genomic record, C=1 and R(X)=1 by the same single-center standard already applied to einkorn, chickpea, and horse (Appendix A.2). κ=1.000 and $\bar{D}$=0 by the branch of §20.7.2 already used for every unanimous C=1 case in this table, giving PI=0. The route to this floor is nonetheless a new

one for Appendix A.2's running list of distinct paths: not a disputed count resolved by testing a named rival (as for C. argyrosperma, §43.2), nor a regionally-inherited location without an independently tested point (as for flax and C. maxima), but a specifically pre-genomic historical/cultural hypothesis of an independent second husbandry tradition, superseded once whole-genome resequencing became available to test it directly.

58.6 Placement in Appendix A.2 as a twenty-fifth entry

Carp is added to Appendix A.2 as a twenty-fifth entry, on a new route distinct from those already catalogued for donkey, chickpea, alpaca, silk moth, coffee, flax, C. maxima, C. argyrosperma, watermelon, and peach. It is this table's first entry from outside Animalia's mammal and bird membership, and this cycle's first case from any ray-finned fish lineage in any appendix.

58.7 Synthesis note

Carp was raised as the alternative candidate to avocado specifically because it offered a structurally different kind of case: not a new center count, but this cycle's first test of its own predicate against a rival hypothesis that is historical and cultural in its original form rather than genomic. That the same single-origin, no-second-center pattern already used for plant cases (date palm, citrus) applies without modification to a vertebrate domesticated for aquaculture rather than for meat, fiber, or traction is itself a small extension of §31.7's and §38.6's own point: this cycle's outcome branches are set by what the cited evidence supports, not by any property specific to a kingdom, a class, or — as carp's own case now shows — a rival hypothesis's evidentiary type.

References newly cited in Chapter 58

Balon, E.K. (1995). Origin and domestication of the wild carp, Cyprinus carpio: from Roman gourmets to the swimming flowers. Aquaculture 129, 3–48.

Xu, P., Zhang, X., Wang, X., Li, J., Liu, G., Kuang, Y., Xu, J., Zheng, X., Ren, L., Wang, G., Zhang, Y., Huo, L., Zhao, Z., Cao, D., Lu, C., Li, C., Zhou, Y., Liu, Z., Fan, Z., Shan, G., Li, X., Wu, S., Song, L., Hou, G., Jiang, Y., Jeney, Z., Yu, D., Wang, L., Shao, C., Song, L., Sun, J., Ji, P., Wang, J., Li, Q., Xu, L., Sun, F., Feng, J., Wang, C., Wang, S., Wang, B., Li, Y., Zhu, Y., Xue, W., Zhao, L., Wang, J., Gu, Y., Lv, W., Wu, K., Xiao, J., Wu, J., Zhang, Z., Yu, J. & Sun, X. (2014). Genome sequence and genetic diversity of the common carp, Cyprinus carpio. Nature Genetics 46(11), 1212–1219.

Chapter 59 — Cassava (Manihot esculenta): A Southern Amazon Single Origin, Reached Without a Contested Second Center

59.1 Admission, continuing the cycle's supplementary practice as a thirteenth case, and a twenty-sixth row within Appendix A.2

Cassava (Manihot esculenta) is admitted here as a thirteenth supplementary case, on the same footing established since donkey (Ch.23): raised on its own evidentiary merits after this cycle's own repeated stopping-rule declarations, rather than as part of any section planned from the outset. Unlike carp (Ch.58), which tested the cycle's predicate against a named historical rival hypothesis, cassava is admitted for a plainer reason: it is a staple root crop for several hundred million people, and its own literature converges on a single origin with a clarity this cycle has previously reserved for potato and donkey.

59.2 A single-copy nuclear gene resolves a long-disputed origin

Olsen and Schaal (1999) investigated cassava's domestication using the single-copy nuclear gene glyceraldehyde-3-phosphate dehydrogenase (G3pdh), identifying 28 haplotypes among 212 individuals (424 alleles) sampled across cultivated cassava and its wild relatives. Their result was stated directly: cassava was domesticated from wild Manihot esculenta populations along the southern border of the Amazon basin; the crop does not appear to derive from several progenitor species, as earlier proposed; and it shares no haplotypes with Manihot pruinosa, a species capable of hybridizing with cassava that some earlier accounts had implicated in its ancestry.

59.3 Independent corroboration, and an earlier multi-progenitor hypothesis set aside

Olsen and Schaal (2001) followed with an independent microsatellite study, genotyping 212 individuals at five loci, comprising cultivated cassava, 27 populations of its closest wild relative (M. esculenta subsp. flabellifolia), and six populations of M. pruinosa. The result reached the same conclusion by a different method: genetic variation in the crop is a subset of that found in the wild subspecies, consistent with a single wild source rather than a composite of several progenitor species. This supersedes an older hypothesis — advanced by Rogers and Appan (1973) and echoed in later reviews (Sauer 1993) — that cassava might derive from hybridization among several wild Manihot species; the genetic evidence available does not require, and does not support, invoking more than the one wild subspecies.

59.4 Archaeobotanical convergence at the proposed source region itself

For a genus whose organic remains preserve poorly in humid tropical sediments, direct archaeobotanical confirmation at a proposed origin is unusual; cassava's case now has one. Lombardo

et al. (2020) report phytolith evidence identifiable as Manihot at roughly 10,350 calibrated years before present at the Llanos de Moxos, in the Bolivian lowlands on the southern margin of the Amazon basin — the same region Olsen and Schaal's genetic data had already implicated, and part of a wider record at the same sites documenting squash cultivation from about 10,250 cal. yr BP and, later, maize from about 6,850 cal. yr BP. This is a genuine corroboration of the genetic reading by an independent archaeological line, on the same footing as the archaeology–genetics convergences already recorded for dromedary (Ch.18) and silk moth (Ch.38), rather than a mere consistency of broad region. Evidence for the crop's subsequent spread is disclosed separately and should not be mistaken for evidence of the founding event itself: starch grains identified as manioc appear on milling stones from the Aguadulce Shelter, Panama, in preceramic strata dated between 7,000 and 5,000 years before present (Piperno et al. 2000), and starch-grain evidence of manioc consumption is reported from the Maya site of La Corona, Guatemala, dated to the Late–Terminal Classic, 8th–9th century CE (Cagnato & Ponce 2017) — both well outside, and much later than, the source region itself.

59.5 Applying §20.7's predicate: C=1, on the same route as potato and donkey

With a single wild source population independently identified by two distinct genetic methods (nuclear-gene phylogeography and microsatellite variation), corroborated by a direct archaeobotanical date at the same region, and no rival center proposed since, C=1 and R(X)=1 by the same "directly tested, unanimous" standard already applied to potato (Ch.24, §24.6) and donkey (Ch.23, §23.5). κ=1.000 and $\bar{D}$=0 follow by the same branch of §20.7.2 used for every unanimous C=1 case in this table, giving PI=0.

59.6 Placement in Appendix A.2 as a twenty-sixth entry

Cassava is added to Appendix A.2 as a twenty-sixth entry, on the same unanimous-from-the-outset route already catalogued for potato, donkey, and — with an archaeology–genetics convergence specifically — dromedary and silk moth, rather than on any of the further routes carp's own chapter (§58.5) most recently distinguished.

59.7 Synthesis note

Cassava is not structurally new to this cycle: it repeats a route to the floor this table has recorded many times over. Its interest is substantive rather than formal — it closes out, on the same clean single-origin footing as potato, one of a small number of staple crops feeding several hundred million people whose geographic origin had once been seriously disputed (an FAO review as late as 1990 still floated Mexico/Central America and northern South America as alternative candidates) before independent genetic and, now, archaeobotanical evidence converged on one answer.

59.8 A real-coordinate check, added in the present pass — illustrative only, an internal-breadth sensitivity measure

Recomputed via great-circle distance (code/Ch59_cassava_distance_check.py; Appendix B.11), using a representative point within the genetic wild-source region Olsen and Schaal (1999, 2001) narrow to "a limited area … between western Mato Grosso and western Rondônia" (Vilhena, Rondônia, Brazil, 12.7406°S, 60.1458°W) and a representative point for the archaeobotanical confirmation region at the Llanos de Moxos, Bolivia (Trinidad, Beni, Bolivia, 14.8292°S, 64.9014°W): 563.6 km. As with dromedary's own internal-breadth check (§18.4), this is not a C=2 distance between rival centers — both points sit inside the single southern Amazon border zone independently implicated by genetics and archaeology — but a disclosed measure of how widely

that single zone is itself drawn, spanning parts of two present-day countries. At 563.6 km this is wider than dromedary's own 20.7 km internal-breadth figure, consistent with cassava's own literature describing a broader source region ("a relatively restricted area," not a single pair of excavated sites) than dromedary's two named localities. This figure does not revise §59.5's own PI=0 result: D̄=0 there follows from C=1 unanimity by §20.7.2's convention, not from this illustrative span, which is reported as a further confirmation of the zone's own narrowness rather than as a D̄ feeding a PI.

References newly cited in Chapter 59

Cagnato, C. & Ponce, J.M. (2017). Ancient Maya manioc (Manihot esculenta Crantz) consumption: Starch grain evidence from late to terminal classic (8th–9th century CE) occupation at La Corona, northwestern Petén, Guatemala. Journal of Archaeological Science: Reports 16, 276–286.

Lombardo, U., Iriarte, J., Hilbert, L., Ruiz-Pérez, J., Capriles, J.M. & Veit, H. (2020). Early Holocene crop cultivation and landscape modification in Amazonia. Nature 581(7807), 190–193.

Olsen, K.M. & Schaal, B.A. (1999). Evidence on the origin of cassava: Phylogeography of Manihot esculenta. Proceedings of the National Academy of Sciences 96(10), 5586–5591.

Olsen, K.M. & Schaal, B.A. (2001). Microsatellite variation in cassava (Manihot esculenta, Euphorbiaceae) and its wild relatives: further evidence for a southern Amazonian origin of domestication. American Journal of Botany 88(1), 131–142.

Piperno, D.R., Ranere, A.J., Holst, I. & Hansell, P. (2000). Starch grains reveal early root crop horticulture in the Panamanian tropical forest. Nature 407, 894–897.

Chapter 60 — Rye (Secale cereale): A Weedy Intermediate the Predicate Was Not Built to Count

60.1 Admission, a fourteenth supplementary case

Rye is admitted as a fourteenth supplementary case, immediately after cassava, on different footing again: not a clean floor case, but a candidate for Appendix A.5's small group of cases lying outside §20.7.1's predicate altogether — and, if it belongs there, on a genuinely new ground.

60.2 A geographic origin not seriously contested, and a long archaeological silence

Wild relatives of rye (Secale vavilovii, S. strictum) are native to eastern Turkey and the Transcaucasus, and domesticated rye is reported to appear by roughly 9,500–8,500 years before present in that same region, with small quantities recovered from Neolithic (Pre-Pottery Neolithic B) contexts at Can Hasan III in Anatolia, a site whose early rye finds were reported by Hillman (1978). Sources reviewed for this chapter consistently place rye's own geographic origin in eastern Anatolia/the Transcaucasus; unlike maize (Ch.6) or Bactrian camel (Ch.19), no rival region is seriously argued in the literature surveyed here. What is unusual is the record's own silence afterward: outside this early Anatolian occurrence, domesticated rye is reported as essentially absent from the archaeological record until the Bronze Age of central Europe, roughly 1800–1500 BCE — a gap of several thousand years, widely explained as rye travelling west as an unintentional admixture in wheat and barley fields (Vavilovian mimicry) long before being sown and harvested in its own right.

60.3 A population-genomic test of Vavilov's own hypothesis

Sun et al. (2022) generated 8.5 Tb of whole-genome resequencing data from 116 worldwide accessions spanning wild, weedy, and

cultivated rye, and tested six demographic scenarios of the crop's origin against this data. The best-supported model does not place cultivated rye as a direct descendant of the wild species; it places cultivated rye as domesticated directly from weedy rye, itself an intermediate population between wild and cultivated forms, with a composite introgression detected from the wild perennial S. strictum into the cultivated genome. Divergence between wild rye and S. cereale is dated to roughly 6,000 years ago in the same study, and no clear genetic bottleneck separates cultivated rye from its weedy source, a pattern the authors attribute to the crop's outcrossing biology.

60.4 A disclosed cross-source tension on timing

One piece of this same population-genomic study's own supporting material reports a radiocarbon date of roughly 4440 BC for an early rye find in central Europe, offered as consistent with the roughly 6,000-year divergence estimate; this sits awkwardly against the archaeological consensus reported above (§60.2) that domesticated rye is otherwise absent from the central European record until the Bronze Age, some two and a half thousand years later. Both figures are reported here as found, rather than adjudicated in either direction: reconciling a single early central European date against a longer, better-attested silence is a question for the primary archaeological literature, not one this cycle's own method is positioned to resolve.

60.5 Why this is neither a location dispute nor a count dispute

Rye's own case does not fit Appendix A.3: no second candidate region competes with eastern Anatolia/the Transcaucasus in the sources reviewed. It does not fit Appendix A.4 either: the disagreement is not over how many centers produced rye, nor over which of two counts is correct. What is unresolved is the domestication event's own structure. Sun et al.'s (2022) best-fitting

model names a third, genetically distinguishable population — weedy rye — standing between wild and cultivated rye, with cultivated rye descending from that intermediate population rather than from the wild species directly. §20.7.1's predicate presupposes a choice among candidate centers for a single wild-to-domesticate event; when the best-supported model itself replaces that single transition with two linked ones, mediated by a population that is neither fully wild nor yet the crop, the predicate has nothing to count. This is a different problem from honey bee's (Ch.31, §31.5): honey bee's difficulty is an absence of any genetic boundary between wild and domesticated populations across most of its management history; rye's difficulty is the opposite in kind — a named, dated, genomically characterized third population, tested by explicit demographic-model comparison against the direct-domestication alternative and found to fit the data better.

60.6 Applying §20.7's predicate: outside the index's domain, on a new ground

No C is meaningfully assigned to a wild-to-domesticate transition here, because the best-supported reading of the evidence denies that a single such transition is what the record shows. Rye is therefore reported outside §20.7.1's predicate, alongside banana, yeast, honey bee, koji, vanilla, sweet potato, and citrus (Appendix A.5) — but on a ground distinct from any of theirs: not a mosaic genome built from several hybridizing taxa (banana, citrus), not several separately dated domestication events drawn from one wild-origin region (yeast), not an absence of any genetic boundary at all (honey bee), but a single wild-origin region feeding a formally tested, better-supported two-stage pathway through a named intermediate population.

60.7 Placement in Appendix A.5 as an eighth entry

Rye is added to Appendix A.5 as an eighth entry, on this new ground.

60.8 Synthesis note

Rye closes this cycle's run of supplementary cases on a note distinct from cassava's: where cassava repeated an established route to the floor, rye supplies this cycle's first exclusion from the index's own domain that rests on a formal, published demographic-model comparison rather than on an absent boundary or a mosaic of hybridizing taxa. It is, in that sense, the most rigorously tested of this appendix's non-computations, and a fitting case on which to close the cycle's own supplementary practice (§61.1).

60.9 A real-coordinate check, added in the present pass — illustrative only, on the wild-range-to-find-site span

Recomputed via great-circle distance (code/Ch60_rye_distance_check.py; Appendix B.12), using a representative point within the wild relatives' own range in eastern Turkey and the Transcaucasus (Erzurum, Turkey, 39.9086°N, 41.2769°E) and a representative point for Can Hasan III's own site region, Karaman Province, Central Anatolia (37.2630°N, 33.3313°E): 750.3 km. Following the same convention as coffee's own wild-origin-to-domestication-pathway check (§39.5), this is reported as an illustrative span between a wild-relative range and an early archaeological find region, not as a $\bar{D}$ feeding a PI. §60.5's own conclusion that no C is assigned to rye holds regardless of this figure: the difficulty identified there is structural — a named, dated, genomically characterized weedy intermediate population standing between wild and cultivated forms — not a matter of an unresolved or contested distance. The span is disclosed here only to give the wild-range/find-site relationship named in §60.2 a real coordinate anchor, in the same spirit as every other illustrative

check in this cycle, and is independent of §60.4's own disclosed cross-source timing tension, which concerns a separate, much later central European find rather than this region.

References newly cited in Chapter 60

Hillman, G.C. (1978). On the origins of domestic rye—Secale cereale: the finds from Aceramic Can Hasan III in Turkey. Anatolian Studies 28, 157–174.

Sun, Y., Shen, E., Hu, Y., Wu, D., Feng, Y., Lao, S., Dong, C., Du, T., Hua, W., Ye, C.-Y., Zhu, J., Zhu, Q.-H., Cai, D., Skuza, L., Qiu, J. & Fan, L. (2022). Population genomic analysis reveals domestication of cultivated rye from weedy rye. Molecular Plant 15(3), 552–561.

Chapter 61 — Closing Synthesis: The Cycle's Final Accounting and Close

61.1 Closing the cycle for the last time

Chapter 1 declared a stopping rule for this cycle's original four cases (§1.3, §1.5); Chapter 8 closed the cycle a first time at seven, as its own title states; and later syntheses carried the running total forward, to eleven cases across seven sections at §13.7 and further still at each count this appendix has recorded since. Every one of those closures was reopened only when a new case was raised on its own evidentiary merits — as Chapter 23 and Chapter 33 each declared explicitly at their own admission (§23.1, §33.1) — rather than to keep the cycle open for its own sake. Cassava (Ch.59) and rye (Ch.60) were admitted on exactly that same basis. This closure differs from every one before it in only one respect: no further supplementary chapter will follow rye's own. Any additional case belongs, if anywhere, to a successor volume, not to this one.

Editorial note, added upon reopening: this limit was subsequently revoked, on the same evidentiary-merits basis already applied at every earlier

reopening of this cycle (§23.1, §33.1) — first for oat and duck (Ch.62–Ch.63), then for taro (Ch.64) — and this closure was in turn superseded by the cycle's third accounting at Ch.65, §65.1–§65.6 (seventy-three tabulated cases across sixty-five chapters), and is now superseded by the cycle's fourth and final accounting at Ch.69, §69.1–§69.6, which carries the tally to seventy-six tabulated cases across sixty-nine chapters. §61.4's own disclaimer, that no monograph of this kind could honestly claim completeness, is not withdrawn by this note; it is the reason the reopening remained possible at all.

61.2 Final tally by outcome group

Across Appendix A's five groups, this cycle now carries sixty-nine tabulated cases: ten with a resolvable, non-zero Polycentricity Index (A.1); twenty-six resolvable at the PI=0 floor (A.2, with cassava's addition); nineteen with a resolvable center count but an unresolved location (A.3); six with a disputed center count rather than a disputed location (A.4); and eight lying outside §20.7.1's predicate altogether (A.5, with rye's addition). No value in this tally is computed for the first time here: each is carried forward from the chapter and appendix section where it was first derived, under the same no-invented-data discipline declared in §1.4 and reaffirmed at each supplementary admission since.

61.3 What the two final cases changed, and what they did not

Cassava changed a count, not a category: it adds a twenty-sixth case to a route already well documented by potato, donkey, and several others, and its own chapter said so directly (§59.7) rather than claiming a novelty it does not have. Rye changed something more structural: it supplies this appendix's first exclusion grounded in an explicit, published demographic-model comparison naming a discrete intermediate population, rather than in an absent genetic boundary (honey bee), a mosaic genome built from several hybridizing taxa (banana, citrus), or several independently dated

domestication events drawn from one wild-origin region (yeast). Appendix A.5's own membership is now organized around a fourth distinct reason for a case falling outside the predicate's domain, alongside the three these seven prior members already supplied.

61.4 Final stopping-rule declaration

This cycle is closed, in the same sense §1.5 and §8.6 first used the term and every later chapter's own admission notice preserved: not because every possible case has been treated — no monograph of this kind could make that claim honestly — but because the sixty-one chapters and sixty-nine tabulated cases assembled here already exercise the Domestication Polycentricity Index, and the predicate it depends on, against every structural difficulty this author has been able to locate real, cited, non-invented evidence for: clean single centers, contested multi-center counts, resolvable and unresolvable locations, mosaic genomes, absent genetic boundaries, and now a formally tested weedy intermediate. Further cases would, at this point, most likely repeat a route already catalogued rather than supply a new one, which is itself the condition §1.5 named for stopping.

61.5 What the cycle shows about the index itself

Of the sixty-nine cases tabulated in Appendix A, thirty-six return a computed Polycentricity Index (A.1's ten non-zero values and A.2's twenty-six zeros) and thirty-three do not (A.3's nineteen, A.4's six, and A.5's eight). A reader expecting an index to resolve nearly every case it is pointed at should take this near-even split as this cycle's own final self-assessment rather than as a shortcoming to explain away: the Domestication Polycentricity Index returns a number only where a center count and a location are both independently resolved by the cited literature, and disclosing a non-computation where that condition fails has been, from §1.4

onward, the discipline this cycle set out to keep — not a fallback adopted when the arithmetic proved inconvenient.

61.6 Closing statement

The furrow this cycle has followed runs from einkorn's single, geographically precise origin (§2.2) to rye's own weedy intermediate (Ch.60), by way of mosaic genomes, absent genetic boundaries, and every gradation of resolved and unresolved center between. What holds sixty-nine cases together is not a single answer about how domestication happened, but a single, consistently applied standard for what counts as knowing the answer — and for saying plainly when it is not yet known. That standard, rather than any total case count, is this monograph's own founder effect, and the reason its author closes it here.

Chapter 62 — Oat (Avena sativa): A Second Weedy-Field Origin the Genomic Record Resolves Differently From Rye's Own

62.1 Admission, a fifteenth supplementary case

Oat is admitted as a fifteenth supplementary case, reopening a cycle Chapter 61 declared closed (§61.1, §61.4). It is raised on a specific, named ground: oat shares with rye (Ch.60) the same textbook description as a “secondary crop,” domesticated from a plant that first spread as a weed of wheat and barley rather than being cultivated in its own right from the outset. Whether that shared narrative also gives oat rye's own structural ground for exclusion from §20.7.1's predicate (§60.5–§60.6) is a genuine question, tested rather than assumed below (§62.5), and the two cases turn out not to resolve the same way.

62.2 A single, late, secondary-crop origin in Anatolia

Cultivated oat (Avena sativa L.) is an allohexaploid (AACCDD, 2n=6x=42) descended from the wild hexaploid oat, A. sterilis, whose ancestral populations are reported in the Fertile Crescent of the Near East. Sources reviewed for this chapter converge on domestication occurring more than 3,000 years ago — substantially later than wheat or barley — while oat grew as a weed in wheat, emmer, and barley fields in Anatolia, before being sown and harvested as a crop in its own right, chiefly as cultivation of the primary cereals spread into the cooler, wetter conditions of Europe where oat outcompetes its former hosts (Kamal et al., 2022; Oxford University Plants 400, citing the same weed-to-crop sequence). The diagnostic domestication trait, as with other cereals, is loss of the wild seed-dispersal mechanism: wild and weedy oats shed their grain at maturity, driven into the soil by a drill-like awned bract, while domesticated oat retains its grain on the plant until harvest.

62.3 The genomic resolution: Kamal et al. (2022) and the wild-oat genome

Kamal et al. (2022) assembled a high-quality reference genome of A. sativa together with its diploid (A. longiglumis) and tetraploid (A. insularis) progenitor relatives, describing the cultivated genome's own “mosaic” internal architecture — numerous large-scale rearrangements among subgenomes — but reporting a single named region, Anatolia, for the weed-to-crop transition itself; no rival geographic center is proposed or tested against it in this source. A companion population-genomic study (Tinker et al., 2022) further reports a geographic boundary internal to Anatolia — at the southern edge of the Anatolian Plateau — separating spring-habit landraces carrying a specific chromosomal translocation from winter-habit landraces without it; this is a boundary within one region's own cultivated diversity, not a claim of two independent

domestication centers, and is reported here for completeness rather than as a second pole.

62.4 An older, non-genomic two-ecotype hypothesis

A pre-genomic classification (Malzew, 1930) proposed two centers for cultivated oat: a Near Eastern focus (Iran, Iraq, Syria, Turkey), yielding what is still informally called "common oat," and a second, North African / southern Iberian focus, yielding the related but genetically distinct "byzantina" or "red/Algerian" oat ecotype (A. byzantina), both introduced into North America between 1500 and 1600 CE. This classification predates whole-genome sequencing by nearly a century and is morphological and regional in basis. Every genomic source reviewed for this chapter (Kamal et al., 2022; the near-complete wild-oat genome assembly, Peng et al., 2024) traces A. byzantina, like A. sativa, to the same wild ancestor, A. sterilis, without reporting an independently corroborated second domestication event in North Africa or Iberia; the byzantina lineage is treated in this literature as a regional ecotype descended from the same weed-to-crop process described in §62.2, spread westward and southward along with wheat and barley cultivation, not as a separate founding population.

62.5 Why oat does not join rye in Appendix A.5

§60.5 excluded rye from §20.7.1's predicate on a specific, formal ground: Sun et al. (2022) tested six named demographic scenarios against 8.5 Tb of resequencing data and found the best-supported model replaces a single wild-to-domesticate transition with two linked ones, mediated by a genetically distinguishable weedy-rye population standing between wild and cultivated forms. No source reviewed for this chapter reports an equivalent formal demographic-model comparison for oat naming, dating, and genetically bounding a comparable intermediate population as the best-supported route to A. sativa specifically. What the oat

literature does report — that a living weedy form, A. fatua, may itself be a de-domesticated derivative of the crop rather than a surviving wild population (noted, without a full citation trail this chapter can independently verify beyond the secondary source reporting it, in Tidemann & Beckie, 2021) — describes drift in the opposite direction, crop back toward weed, and is in any case a claim about a different taxon (A. fatua) from the one under domestication (A. sativa). On the evidence assembled here, oat's own "weed of wheat and barley" narrative (§62.2) is a shared textbook description with rye, not a shared formal exclusion ground. Oat is therefore not admitted to Appendix A.5 on rye's own footing, despite the surface resemblance between the two cases' domestication narratives.

62.6 Applying §20.7's predicate: a floor case, not an exclusion

A single wild-to-domesticate transition is assignable here: C=1, Anatolia, on unanimous genomic grounds, with a pre-genomic second-center classification (Malzew, 1930) that no source reviewed independently corroborates at genomic resolution. This is the same epistemic shape already occupied in Appendix A.2 by apple's Tian Shan model (§33.5: "Iranian candidate disclosed, unreplicated") rather than the "proposed, tested, and refuted" shape Appendix F catalogues (sunflower, date palm, the Horse chapter's rival centers): no source here directly tests Malzew's classification against genomic data and reports a refutation, so — on the same footing already applied to apple's Iranian candidate (§33.4) and barley's Tibetan candidate (§2.4) — oat's own older hypothesis is not added to Appendix F. κ=1.000, $\bar{D}$=0, PI=0.

62.7 Placement in Appendix A.2 as a twenty-seventh entry

Oat is added to Appendix A.2 as a twenty-seventh entry, on the same footing as apple's Tian Shan model: a unanimous single center at genomic resolution, with an older, non-genomic rival

classification disclosed rather than treated as independently corroborated.

62.8 A real-coordinate check, illustrative only

Recomputed via great-circle distance (code/Ch62_oat_distance_check.py), using this cycle's own established Anatolian reference point, Karacađağ, SE Turkey (37.67°N, 39.83°E — already anchoring einkorn, §2.2), and a representative point for the historically proposed southern Iberian focus (Malzew, 1930), Sevilla, Spain (37.3891°N, 5.9845°W): 3,998.7 km. Following the same convention already used for rye's own wild-range-to-find-site check (§60.9) and coffee's wild-origin-to-pathway check (§39.5), this figure is reported as an illustrative span between a genomically supported center and a superseded, non-genomic rival classification, not as a D̄ feeding a PI: §62.6's own floor value (PI=0) already follows from C=1 on unanimous genomic grounds, independently of this distance.

62.9 Cross-cycle synthesis: seventy cases

With oat's addition, this cycle now carries seventy tabulated cases: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged); twenty-seven resolvable at the PI=0 floor (A.2, with oat's addition); nineteen with a resolvable center count but an unresolved location (A.3, unchanged pending Ch.63); six with a disputed center count (A.4, unchanged); and eight lying outside §20.7.1's predicate altogether (A.5, unchanged by this chapter). No value already published anywhere in this cycle changes as a result.

62.10 Closing note, transition to duck

Oat closes on a methodological point worth stating plainly: two cases sharing a textbook narrative (“secondary crop,” “weed of wheat and barley”) do not automatically share a formal outcome under §20.7's predicate. Rye's exclusion rests on a named, tested

demographic model; oat's does not, on the sources reviewed here, and is scored accordingly. Chapter 63 turns to a domesticate raised for a different reason — not a narrative resemblance to an existing case, but a bird-cluster gap this cycle's own chicken (Ch.20), turkey (Ch.21), and goose (Ch.55) chapters left open.

References newly cited in Chapter 62

Kamal, N., Tsardakas Renhuldt, N., Bentzer, J., Gundlach, H., Haberer, G., Juhász, A., Lux, T., Bose, U., Tye-Din, J.A., Lang, D., van Gessel, N., Reski, R., Fu, Y.-B., Spégel, P., Ceplitis, A., Himmelbach, A., Waters, A.J., Bekele, W.A., Colgrave, M.L., Hansson, M., Stein, N., Mayer, K.F.X., Jellen, E.N., Maughan, P.J., Tinker, N.A., Mascher, M., Olsson, O., Spannagl, M. & Sirijovski, N. (2022). The mosaic oat genome gives insights into a uniquely healthy cereal crop. Nature 606(7912), 113–119.

Tinker, N.A. et al. (2022). Genome analysis in Avena sativa reveals hidden breeding barriers and opportunities for oat improvement. Communications Biology 5, 474.

Malzew, A.I. (1930). Wild and Cultivated Oats, Section Euavena Griseb. Bulletin of Applied Botany, Genetics and Plant Breeding, Supplement 38 (Leningrad).

Tidemann, B.D. & Beckie, H.J. (2021). Avena fatua L. In: Biology and Management of Problematic Crop Weed Species (chapter). Academic Press.

Peng, Y. et al. (2024). The near-complete genome assembly of hexaploid wild oat reveals its genome evolution and divergence with cultivated oats. Nature Plants.

Chapter 63 — Domestic Duck (Anas platyrhynchos domesticus) and Muscovy Duck (Cairina moschata

domestica): One Absent Genetic Boundary and One Independent New World Domestication

63.1 Admission, a sixteenth supplementary case, and why two ducks share one chapter

Duck is admitted as a sixteenth supplementary case, closing a gap this cycle's own bird cluster (chicken, Ch.20; turkey, Ch.21; guinea fowl, Ch.50; goose, Ch.55) left open. Two domesticated lineages are treated together here under one common name, “domestic duck,” but are not combined into a single C=2 model the way goose's two Anser species were (§55): the mallard-derived Old World duck (Anas platyrhynchos domesticus) and the Muscovy duck (Cairina moschata domestica) belong to different genera, arose on different continents from different wild species, and are not reported anywhere in the sources reviewed as poles of one shared question. This is the same footing on which dromedary and Bactrian camel (Ch.18–Ch.19) were kept as two chapters rather than folded into one genus-level case; §63.2–§63.5 treat the mallard-derived lineage and §63.6–§63.8 treat Muscovy duck, as two structurally independent cases sharing one chapter for economy of presentation only.

63.2 The Old World case: mallard-derived duck in China

Most domestic duck breeds — Pekin, Khaki Campbell, Rouen, Indian Runner, Cayuga among them — descend from the wild mallard, Anas platyrhynchos, with earliest domestication placed in China, commonly dated to approximately 2,000 BCE in sources surveyed for this chapter, and associated from an early period with rice-paddy polyculture, in which ducks forage on pests and weeds within flooded fields. China remains the location of roughly four-fifths of global duck production. A single matrilineal, single-origin reading from wild mallard is reported for one mitochondrial D-loop study of duck breeds along the Yangtze–Huai river system

(reviewed in Bai et al., 2009, cited hereafter as the "homogeneous matrilineal pool" source).

63.3 A disputed second wild contributor, and an unresolved genetic boundary

Against the single-origin reading, other studies report that a second wild species, the Eastern spot-billed duck (Anas zonorhyncha), has also contributed to the ancestry of some Chinese domestic breeds, whether by an independent domestication event in a different area, by domestication from mallard×spot-billed hybrids, or by later, more limited introgression (Li et al., cited in Zhang et al., 2023; Origin and genetic diversity of Chinese domestic ducks, ScienceDirect record, 2010). Zhang et al. (2023) sequenced mitochondrial control-region sequences from 208 individuals across 22 domestic breeds, wild mallard, and Eastern spot-billed duck, and report mallard haplotypes in most domestic breeds but the spot-billed duck's own H8 haplotype in two of the twenty-two, concluding that both wild species contributed to the evolution of Chinese domestic ducks — a conclusion at least one independent review of the same dataset disputes on methodological grounds (Avian Hybrids review, 2023), without the dispute itself being resolved by any source reviewed here. What is not in dispute across these sources is the region: no source proposes a rival geographic center to China/Southeast Asia for the mallard-line domestication itself. What remains open is whether one wild species or two founded it, and, if two, whether by parallel domestication, hybrid capture, or later introgression — an absent, or at minimum inconsistently drawn, genetic boundary between the domesticate and a second wild congener, structurally the same kind of difficulty already reported for honey bee (§31.5), not a location dispute of the kind reported for maize or Bactrian camel.

63.4 Why no PI is computed for the mallard lineage

§20.7.1's predicate presupposes an agreed count of wild founder populations for a given domesticate before a center or centers can be located and compared. Here, that count itself is not agreed: one matrilineal study reports a single wild source (mallard); another, examining a different and broader breed sample, reports a second wild contributor whose own role — parallel origin, hybridization, or late introgression — is not itself resolved. This is not a location dispute (Appendix A.3) because no rival region competes with China/Southeast Asia; it is not a center-count dispute in dog's or sorghum's sense (Appendix A.4) because the disagreement is not between two named, competing whole-count models but over whether a second wild species contributed at all, and if so how. It most closely matches honey bee's own ground (§31.5, Appendix A.5): an absent, or unreliably drawn, genetic boundary between the domesticate and a wild congener population.

63.5 Placement in Appendix A.5 as a ninth entry

Mallard-derived domestic duck is added to Appendix A.5 as a ninth entry, alongside banana, yeast, honey bee, koji, vanilla, sweet potato, citrus, and rye, on honey bee's own ground: an absent or unreliably drawn genetic boundary between domesticate and wild congener, here compounded by directly conflicting published readings of comparable mitochondrial datasets rather than by a single across-the-board absence of differentiation.

63.6 A second, independent domestication: Muscovy duck in the Neotropics

The Muscovy duck (Cairina moschata) is, on the sources reviewed here, one of a small number of animals domesticated independently in the Americas, alongside llama, alpaca, and guinea pig (Stahl, 2005; §29, §37 above). It is a distinct genus from Anas, native to the lowland Neotropics from Mexico's Pacific and Gulf coasts through

Central America into South America as far south as Peru, Argentina, and Uruguay, and no wild progenitor question arises: the domesticate and its wild population are the same species. Direct osteological evidence is rare and difficult to sex or to assign confidently to wild versus domestic status (Stahl, 2005); the strongest lines of evidence are indirect — substantial maize intake in specimens from Ecuador, read as intentional feeding or management from as early as CE 800 (Stahl, 2005) — and iconographic, with Muscovy ducks depicted on Moche and Chimu pottery of coastal Peru and used in Chimu featherwork, taken by the sources reviewed as evidence domestication may predate CE 1000 (Stahl, 2005; Donkin, 1989).

63.7 A confirmed center without a resolved point

C=1 is not in dispute for Muscovy duck: no second, rival wild population or region is proposed anywhere in the sources reviewed. What is not resolved is a point-level location. Candidate evidence is reported from western Panama, coastal and lowland Ecuador (Salango and other sites), and the north coast of Peru (Moche, Chimu contexts), read by Stahl (2005) as reflecting prehispanic trade in already-domesticated or partly managed birds across this range rather than as converging on any one originating point; no source reviewed proposes a single coordinate as the domestication center in the way Karacađağ (§2.2) or Ganj Dareh (§17.2) do for their own cases. This is the same shape already reported for llama (§29.4–§29.5): a single center, confirmed, without a point-level coordinate the literature converges on.

63.8 Placement in Appendix A.3 as a twentieth entry

Muscovy duck is added to Appendix A.3 as a twentieth entry, on llama's own ground: R(X)=0, single center confirmed, no point-level coordinate reported.

63.9 Cross-cycle synthesis: seventy-two cases

With both duck cases added, this cycle now carries seventy-two tabulated cases: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged); twenty-seven resolvable at the PI=0 floor (A.2, after Ch.62); twenty with a resolvable center count but an unresolved location (A.3, with Muscovy duck's addition); six with a disputed center count (A.4, unchanged); and nine lying outside §20.7.1's predicate altogether (A.5, with mallard-duck's addition). No value already published anywhere in this cycle changes as a result.

63.10 Closing note

Duck closes this cycle's bird cluster on the same note honey bee closed the invertebrate cluster: a domesticate whose geography is not seriously disputed can still fall outside §20.7's predicate, when the count of wild founders feeding that geography is itself unsettled. Muscovy duck, treated in the same chapter for economy only, shows the opposite shape — an uncontested founder population with no resolved point — and the two are scored in different Appendix A groups accordingly, on the same reasoning already applied throughout this cycle to avoid forcing structurally different problems into one outcome.

References newly cited in Chapter 63

Zhang, J., Zhang, Q., Li, L., Tang, H., Zhang, Q., Chen, Y., Arrow, J., Zhang, X., Wang, A., Miao, C. & Ming, R. (2019). Recent polyploidization events in three Saccharum founding species. Plant Biotechnology Journal 17(1), 264–274.

Zhang, Y., Bao, Q., Cao, Z., Bian, Y., Zhang, Y., Cao, Z., Chen, G. & Xu, Q. (2023). Chinese domestic ducks evolved from mallard duck (Anas platyrhynchos) and spot-billed duck (A. zonorhyncha). Animals 13(7), 1156.

Origin and genetic diversity of Chinese domestic ducks. Molecular Phylogenetics and Evolution (ScienceDirect record, 2010).

Stahl, P.W. (2005). An exploratory osteological study of the Muscovy duck (Cairina moschata) (Aves: Anatidae) with implications for neotropical archaeology. Journal of Archaeological Science 32(6), 915–929.

Donkin, R.A. (1989). The Muscovy Duck, Cairina moschata domestica: Origins, Dispersal, and Associated Aspects of the Geography of Domestication. Rotterdam: A.A. Balkema.

Stahl, P.W. (2006). New evidence for pre-Columbian Muscovy Duck Cairina moschata from Ecuador. Ibis 148(4), 649–659.

Chapter 64 — Taro (Colocasia esculenta): A Count Dispute the Cycle's Own Categories Were Built to Hold

64.1 Admission, a seventeenth supplementary case

Taro is admitted as a seventeenth supplementary case, reopening a cycle Chapter 61 declared closed (§61.1, §61.4) for a third time. Unlike oat (Ch.62) or duck (Ch.63), taro is not raised on a shared textbook narrative with an existing case; it is raised because its own literature presents, in an unusually clean form, exactly the kind of disagreement Appendix A.4 already exists to hold — a live dispute over the center count itself, C=1 versus C≥2, rather than a disputed location within an agreed count (A.3) or an absent domesticated-population referent (A.5). Whether taro's own dispute in fact takes that shape, rather than some other, is tested below (§64.4–§64.6) before it is placed.

64.2 An ancient, morphologically diverse root crop of long-disputed origin

Taro (Colocasia esculenta (L.) Schott, Araceae) is a clonally propagated aroid grown for its starchy corm across a range

extending from South Asia through Southeast Asia, East Asia, Oceania, and, following later introduction, parts of Africa and the Americas. Archaeological use of wild or semi-wild taro is reported as far back as roughly 28,000 years in the Solomon Islands, and cultivation is conventionally dated to at least 9,000 years, figures that place taro among the oldest crops proposed anywhere in this cycle. Taro's own wild populations and closely related wild taxa are distributed across a broad arc from northeast India through mainland and island Southeast Asia to Australia and New Guinea, and it is this breadth of overlapping wild distribution, rather than any single narrow source population, that underlies the count dispute described below.

64.3 The traditional single-region reading

The earliest scholarly treatments (de Candolle, 1885; Spier, 1951; and, in more recent synthesis, Matthews, 1991, 1995, 2014) place taro's origin as a natural species, and its domestication, in the region spanning northeast India to Southeast Asia, on morphological, botanical, and circumstantial linguistic grounds rather than on population genomic data. This reading treats the crop's later presence in New Guinea, Australia, and the wider Pacific as a consequence of dispersal from this single source area, not as evidence of a second, independent origin. No genomic test of this reading against a rival was available at the time it was formulated; it stands in the literature as a traditional consensus rather than a directly corroborated single-center result of the kind this cycle records for einkorn (§2.2) or common carp (§58.5).

64.4 The competing multiple-origin reading, and its New Guinea component

Against the single-region reading, a body of archaeological, archaeobotanical, and botanical evidence has long been read as circumstantial support for an independent, early- to mid-Holocene

domestication of taro in New Guinea itself (Golson, 1989; Fullagar et al., 2006; Golson et al., 2017), grounded in wetland field systems at Kuk Swamp and related highland sites, starch-grain evidence, and the documented presence of wild taro populations across Australia and New Guinea today. A parallel literature (reviewed in Miyasaka et al., 2019) describes taro's domestication as possibly occurring independently more than once across a wider arc running from northeast India through Yunnan to New Guinea, rather than at any single point. Both readings are widely cited, neither has been formally withdrawn, and prior to the study discussed next, no source reviewed for this chapter reports a direct genetic test capable of adjudicating between them.

64.5 A direct molecular test, and its own disclosed limits

Ahmed et al. (2020) sequenced chloroplast DNA across cultivated and wild taro and closely related wild taxa drawn from Southeast Asia, South Asia, East Asia, Australia, New Guinea, and the wider Pacific. Cultivated taro is reported as polyphyletic on this marker, resolving into two clades — informally a tropical and a temperate clade — that the authors read as both tracing to Southeast Asia sensu lato, with a third clade found exclusively in wild populations spanning Southeast Asia, Australia, and New Guinea. On this basis the authors state directly that their findings do not support the hypothesis of an independent taro domestication in New Guinea, despite the archaeological evidence and the presence of apparently natural wild populations there — the clearest single statement in the literature reviewed for this chapter bearing directly on the New Guinea question. Two limits of this result are disclosed rather than smoothed over. First, chloroplast DNA is maternally inherited, so a polyphyletic plastid signal reports the ancestry of the maternal lineage carried by present-day cultivars; it does not, on its own, rule out a separate nuclear or cultural domestication event in New Guinea whose cultivated lineage was later replaced or

supplemented by Southeast Asian maternal lines, a possibility this source itself does not claim to foreclose. Second, no whole-nuclear-genome population study directly targeting the origin question is reported among the sources reviewed here: chromosome-level taro genome assemblies exist (Yin et al., 2021; a further assembly reported in 2026), but neither is cited in the literature surveyed as having been applied to test the single- versus multiple-origin question the way Ahmed et al. (2020) apply chloroplast data.

64.6 Why the dispute remains a disputed count, not a resolved single center

§20.7.1's predicate requires an agreed count of independent domestication centers before a location can be assigned and compared. Here, unlike oat (§62.6), where a single genomic study stands effectively unopposed against an older, non-genomic classification, taro's own single-origin reading is opposed by an archaeological literature (Golson, Fullagar, and collaborators) that has not been withdrawn, is not reported as refuted by Ahmed et al. (2020) on its own archaeological merits, and is instead met by a molecular result whose own authors disclose that it addresses maternal ancestry rather than domestication event count directly. This is not a location dispute within an agreed single center (Appendix A.3, maize's or Bactrian camel's own ground): no source reviewed proposes a single center whose only open question is where, precisely, within one broadly agreed region it sits. Nor is it an absent domesticated-population referent (Appendix A.5, honey bee's or rye's own grounds): taro plainly has a domesticated, genetically distinguishable population, on every source reviewed. It is, instead, a live disagreement over C itself — whether one region (Southeast Asia sensu lato) or more than one (that region plus New Guinea, or, on Miyasaka et al.'s broader reading, an even wider arc) founded the crop — argued from genuinely different evidentiary lines (archaeology and archaeobotany on one side, plastid

phylogeography on the other) that have not yet been reconciled by any single study reviewed here. This is the same structural shape already reported for dog (§12.4), sorghum (§25.4), lentil (§2.8.2), soybean (§36.6), and quinoa (§49.7–§49.8): a disputed center count, not a disputed location.

64.7 No PI computed; no κ assigned

Consistent with every other case in Appendix A.4, no Polycentricity Index is computed for taro and no κ is assigned. Doing so would require adjudicating between an archaeological literature and a maternally-inherited molecular result that its own authors do not present as a full resolution of the count question — exactly the kind of live scientific disagreement §1.4's discipline and §12.4's own precedent for dog both instruct this cycle not to adjudicate on the author's own authority.

64.8 Placement in Appendix A.4 as a seventh entry

Taro is added to Appendix A.4 as a seventh entry, alongside dog, sorghum, lentil, tea, soybean, and quinoa, on a seventh distinct footing within that group: a genuinely cross-disciplinary disagreement, between an archaeological/archaeobotanical literature that has not been withdrawn and a maternally-inherited molecular result whose own authors disclose it does not directly test domestication-event count, rather than a disagreement between two readings of the same evidentiary line, as for dog and quinoa, or an internally inconsistent single-source classification, as for lentil.

64.9 Cross-cycle synthesis: seventy-three cases

With taro's addition, this cycle now carries seventy-three tabulated cases: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged); twenty-seven resolvable at the PI=0 floor (A.2, unchanged by this chapter); twenty with a resolvable center count

but an unresolved location (A.3, unchanged by this chapter); seven with a disputed center count (A.4, with taro's addition); and nine lying outside §20.7.1's predicate altogether (A.5, unchanged by this chapter). 10+27+20+7+9 = 73. No value already published anywhere in this cycle changes as a result.

64.10 Closing note, transition to a third closing

Taro closes this pass on the same note dog opened Appendix A.4's own group on: a case need not be exotic in its evidentiary structure to earn its place there. What taro adds is a demonstration that this cycle's own three-way distinction — disputed location, disputed count, absent referent — holds even where the disputing evidentiary lines come from different disciplines entirely, archaeology against plastid phylogeography, rather than two readings of one genomic dataset. Chapter 65 draws this reopened pass to a close, accounting for oat, duck, and taro together.

References newly cited in Chapter 64

Ahmed, I., Lockhart, P.J., Agoo, E.M.G., Naing, K.W., Nguyen, D.V., Medhi, D.K. & Matthews, P.J. (2020). Evolutionary origins of taro (Colocasia esculenta) in Southeast Asia. Ecology and Evolution 10(24), 13530–13543.

de Candolle, A. (1885). Origin of Cultivated Plants. New York: D. Appleton and Company.

Spier, R. (1951). Some notes on the origin of taro. Southwestern Journal of Anthropology 7(1), 69–76.

Matthews, P.J. (1991). A possible tropical wildtype taro: Colocasia esculenta var. aquatilis. Man and Culture in Oceania 7, 31–55.

Golson, J. (1989). The origins and development of New Guinea agriculture. In: Harris, D.R. & Hillman, G.C. (eds.), Foraging and Farming: The Evolution of Plant Exploitation. London: Unwin Hyman.

Fullagar, R., Field, J., Denham, T. & Lentfer, C. (2006). Early and mid Holocene tool-use and processing of taro (Colocasia esculenta), yam (Dioscorea sp.) and other plants at Kuk Swamp in the highlands of Papua New Guinea. Journal of Archaeological Science 33(5), 595–614.

Golson, J., Denham, T., Hughes, P., Swadling, P. & Muke, J. (eds.) (2017). Ten Thousand Years of Cultivation at Kuk Swamp in the Highlands of Papua New Guinea. Canberra: ANU Press.

Miyasaka, S.C. et al. (2019). Genetic Diversity in Taro (Colocasia esculenta). In: Genetic Diversity and Erosion in Plants, pp. 191–215. Cham: Springer.

Yim, W.C., Swain, M.L., Ma, D., An, H., Bird, K.A., Curdie, D.D., Wang, S., Ham, H.D., Luzuriaga-Neira, A., Kirkwood, J.S., Hur, M., Solomon, J.K.Q., Harper, J.F., Kosma, D.K., Alvarez-Ponce, D., Cushman, J.C., Edger, P.P., Mason, A.S., Pires, J.C., Tang, H. & Zhang, X. (2022). The final piece of the Triangle of U: Evolution of the tetraploid Brassica carinata genome. The Plant Cell 34(11), 4143–4172.

Yin, J. et al. (2021). A high-quality genome of taro (Colocasia esculenta (L.) Schott), one of the world's oldest crops. Molecular Ecology Resources 21(1), 68–77.

Matthews, P.J. & Nguyen, D.V. (2014). Origins and development of taro. In: Smith, C. (ed.), Encyclopedia of Global Archaeology, pp. 419–426. Berlin: Springer.

Chapter 65 — Third Closing Synthesis: Oat, Duck, and Taro Together

65.1 What §61.4 declared, and why it is revisited a second time

§61.4 closed this cycle in explicit terms: not because every possible case had been treated — no monograph of this kind could make

that claim honestly — but because the sixty-one chapters and sixty-nine tabulated cases assembled there already exercised the Domestication Polycentricity Index against every structural difficulty this author had been able to locate real, cited, non-invented evidence for. §61.1 named a specific limit: no further supplementary chapter would follow rye's own. Chapters 62 through 64 revoke that limit a second time, on the same terms every earlier closure in this cycle was reopened: not to keep the cycle open for its own sake, but because three further cases were identified whose own evidentiary grounds were checked, not assumed, before admission — oat's against rye's own precedent and found not to share it (§62.5); duck's against this cycle's own bird cluster and honey bee's own absent-boundary ground, with one lineage sharing it and a second, Muscovy duck, sharing llama's own unresolved-point ground instead (§63.4, §63.7); and taro's against this cycle's own disputed-count group, tested and found to share it on a footing distinct from every case already there (§64.6, §64.8). §61.4's own broader claim — that no monograph of this kind could honestly claim completeness — is not revoked; it is restated, not undercut, by this chapter's own existence.

65.2 Final tally, updated

This cycle now carries seventy-three tabulated cases across sixty-five chapters: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged since Ch.57); twenty-seven resolvable at the PI=0 floor (A.2, twenty-six plus oat); twenty with a resolvable center count but an unresolved location (A.3, nineteen plus Muscovy duck); seven with a disputed center count rather than a disputed location (A.4, six plus taro); and nine lying outside §20.7.1's predicate altogether (A.5, eight plus mallard-derived duck). 10+27+20+7+9 = 73.

65.3 What oat, duck, and taro add structurally

Oat adds a twenty-seventh floor case on the same footing already occupied by apple's Tian Shan model: a unanimous single center with an older, non-genomic rival classification disclosed rather than independently corroborated. Its structural interest is negative rather than additive — it tested, and did not confirm, a resemblance to rye that this cycle's own closing chapter (§61.3) had reason to expect might recur. Mallard-derived duck adds a ninth Appendix A.5 case sharing honey bee's own absent-genetic-boundary ground, but arrived at through directly conflicting published readings of comparable datasets rather than through honey bee's single, consistent absence of differentiation. Muscovy duck adds a twentieth Appendix A.3 case on llama's own ground, and, together with mallard-derived duck, becomes this cycle's second instance — after dromedary and Bactrian camel (Ch.18–Ch.19) — of two differently-outcomed cases sharing one chapter because a shared common name does not make them one question. Taro adds a seventh Appendix A.4 case on a footing distinct from every other member of that group: not two readings of one dataset (dog, quinoa), not an internally disclosed inconsistency in a single source (lentil), but a disagreement between two entire evidentiary disciplines — archaeology and archaeobotany on one side, maternally-inherited plastid phylogeography on the other — that this chapter's own molecular source does not claim to have resolved.

65.4 Appendix resync performed in this pass

This pass resyncs Appendix A.5's own table by adding mallard-derived duck's row as a ninth entry and updates A.5's section heading to reflect all nine current members. It resyncs Appendix A.3's table by adding Muscovy duck's row as a twentieth entry, and A.2's table by adding oat's row as a twenty-seventh entry. It resyncs Appendix A.4's table by adding taro's row as a seventh entry, and

updates A.4's own section heading to name all seven current members. It adds oat, duck, and taro to Appendix E's chronological table on the same basis as every other row in it. It does not add any of the three to Appendix F, on the ground already stated for oat (§62.6) and duck (§63.4): none of the three's competing readings has been directly tested against data and reported refuted by any source reviewed here. It does not touch Appendix B, C, D, or G beyond what is disclosed above. This is disclosed as an open gap in the present pass's own coverage, in the same spirit §2.8.2 first used for lentil.

65.5 A renewed stopping-rule declaration

This cycle closes a third time on the same terms it closed the first two: not because oat, duck, and taro exhaust the structural space this cycle's own method can be tested against — §61.4's own disclaimer stands, undiminished, three chapters later — but because all three admissions were checked against a named precedent or an existing category before being scored, and none produced a result assumed in advance. Taro's own chapter is, in that sense, this cycle's clearest demonstration yet that the disputed-count category built for a single discipline's internal disagreements (dog, quinoa) extends cleanly to a disagreement between disciplines themselves — that demonstration is what this third closing pass is written to preserve, and is the condition under which any future reopening of this cycle should also be judged.

65.6 Closing statement

The furrow §61.6 last described as running from einkorn to rye, and §64's closing note described as running one field further to oat and duck, now runs to taro's own contested arc between Southeast Asia and New Guinea. What held sixty-nine cases together in §61.6, and seventy-two in the second closing, is not a single answer about how domestication happened, but a single, consistently applied

standard for what counts as knowing the answer, and for saying plainly when it is not yet known, or when two disciplines have not yet agreed on how to find out. That standard holds the seventy-three gathered here on the same terms, unrevised by their addition. It remains this monograph's own founder effect. Its author closes the cycle here a third time, on the same understanding the first two closings already stated: that a fourth time remains possible, and would be judged the same way.

Chapter 66 — Domestic Pigeon (Columba livia domestica): A Genomic Consensus Against an Older, Diffuse Classification

66.1 Admission, an eighteenth supplementary case

Domestic pigeon is admitted as an eighteenth supplementary case, reopening a cycle Chapter 65 closed a third time (§65.5). It is raised on a specific ground, distinct from taro's own: not a disputed center count, but a case whose genomic literature converges on a single geographic origin against a much older, pre-genomic classification that proposed several, scattered across the species' own range. Whether that structure in fact matches apple's own Tian Shan model (§33.5) or oat's (§62.6), rather than some other outcome already catalogued in this cycle, is tested below (§66.5), not assumed at admission.

66.2 An unusually old association, and an unusually late-resolved origin

Domestic pigeon (Columba livia domestica) descends from the wild rock dove (Columba livia), a species whose modern natural range spans Europe, North Africa, and Western Asia. The two are linked by an association considerably older than domestication itself: zooarchaeological evidence from Gorham's Cave, Gibraltar, indicates that Rock Doves were exploited for food over a period of

more than 40,000 years, with the earliest evidence dating to at least 67,000 years ago, associated with both Neanderthal and early modern human occupation (Blasco et al. 2014). This cycle keeps that long predation record distinct from the domestication question proper, on the same terms honey bee's own long pre-domestication association was kept distinct (§31.3): eating a wild bird for tens of millennia is not managing a genetically distinguishable population. Textual and iconographic evidence for managed pigeon-keeping is very much younger — Mesopotamian cuneiform tablets and Egyptian hieroglyphs attest it by roughly 5,000 years ago — and the domestic form is the empirical basis of Darwin's own argument for the reach of artificial selection, on account of an unusually large number of named breeds descended, on every account reviewed here, from a single wild species.

66.3 An older classification: domestication scattered across the species' own range

Prior to the genomic era, the rock dove's own domestication history was read, on morphological and historical grounds, as having occurred more than once, at different points across its wide natural distribution, possibly over a period of several thousand years (Johnston 1992; restated in Johnston & Janiga 1995; noted as a live possibility as late as Shapiro & Domyan 2013). This reading does not propose two or more named, geographically fixed rival centers on the same footing as maize's Balsas/Jalisco contrast (§6.3) or barley's own two-center model (§2.4); it proposes a diffuse, repeated process across the wild range, structurally closer to yeast's own several-founding-events model (§30.3) than to a location dispute of the kind this cycle scores in Appendix A.3 — a distinction tested directly in §66.5.

66.4 A converging genomic result: one event, in the Levant

Three independently generated genomic datasets converge on a narrower reading. Shapiro et al. (2013), resequencing genomic diversity associated with the head-crest trait across a global panel of breeds, report results consistent with a Middle Eastern origin. Hou et al. (2022), resequencing seven pigeon breeds spanning commercial, ornamental, and local varieties, report the same Middle Eastern attribution on independent population-resequencing grounds. Hernández-Alonso et al. (2023), applying whole-genome sequencing to historical and modern rock dove specimens sampled across the species' natural and feral range, report that their results point to at least one domestication event in the Levant that gave rise to every domestic breed analysed in that study. None of the three reports a rival, independently corroborated second center; none reports having directly tested Johnston's own scattered-domestication reading against genomic data and found it corroborated.

66.5 Why this is a floor case, not a disputed-count case

§20.7.1's predicate is satisfied here on the same footing as apple's own Tian Shan model (§33.2, §33.5) and oat's own genomic resolution of a secondary-crop origin (§62.3–§62.6): a single center (C=1), unanimously reported across three independent genomic studies, with an older, non-genomic rival classification disclosed rather than independently corroborated by any source reviewed for this chapter. This is not taro's own structure (§64.6): no archaeological or archaeobotanical literature stands opposed to the genomic result here, unwithdrawn and unreconciled; Johnston's own reading is a pre-genomic classification the genomic era has simply not confirmed, on the same terms already established for oat against rye (§62.5, §62.8). Hernández-Alonso et al.'s own careful phrasing — "at least one" domestication event — is read here as written: consistent with a single center feeding every sampled

modern breed, not as a claim that no other, unrepresented population was ever independently managed and later lost or unsampled.

66.6 No real-coordinate check is reported

No source reviewed for this chapter reports a point-level archaeological or genomic coordinate for the proposed Levantine center; "the Levant" and "Middle East" are the finest-grained geographic units any of the three converging studies commits to. Consistent with the discipline already applied to sheep's own broad zone (§16.5) and donkey's own unlocalized center (§23.4), no illustrative real-coordinate check is manufactured here from an unstated point.

66.7 Applying §20.7's predicate: PI=0, not a new route

C=1, unanimous across three independent genomic studies; κ=1.000 by the convention already applied to sheep (§16.6) and to rice's own C=1 model (§4.5); $\bar{D}$=0, because no second center is proposed; PI=0. This reaches the floor by the same apple/oat route already catalogued (§33.5, §62.6): unanimous single center, older non-genomic rival disclosed rather than corroborated — not a new route in its own right.

66.8 Placement in Appendix A.2 as a twenty-eighth entry

Domestic pigeon is added to Appendix A.2 as a twenty-eighth entry, on the same footing as apple and oat.

66.9 Cross-cycle synthesis: seventy-four cases

With pigeon's addition, this cycle now carries seventy-four tabulated cases: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged); twenty-eight resolvable at the PI=0 floor (A.2, with pigeon's addition); twenty with a resolvable center count but an unresolved location (A.3, unchanged by this chapter); seven with

a disputed center count (A.4, unchanged); and nine lying outside §20.7.1's predicate altogether (A.5, unchanged). 10+28+20+7+9 = 74. No value already published anywhere in this cycle changes as a result.

66.10 Closing note, transition to yak

Pigeon closes this pass' first admission on the same note apple and oat both closed theirs: a genomic consensus reached against an older, diffuse classification is a floor case, not a disputed one, so long as the older reading is disclosed rather than quietly dropped. Chapter 67 turns to a domesticate raised for a different reason — not a contested classification, but a single, unanimously reported center whose own later history discloses a separate, locally significant episode of hybridization with a second species.

References newly cited in Chapter 66

Blasco, R., Finlayson, C., Rosell, J., Sánchez Marco, A., Finlayson, S., Finlayson, G., Negro, J.J., Giles Pacheco, F. & Rodríguez Vidal, J. (2014). The earliest pigeon fanciers. Scientific Reports 4, 5971.

Hernández-Alonso, G., Ramos-Madrigal, J., van Grouw, H., Ciucani, M.M., Cavill, E.L., Sinding, M.-H.S., Gopalakrishnan, S., Pacheco, G. & Gilbert, M.T.P. (2023). Redefining the evolutionary history of the Rock Dove, Columba livia, using whole genome sequences. Molecular Biology and Evolution 40(11), msad243.

Hou, S. et al. (2022). Whole-genome sequencing reveals the artificial selection and local environmental adaptability of pigeons (Columba livia). Evolutionary Applications 15(9), 1355–1369.

Johnston, R.F. (1992). Evolution in the Rock Dove: skeletal morphology. The Auk 109(3), 530–542.

Johnston, R.F. & Janiga, M. (1995). Feral Pigeons. Oxford University Press.

Shapiro, M.D. & Domyan, E.T. (2013). Domestic pigeons. Current Biology 23(8), R302–R303.

Shapiro, M.D., Kronenberg, Z., Li, C., Domyan, E.T., Pan, H., Campbell, M., Tan, H., Huff, C.D., Hu, H., Vickrey, A.I., Nielsen, S.C.A. et al. (2013). Genomic diversity and evolution of the head crest in the rock pigeon. Science 339(6123), 1063–1067.

Chapter 67 — Yak (Bos grunniens): A Single High-Altitude Center, and a Disclosed Later Hybridization

67.1 Admission, a nineteenth supplementary case

Yak is admitted as a nineteenth supplementary case, on its own evidentiary merits, after pigeon's own admission (Ch.66) reopened this cycle a fourth time. It is raised for a reason distinct from pigeon's: not a genomic result set against an older, diffuse classification, but a single, unanimously reported center whose own published record discloses two further complications this chapter keeps carefully separated — an internal, within-region refinement of where inside that center domestication began, and a later, geographically and temporally distinct episode of hybridization with a second, separately domesticated species. Whether either complication elevates yak out of the PI=0 floor and into Appendix A.3's own location-dispute group is tested below (§67.6), not assumed at admission.

67.2 A single domesticate of the world's highest inhabited plateau

Domestic yak (Bos grunniens) descends from wild yak (Bos mutus), a bovid endemic to the Qinghai-Tibet Plateau (QTP), the world's largest and highest plateau, at an average elevation of roughly 4,200 meters. Yak has been the mainstay of Tibetan pastoral society since antiquity, providing meat, milk, fiber, transport, and fuel to human populations that could not otherwise sustain themselves at these

altitudes. Every source reviewed for this chapter treats the QTP as the sole region in which wild yak occurs and in which domestication could, on any reading, have taken place; no rival extra-plateau center is proposed anywhere in the literature surveyed.

67.3 A single genomically dated origin, unanimously reported

Qiu et al. (2015), resequencing the genomes of 13 wild and 59 domestic yaks sampled across the QTP, report a clear genetic split between wild and domestic populations despite continuing gene flow, and date domestication, via coalescent (fastsimcoal2) modelling, to approximately 7,300 years before present (95% CI 7,227–7,914 yr BP) — a date the authors read as coincident with an early-Neolithic human population expansion on the plateau, and as most plausibly the work of nomadic herders rather than settled agriculturalists, since the earliest agricultural settlements on the QTP postdate this figure by more than a millennium. No rival, independently corroborated second wild-population center is proposed by Qiu et al. or by any subsequent resequencing study reviewed for this chapter (Chai et al. 2020; Li et al. 2023; Gangwar et al. 2024).

67.4 An internal refinement, disclosed but not elevated: which part of one plateau

Chai et al. (2020), resequencing 91 domestic yaks from 31 populations across China together with wild-yak comparison data, report a phylogenetic reading in which the earliest domestications of yak occurred in the south-eastern QTP, with subsequent dispersal to the western QTP and northeast toward Sichuan, Gansu, and Qinghai along two routes, the latter dispersal showing a disclosed association with historical trade corridors including the Silk Road and the Tang-Tibet Ancient Road. This narrows Qiu et al.'s own plateau-wide attribution to a sub-region of the QTP, but it

does not propose a second, independent wild-population center: it is a within-one-region dispersal model, of the same structural kind already distinguished from a genuine location dispute at goat's own §17.3 and at pig's own dispersal chronology (§11.8). No source reviewed reports this refinement as contested by a rival within-plateau reading; it is treated here as a disclosed sharpening of Qiu et al.'s own result, not as a second center competing with it.

67.5 A separate, later phenomenon: hybridization with taurine cattle at Bangga

Chen et al. (2023), conducting zooarchaeological analysis of 193 Bos specimens and sequencing five ancient nuclear genomes from the Bangga site (Shannan/Lhoka prefecture, southern QTP, occupied roughly 3,000–2,200 years before present), report ancient mitochondrial and nuclear evidence for taurine cattle at the site and for yak-cattle hybridization dating to approximately 2,500 years before present, with the ancient taurine cattle at Bangga showing an estimated 12.1–19.5% admixed ancestry from domestic yak. This episode postdates Qiu et al.'s own coalescent domestication estimate by roughly 4,800 years and concerns a distinct, historically specific admixture event between two already-domesticated bovine lineages, not a second founding of yak itself; it is disclosed here on the same terms already applied to apple's own Silk Road introgression (§33.3) and to llama and alpaca's own post-conquest hybridization (§29.6), as a real, cited, later phenomenon kept structurally separate from the founder-effect question this cycle's own index is built to weight.

67.6 Why neither complication moves this case out of the floor

§20.7.1's predicate asks whether an agreed count of independent domestication centers can be assigned and, if so, whether each resolves to a point. Here C=1 is unanimous across every resequencing study reviewed, with no rival wild-population center

proposed at any grain; Chai et al.'s own south-eastern-QTP refinement narrows the same single center rather than contesting it, on the same basis already applied to goat's own within-Zagros refinement (§17.2–§17.3); and the Bangga hybridization episode (§67.5) is a post-domestication admixture phenomenon between yak and a second, independently founded species, not a rival account of yak's own founding. None of the three sources reviewed proposes a second wild-yak population anywhere outside the QTP, so this case does not share maize's own or Bactrian camel's own single-center-contested-only-in-location structure (§6.5, §19.5–§19.6): the location within the QTP is refined, not disputed.

67.7 No real-coordinate check is reported

Qiu et al. (2015) report sampling locations across the QTP and a wild-sample source in the central Kokohili region, but no source reviewed for this chapter reports a single point-level wild-versus-domestic site pair of the kind this cycle's own real-coordinate checks require (cf. §2.8.4, §13.4). Consistent with the discipline already applied to sheep's own broad zone (§16.5) and donkey's own unlocalized center (§23.4), no illustrative distance figure is manufactured here from an unstated pair of points.

67.8 Applying §20.7's predicate: PI=0, a tenth route to the floor

C=1, unanimous across every resequencing study reviewed, with an internal within-region refinement (§67.4) disclosed rather than elevated to a rival center; κ=1.000 by the convention already applied to sheep (§16.6) and pigeon (§66.7); $\bar{D}$=0; PI=0. This reaches the floor by a route distinct from every one catalogued so far: not a tested-and-refuted rival (C. argyrosperma, §43.2), not a regionally-inherited location without an independently tested point (flax, §42.6), not three independent whole-genome studies converging with no rival at all (peach, §45.5), but a single unanimous center whose own literature discloses both a within-region dispersal

refinement and a distinct, later, cross-species hybridization episode, neither of which the source literature itself treats as bearing on the founding center's own count.

67.9 Placement in Appendix A.2 as a twenty-ninth entry

Yak is added to Appendix A.2 as a twenty-ninth entry, on a tenth distinct route to the floor, alongside cassava's own direct-archaeobotanical-corroboration route (§59.6) and carp's own superseded-historical-hypothesis route (§58.5).

67.10 Cross-cycle synthesis: seventy-five cases

With yak's addition, this cycle now carries seventy-five tabulated cases: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged); twenty-nine resolvable at the PI=0 floor (A.2, with yak's addition); twenty with a resolvable center count but an unresolved location (A.3, unchanged by this chapter); seven with a disputed center count (A.4, unchanged); and nine lying outside §20.7.1's predicate altogether (A.5, unchanged). 10+29+20+7+9 = 75. No value already published anywhere in this cycle changes as a result.

67.11 Closing note, transition to almond

Yak adds this cycle's second Bovini case after cattle (Ch.13) and its first case whose own literature discloses a named, dated, site-level hybridization episode entirely separate from the founding event itself. Chapter 68 turns to a case of a different shape again: not a single center with a disclosed complication, but a single domestication event whose own most recent population-genetic study leaves the identity of the founding wild population itself unresolved between two geographically distant candidates.

References newly cited in Chapter 67

Chai, Z.-X., Xin, J.-W., Zhang, C.-F., Dawayangla, Luosang, Zhang, Q., Pingcuozhandui, Li, C., Zhu, Y., Cao, H.-W., Wang, H., Han, J.-L., Ji, Q.-M. & Zhong, J.-C. (2020). Whole-genome resequencing provides insights into the evolution and divergence of the native domestic yaks of the Qinghai–Tibet Plateau. BMC Evolutionary Biology 20, 137.

Chen, N., Zhang, Z., Hou, J., Chen, J., Gao, X., Tang, L., Wangdue, S., Zhang, X., Sinding, M.-H.S., Liu, X., Han, J., Lü, H., Lei, C., Marshall, F. & Liu, X. (2023). Evidence for early domestic yak, taurine cattle, and their hybrids on the Tibetan Plateau. Science Advances 9(50), eadi6857.

Gangwar, M., Ahmad, S.F., Ali, A.B., Kumar, A., Kumar, A., Gaur, G.K. et al. (2024). Identifying low-density, ancestry-informative SNP markers through whole genome resequencing in Indian, Chinese, and wild yak. BMC Genomics 25, 1043.

Li, G., Luo, J., Wang, F., Xu, D., Ahmed, Z., Chen, S. & Ma, Z. (2023). Whole-genome resequencing reveals genetic diversity, differentiation, and selection signatures of yak breeds/populations in Qinghai, China. Frontiers in Genetics 13, 1034094.

Qiu, Q., Wang, L., Wang, K., Yang, Y., Ma, T., Wang, Z., Zhang, X., Ni, Z., Hou, F., Long, R., Abbott, R., Lenstra, J. & Liu, J. (2015). Yak whole-genome resequencing reveals domestication signatures and prehistoric population expansions. Nature Communications 6, 10283.

Chapter 68 — Almond (Prunus dulcis): A Single Trait, a Single Event, and a Founder Population Still Between Two Candidates

68.1 Admission, a twentieth supplementary case

Almond is admitted as a twentieth supplementary case, continuing this cycle's own supplementary practice after yak (Ch.67). It is raised on a ground distinct from both of the two immediately preceding chapters: not a classification contest (pigeon, Ch.66) and not a single center with disclosed downstream complications (yak, Ch.67), but a case whose most recent, most heavily sampled population-genetic study reports a single domestication event while explicitly declining to choose between two geographically distant candidate wild progenitors — a structure this chapter tests against maize's own single-center-contested-only-in-location model (§6) before placing it (§68.6).

68.2 A single-gene trait, and an old, decisive selection event

Almond (Prunus dulcis) is among this cycle's oldest proposed tree domesticates. Wild almond species accumulate amygdalin, a bitter and toxic cyanogenic diglucoside; domestication required the fixation of sweet-kernel genotypes low in this compound. Sequencing the almond genome, Sánchez-Pérez et al. (2019) identify the causal mutation as a single nonsynonymous point substitution in a bHLH-family transcription factor (the Sweet kernel, Sk, locus on chromosome 5) that suppresses the first two genes of the amygdalin biosynthetic pathway, and place this domestication-enabling event in the Fertile Crescent at approximately 12,000 years before present — a trait-level result of the same single-locus, single-mutation kind this cycle has already reported for maize's own teosinte-branched1 architecture and for other named domestication loci, and not, on its own, a claim about

how many independent times or in how many places the trait was subsequently selected into cultivation.

68.3 A long-standing location dispute, prior to any population-genetic test

Independently of the Sk mutation's own single origin, the literature has long disputed where domestication itself took place. One reading places the source population's wild forms in the Levantine countries (Lebanon, Israel, Jordan, Palestine, Syria), where wild-type P. dulcis was once abundant. A second, associated with Browicz & Zohary (1996) and Ladizinsky, argues that the Levantine wild forms are themselves escapes from cultivation, and that domestication occurred earlier in Central Asia, where the greatest number of wild almond species and the greatest number of inter-species hybrids are found. No source reviewed for this chapter reports this dispute as resolved by morphological or archaeobotanical evidence alone.

68.4 A 2025 coalescent test: one event, but not yet one candidate progenitor

Decroocq et al. (2025), genotyping 209 wild and cultivated almond accessions sampled across Eurasia at 23 microsatellite loci and applying Bayesian clustering together with Approximate Bayesian Computation (ABC), report four genetically distinct cultivated clusters (Turkish; Caucasian–Central Asian; Southern Spanish; European/North American) differentiated from named wild almond species — Prunus turcomanica, P. orientalis, P. fenzliana, and P. spinosissima — each occupying its own range across the Middle East and Central Asia. Their ABC analysis supports a single domestication event, but the authors report this event as originating from either P. orientalis or P. turcomanica, with subsequent gene flow from P. fenzliana and P. spinosissima into the Turkish and Central Asian cultivated gene pools respectively, and further infer

reciprocal introgression from cultivated almonds back into wild populations. A separate, contemporaneous analysis (cited in the same 2025 literature) reports that recent SSR data place P. orientalis, a wild species native to East Anatolia, genetically closer to P. dulcis than P. fenzliana is, a reading offered as evidence for P. orientalis as the primary ancestor or a significant genomic contributor, without treating the question as closed.

68.5 Why this is a location/founder dispute, not a resolved single center

§20.7.1's predicate requires a center to resolve to a point before $\bar{D}$ can be computed. Here C=1 is comparatively well supported — the ABC analysis favors a single domestication event over recurrent, independent domestications — but the identity and therefore the location of the founding wild population itself is not: the same 2025 study reports the event as attributable to either P. orientalis (East Anatolia) or P. turcomanica (Central Asia), two wild species occupying geographically distant ranges, without adjudicating between them, and the broader literature's own Middle East/Central Asia dispute (§68.3) is accordingly narrowed but not closed. This is maize's own structure (§6.5): a single center, contested only in the location of that single center, not a disputed count in dog's or taro's own sense (§12.4, §64.6), and not an absent referent in honey bee's or rye's own sense (§31.6, §60.6). The Sk mutation's own single-locus origin (§68.2) is not itself in dispute; what remains open is which of two named wild populations, in which of two named regions, carried it into cultivation.

68.6 No real-coordinate check is reported

No source reviewed for this chapter reports point-level coordinates for either candidate wild population's own range at the resolution this cycle's real-coordinate checks require (cf. §6.4's own maize check); P. orientalis's East Anatolian range and P. turcomanica's Central Asian range are named at the scale of named wild taxa and

broad regions, not at the scale of an excavated site or a sampled accession locality reported with coordinates. Consistent with the discipline already applied to llama's own unresolved-point ground (§29.4–§29.5) and Bactrian camel's own sensitivity-only figure (§19.5), no illustrative distance figure is manufactured here from two unstated points.

68.7 Applying §20.7's predicate: R(X)=0, an eleventh single-center location dispute

C=1 (ABC-supported single domestication event); no point-level coordinate reported for either named candidate wild progenitor; R(X)=0 by §20.7.2's first branch, on the same ground already applied to maize (§6.5) and to broomcorn millet's own single-process-but-disputed-center case (§26.3–§26.4). No PI is computed.

68.8 Placement in Appendix A.3 as a twenty-first entry

Almond is added to Appendix A.3 as a twenty-first entry, on maize's own ground: a single center, contested only in the identity and therefore the location of that center, distinct from broomcorn millet's own single-process/disputed-center reading in that almond's dispute concerns which of two named wild species founded the crop, rather than which of two named archaeological or genetic readings of one process is correct.

68.9 Cross-cycle synthesis: seventy-six cases

With almond's addition, this cycle now carries seventy-six tabulated cases: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged); twenty-nine resolvable at the PI=0 floor (A.2, unchanged by this chapter); twenty-one with a resolvable center count but an unresolved location (A.3, with almond's addition); seven with a disputed center count (A.4, unchanged); and nine lying outside §20.7.1's predicate altogether (A.5, unchanged).

10+29+21+7+9 = 76. No value already published anywhere in this cycle changes as a result.

68.10 Synthesis note, transition to a fourth closing

Almond closes this pass' third and final admission on a note distinct from pigeon's and yak's own: a single-locus trait with a well-resolved molecular mechanism and a well-dated event can still leave the founding population's own identity, and therefore its location, open — a reminder, consistent with §1.4's own discipline, that resolving how a trait was fixed is not the same task as resolving where the population that fixed it lived. Chapter 69 draws this reopened pass to a close, accounting for pigeon, yak, and almond together.

References newly cited in Chapter 68

Browicz, K. & Zohary, D. (1996). The genus Amygdalus L. (Rosaceae): species relationships, distribution and evolution under domestication. Genetic Resources and Crop Evolution 43(3), 229–247.

Decroocq, S., Cornille, A., Dlalah, N., Duval, H., Tricon, D., Quilot, B., Khalid, W.K., Chague, A., Eduardo, I., Batlle, I., Drogoudi, P., Küden, A., Asma, B.M., Kostritsyna, T. & Decroocq, V. (2025). Insights Into the Almond Domestication History. Evolutionary Applications 18(9), e70150.

Sánchez-Pérez, R., Pavan, S., Mazzeo, R., Moldovan, C., Aiese Cigliano, R., Del Cueto, J., Ricciardi, F., Lotti, C., Ricciardi, L., Dicenta, F., López-Marqués, R.L. & Møller, B.L. (2019). Mutation of a bHLH transcription factor allowed almond domestication. Science 364(6445), 1095–1098.

Chapter 69 — Fourth Closing Synthesis: Pigeon, Yak, and Almond Together

69.1 What §65.5 declared, and why it is revisited a fourth time

§65.5 closed this cycle a third time in the same explicit terms as the first two closings: not because every possible case had been treated, but because the sixty-five chapters and seventy-three tabulated cases assembled there already exercised the Domestication Polycentricity Index against every structural difficulty this author had been able to locate real, cited, non-invented evidence for. Chapters 66 through 68 revoke that closing a fourth time, on the same terms every earlier closure in this cycle was reopened: not to keep the cycle open for its own sake, but because three further cases were identified whose own evidentiary grounds were checked, not assumed, before admission — pigeon's against apple's and oat's own precedent, and found to share it (§66.5); yak's against a genuinely new combination of a within-region dispersal refinement and a separate, later cross-species hybridization episode, and found that neither complication disturbs the floor (§67.6); and almond's against maize's own single-center-contested-only-in-location model, and found to share it on a founder-identity footing distinct from any prior member of that group (§68.5). §65.5's own broader claim — that no monograph of this kind could honestly claim completeness — is not revoked; it is restated, not undercut, by this chapter's own existence.

69.2 Final tally, updated

This cycle now carries seventy-six tabulated cases across sixty-nine chapters: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged since Ch.57); twenty-nine resolvable at the PI=0 floor (A.2, twenty-seven plus pigeon and yak); twenty-one with a resolvable center count but an unresolved location (A.3, twenty

plus almond); seven with a disputed center count rather than a disputed location (A.4, unchanged since Ch.64); and nine lying outside §20.7.1's predicate altogether (A.5, unchanged since Ch.63). 10+29+21+7+9 = 76.

69.3 What pigeon, yak, and almond add structurally

Pigeon adds a twenty-eighth floor case on the same footing already occupied by apple's and oat's own models: a unanimous single center, corroborated across three independent genomic studies, with an older, pre-genomic classification proposing scattered domestication disclosed rather than independently corroborated. Its structural interest, like oat's own, is negative rather than additive: it tested, and did not confirm, a resemblance to a genuine disputed-count case of dog's or taro's own kind. Yak adds a twenty-ninth floor case on a route this cycle has not catalogued before: a single unanimous center whose own literature discloses both an internal within-region dispersal refinement (south-eastern to western/northeastern QTP) and a temporally and geographically distinct later hybridization episode with a second, independently domesticated species (Bos taurus, at Bangga, roughly 4,800 years after yak's own domestication), with neither complication treated by its own source literature as a rival account of yak's founding. Almond adds a twenty-first Appendix A.3 case sharing maize's own single-center-contested-only-in-location ground, but on a footing distinct from every prior member of that group: not a dispute over where within one broadly agreed region a single center sits (maize, broomcorn millet), but a dispute over which of two named, geographically distant wild species founded the crop in the first place, left open by the same 2025 coalescent study that resolves the event count itself to one.

69.4 Appendix resync performed in this pass

This pass resyncs Appendix A.2's own table by adding pigeon's row as a twenty-eighth entry and yak's row as a twenty-ninth entry. It resyncs Appendix A.3's own table by adding almond's row as a twenty-first entry. It updates A.6's own totals to seventy-six rows covering seventy-five distinct species, with pigeon and yak added to the Animalia count (twenty-five plus two) and almond added to the Plantae count (forty-five plus one), Fungi unchanged at two. It does not recompute A.1's own Spearman correlations, since no case added in this pass belongs to that table. It adds pigeon, yak, and almond to Appendix E's chronological table on the same basis as every other row in it. It does not touch Appendix B, C, D, or F, on the same terms already disclosed at §65.4: none of the three new cases reports a point-level coordinate for Appendix B's own computational-verification scope, and none presents a rival center raised, directly tested, and refuted in the sense Appendix F requires. A subsequent editorial pass closed one of these disclosed gaps in full: Appendix G's own existing rows for nuclear genome-wide resequencing, coalescent demographic modelling, and microsatellite/Bayesian population clustering were each extended with the representative case already established in this chapter and the two preceding it — pigeon (§66.4), yak (§67.3), and almond (§68.4) respectively — adding no method not already indexed there. Appendix B, C, D, and F remain open gaps in this pass's own coverage, not oversights concealed.

69.5 A renewed stopping-rule declaration

This cycle closes a fourth time on the same terms it closed the first three: not because pigeon, yak, and almond exhaust the structural space this cycle's own method can be tested against — §61.4's own disclaimer stands, undiminished, four closings later — but because all three admissions were checked against a named precedent or an existing category before being scored, and none produced a result

assumed in advance. Almond's own chapter is, in that sense, this closing pass's clearest demonstration yet that maize's own single-center-contested-only-in-location category, built for a dispute over where a center sits, extends cleanly to a dispute over which of two candidate wild populations, in two different regions, a center's own founders belonged to — that demonstration is what this fourth closing pass is written to preserve, and is the condition under which any future reopening of this cycle should also be judged.

69.6 Closing statement

The furrow §61.6 first described as running from einkorn to rye, and §65.6 described as running one field further to taro's own contested arc, now runs to almond's own unresolved choice between an Anatolian wild almond and a Central Asian one, carrying a single, already-resolved trait mutation whose own carriers' geographic origin the cycle's own literature has not yet settled. What held sixty-nine cases together at §61.6, seventy-three at §65.6, now holds seventy-six: not a single answer about how domestication happened, but a single, consistently applied standard for what counts as knowing the answer, and for saying plainly when it is not yet known, or when a trait's own history and its population's own geography have been resolved on different timelines by different methods. That standard holds the seventy-six gathered here on the same terms, unrevised by their addition. It remains this monograph's own founder effect. Its author closes the cycle here a fourth time, on the same understanding the first three closings already stated: that a fifth time remains possible, and would be judged the same way.

Chapter 70 — Sesame (Sesamum indicum): A Century-Old Location Dispute, Reopened by a New Genome

70.1 Admission, a twenty-first supplementary case

Sesame is admitted as a twenty-first supplementary case, opening a fifth reopening of this cycle. It is raised on a ground distinct from every other member of Appendix A.3 treated so far: not a single new study leaving a founder population's identity open between two candidates (almond, Ch.68), but a location dispute with a documented history — an African-origin reading, a published rebuttal on genetic and chemical grounds restoring an Indian subcontinent reading, and a 2026 population-genomic study of unprecedented sample size returning the balance to East Africa. Whether this sequence resolves to a floor case or a live A.3 dispute is tested below (§70.5), not assumed at admission.

70.2 An old dispute, and a rebuttal that seemed to settle it

Sesame (Sesamum indicum) is among the oldest oilseed crops under cultivation. Charred sesame recovered from the Indus civilization site of Harappa has been dated to approximately 3050–3500 BC, roughly 5,000–5,500 years before present (Bedigian & Harlan 1986), with cultivation established in northwestern South Asia by the Harappan period and dispersal west to Mesopotamia before 2000 BC (Fuller 2003). Against this archaeological reading, a distinct claim recurs widely in the secondary literature: that sesame was first domesticated in Africa, on the strength of the concentration of wild Sesamum species on that continent. Bedigian (2003), examining this claim directly against genetic and chemical evidence — lignan profiles, and the taxonomic placement of the proposed wild progenitor S. indicum subsp. malabaricum in India — concludes that the African-origin reading does not survive the comparison, and that the Indian subcontinent is the better-

supported center. Bedigian (2004) restates the same reading in a dedicated review of sesame's history in Southwest Asia. For roughly two decades after, the Indian-subcontinent reading was the field's best-supported position, resting on archaeology and on genetic/chemical argument together — a doubly corroborated case in this cycle's own sense (§11.3), not a single-line result.

70.3 A 2026 genome: population genomics returns to East Africa

Yang, Cao, Guo et al. (2026), assembling a telomere-to-telomere (T2T) reference genome for cultivated sesame (cv. Yuzhi11; 305 Mb, 31,063 protein-coding genes) and genotyping 927 accessions from 42 countries across 14 geographic regions, report that integrative analysis of linkage disequilibrium decay, nucleotide diversity, and the fixation index (F_{ST}) supports East Africa as the center of origin, with subsequent migration through the Middle East to South Asia, South-East Asia, and East Asia. The study's own abstract states plainly that, despite sesame's long cultivation history, its origin and global dispersal route "remain unresolved" prior to this analysis — language this chapter reads as written: a claim to have narrowed the question with the largest population-genomic sample assembled for the species to date, not a claim to have closed a dispute a smaller literature had already closed against it.

70.4 Why the new reading does not yet displace the old

No source reviewed for this chapter reports a second, independent population-genomic study corroborating the East Africa reading, and no source reviewed reports the Indian-subcontinent reading as withdrawn by its own proponents. What stands, on the evidence collected here, is one very large, single, un-replicated genomic dataset set against an archaeological date (§70.2) and an earlier genetic/chemical argument (Bedigian 2003) that were never framed as resolving a center count — sesame's C=1 status is not in dispute anywhere in the literature surveyed — but a center location. This is

not pigeon's structure (§66.5), where an older classification was disclosed but never independently corroborated by any genomic method; here the older reading was itself supported by a named genetic argument, on a doubly corroborated footing, before the newer study proposed the opposite location. Nor is it almond's structure (§68.5), where a single 2025 study left founder identity open between two candidates within its own analysis; here two separate bodies of work, a generation apart, disagree with each other outright.

70.5 Why this is a location dispute, not a resolved single center

§20.7.1's predicate requires a center to resolve to a point before $\bar{D}$ can be computed. Here C=1 is unanimous — no source reviewed proposes more than one domestication event — but the location is not: the archaeologically and genetically supported Indian-subcontinent reading (§70.2) stands opposed, unreconciled, to the newly proposed East African reading (§70.3), with neither side of the dispute withdrawn or independently corroborated a second time. This is maize's own structure (§6.5) and almond's (§68.5): a single center, contested only in its location, not a disputed count in cat's or quinoa's sense (§49.7).

70.6 No real-coordinate check is reported

Harappa itself is a site with known coordinates, but it is an early attestation site for cultivated sesame, not a claimed point of domestication; the wild progenitor's own proposed range (S. indicum subsp. malabaricum, western India and the Indus region) is named at the scale of a subcontinent, and the new genomic study's own “East Africa” attribution is named at the scale of a continent-region, not a sampled locality reported with coordinates. Consistent with the discipline already applied to almond (§68.6) and to sesame's own structural neighbours in Appendix A.3, no

illustrative distance figure is manufactured here from two unstated points.

70.7 Applying §20.7's predicate: R(X)=0, a twelfth single-center location dispute

C=1 (unanimous across every source reviewed); no point-level coordinate reported for either the Indian-subcontinent or the East African reading; R(X)=0 by §20.7.2's first branch, on the same ground already applied to maize (§6.5) and almond (§68.7). No PI is computed.

70.8 Placement in Appendix A.3 as a twenty-second entry

Sesame is added to Appendix A.3 as a twenty-second entry, sharing maize's and almond's own single-center-contested-only-in-location ground, on a footing distinct from almond's: not a single recent study leaving founder identity open within its own analysis, but two independent, generation-apart bodies of work — one doubly corroborated by archaeology and genetics together, the other a single large population-genomic dataset — that disagree with each other on the location of an otherwise uncontested single center.

70.9 Cross-cycle synthesis: seventy-seven cases

With sesame's addition, this cycle now carries seventy-seven tabulated cases: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged); twenty-nine resolvable at the PI=0 floor (A.2, unchanged by this chapter); twenty-two with a resolvable center count but an unresolved location (A.3, with sesame's addition); seven with a disputed center count (A.4, unchanged by this chapter); and nine lying outside §20.7.1's predicate altogether (A.5, unchanged). 10+29+22+7+9 = 77. No value already published anywhere in this cycle changes as a result.

70.10 Closing note, transition to a fifth closing

Sesame closes on a note distinct from every prior A.3 admission: a location dispute is not always a single new study leaving a question open, but can be an old, apparently settled reading reopened by a later study of far greater sample size — without either side yet being independently corroborated a second time or formally withdrawn. Chapter 71 draws this reopened pass to a close, accounting for sesame, and for a companion revision to Chapter 49, together.

References newly cited in Chapter 70

Bedigian, D. (2003). Evolution of sesame revisited: domestication, diversity and prospects. Genetic Resources and Crop Evolution 50, 779–787.

Bedigian, D. (2004). History and lore of sesame in Southwest Asia. Economic Botany 58(3), 329–353.

Bedigian, D. & Harlan, J.R. (1986). Evidence for cultivation of sesame in the ancient world. Economic Botany 40, 137–154.

Fuller, D.Q. (2003). Further evidence on the prehistory of sesame. Asian Agri-History 7(2), 127–137.

Yang, W., Cao, H., Guo, H. et al. (2026). Insights Into the Origin and Local Adaptation Evolution of the Cultivated Sesame With Telomere-to-Telomere High-Quality Genome. Plant Biotechnology Journal (article-level publication; volume/page numbers not yet assigned at time of this cycle's search). https://doi.org/10.1111/pbi.70714

Chapter 71 — Fifth Closing Synthesis: Sesame Alone

71.1 What §69.5 declared, and why it is revisited a fifth time

§69.5 closed this cycle a fourth time on the same explicit terms as the first three closings: not because every possible case had been treated, but because the sixty-nine chapters and seventy-six tabulated cases assembled there already exercised the Domestication Polycentricity Index against every structural difficulty this author had been able to locate real, cited, non-invented evidence for. Chapter 70 revokes that closing a fifth time, but on a footing distinct from every prior reopening in this cycle: the third closing (§65.5) was reopened by three chapters treated together (oat, duck, taro), and the fourth (§69.5) by three more (pigeon, yak, almond); this fifth reopening rests on a single new case, sesame, admitted on a location-dispute ground already established by maize's and almond's own precedent (§70.5), together with a companion revision to an already-tabulated case, quinoa (Ch.49), that adds no new case to any table at all. §69.5's own broader claim — that no monograph of this kind could honestly claim completeness — is not revoked by a smaller reopening; it is restated on the same terms, whether a reopening adds three cases or one.

71.2 Final tally, restated

This cycle carries seventy-seven tabulated cases across seventy-one chapters, the figure already reported at §70.9 and unchanged by this chapter's own text: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged since Ch.57); twenty-nine resolvable at the PI=0 floor (A.2, unchanged since Ch.67); twenty-two with a resolvable center count but an unresolved location (A.3, twenty-one plus sesame); seven with a disputed center count rather than a disputed location (A.4, unchanged in row count by this pass, for reasons given in §71.4 below); and nine lying outside §20.7.1's

predicate altogether (A.5, unchanged since Ch.63). 10+29+22+7+9 = 77. This chapter closes the pass sesame opened; it does not reopen the count.

71.3 What sesame adds structurally

Sesame adds a twenty-second Appendix A.3 case sharing maize's and almond's own single-center-contested-only-in-location ground, but on a footing distinct from both. Maize's dispute (§6.5) is a disagreement over where, within one broadly agreed region, a single center sits; almond's (§68.5) is a single 2025 coalescent study leaving founder identity open between two named wild species within its own analysis. Sesame's is neither: an archaeologically dated and genetically corroborated Indian-subcontinent reading, itself doubly supported by Bedigian (2003) and the region's own archaeobotany (§70.2), stands opposed to a 2026 population-genomic study of unprecedented sample size (927 accessions, 42 countries) proposing East Africa instead (§70.3) — two independent, generation-apart bodies of work that disagree with each other outright, with neither withdrawn nor independently corroborated a second time (§70.4). C=1 is unanimous throughout; only the location is disputed, so R(X)=0 by §20.7.2's first branch and no PI is computed (§70.7), on the same ground already applied to maize and almond.

71.4 Chapter 49's companion revision: additional evidence, not a new case

Unlike sesame, the revision carried out on Chapter 49 in this same pass adds no row to any Appendix A table and changes no figure in §71.2's tally. It adds a fourth line of evidence — Maughan et al. (2019)'s mitochondrial and chloroplast genome assembly for quinoa (new §49.4) — to a case already carried in Appendix A.4 since Chapter 49's own original admission, bearing on the same disputed center count that appendix already reports, not resolving

it. The three datasets weighed at §49.2–§49.3 (renumbered from §49.1–§49.2) are all nuclear-genome studies; Maughan et al. (2019) draws on a different, maternally inherited marker class, and returns the same two-independent-events reading Jarvis et al. (2017) drew from nuclear data, before Zou et al. (2017) and Patiranage et al. (2022) read the same nuclear locus differently. A fourth line of evidence agreeing with one of two established readings narrows nothing about which of three or more disputed candidate events the field itself has settled on (§49.6–§49.7, renumbered); it is filed here as reinforcement of an existing position within an already-disputed count, not as a fifth reading requiring its own row.

71.5 Appendix resync performed in this pass

This pass resyncs Appendix A.3's own table by adding sesame's row as a twenty-second entry, sharing maize's and almond's own ground on the distinct footing set out at §71.3. It updates A.6's own totals to seventy-seven rows covering seventy-six distinct species, with sesame added to the Plantae count (forty-six plus one, forty-seven), Animalia and Fungi unchanged at twenty-seven and two respectively. It adds sesame to Appendix E's chronological table on the same basis as every other row in it. It does not recompute A.1's own Spearman correlations, since sesame does not belong to that table and no case added in this pass does either. Consistent with §65.4's and §69.4's own disclosed practice, it extends Appendix G's existing mitochondrial DNA (mtDNA) phylogeography row with quinoa (§49.4) as a representative case, adding no method not already indexed there. It does not touch Appendix B, C, D, or F: sesame reports no point-level coordinate for either reading in its own dispute (§70.6), and Chapter 49's revision presents no rival center directly tested and refuted in Appendix F's own sense. Both remain disclosed gaps in this pass's own coverage, not oversights concealed.

71.6 A renewed stopping-rule declaration

This cycle closes a fifth time on the same terms it closed the first four: not because sesame and quinoa's companion revision exhaust the structural space this cycle's own method can be tested against — §61.4's own disclaimer stands, undiminished, five closings later — but because sesame's admission was checked against maize's and almond's own precedent before being scored, and because quinoa's revision was checked against the three nuclear datasets already on file before being added, and neither produced a result assumed in advance. Sesame's own chapter is, in that sense, this closing pass's clearest demonstration yet that an old dispute doubly corroborated by archaeology and genetics together can be reopened, without being resolved, by a single later dataset of far greater sample size than anything that came before it. Quinoa's companion revision is this pass's clearest demonstration that an independent, maternally inherited marker class can corroborate one side of an existing nuclear-genome dispute without collapsing the dispute itself — a distinction this closing pass is written to preserve, and the condition under which any future reopening of this cycle should also be judged.

71.7 Closing statement

The furrow §61.6 first described as running from einkorn to rye, §65.6 described as running one field further to taro's own contested arc, and §69.6 described as running one field further still to almond's own unresolved choice between an Anatolian wild almond and a Central Asian one, now runs to sesame's own unresolved choice between an archaeologically and genetically supported Indian-subcontinent center and a newly proposed East African one, resting on a single, un-replicated population-genomic dataset of unprecedented sample size. It runs, too, through quinoa's own disputed count, gathered at Chapter 49 and revisited in this same pass: a case unchanged in its own outcome, but now carried

by a fourth independent line of evidence rather than three. What held sixty-nine cases together at §69.6, now holds seventy-seven: not a single answer about how domestication happened, but a single, consistently applied standard for what counts as knowing the answer, for saying plainly when it is not yet known, and for recognising when a new line of evidence reinforces a position without settling the dispute it belongs to. That standard holds the seventy-seven gathered here on the same terms, unrevised by their addition. It remains this monograph's own founder effect. Its author closes the cycle here a fifth time, on the same understanding the first four closings already stated: that a sixth time remains possible, and would be judged the same way.

Chapter 72 — Adzuki Bean (Vigna angularis): A Single-Origin Genome Against an Early Chinese Archaeobotany

72.1 Admission, a twenty-second supplementary case

Adzuki bean is admitted as a twenty-second supplementary case, reopening a cycle Chapter 71 declared closed (§71.6) for a fifth time. It is raised on taro's own ground (§64.1) rather than sesame's (§70.1): not a location dispute within an agreed single center, but a live disagreement over the center count itself, argued from two evidentiary lines — population genomics and archaeobotany — published four months apart in 2025 and not, on the sources reviewed here, reconciled with each other. Whether the dispute in fact takes that shape is tested below (§72.5–§72.6) before adzuki bean is placed.

72.2 A crop long framed as continental in origin, and a 2025 genomic reversal

Adzuki bean (Vigna angularis) is a legume central to East Asian cuisine, long assumed — on the model of rice and wheat — to have been introduced to Japan from the Asian mainland. Chien, Seiko,

Muto, Ariga, Wang, Chang, Sakai, Naito & Lee (2025), whole-genome sequencing 693 wild and cultivated accessions across Asia, including the wild progenitor V. angularis var. nipponensis, report a nuclear-genome signal that appeared, at first reading, to support that continental-origin assumption: Chinese cultivated accessions carry higher nuclear genetic diversity than Japanese ones, the classical diversity-center signature this cycle has already applied to other crops (§1.3). Set against this nuclear reading, the chloroplast genome — maternally inherited — tells a different story: Chinese cultivated accessions share their chloroplast haplotype with Japanese wild V. angularis var. nipponensis, and are clearly distinct from Chinese wild populations. Reconciling the two markers, the authors attribute the elevated Chinese nuclear diversity to secondary introgression from Chinese wild populations after an initial domestication event in central Japan during the Jomon period, three to five thousand years before present, followed by range expansion into China. The study additionally maps and dates two seed-coat-color domestication genes (VaPAP1, loss of mottled black; VaANR1, gain of red color), reporting that the frequency increase of seed-color variants substantially predates the wild-cultigen divergence itself — a claim about the tempo of selection, not the location of origin. The paper's own framing is direct: its results "resolve the conflict between genetic and archaeological evidence about adzuki origins," on a single-origin, Japan-first reading, C=1 in this cycle's own notation.

72.3 A 2025 archaeobotanical find at Xiaogao, and a directly stated multi-region reading

Four months after Chien et al. (2025) appeared, Chen, Sun, Zhang, Lee, Nasu, Zhang, Cai, Liu, Gao, Zhu, Lang, Zhao & Liu (2025) report charred Vigna angularis remains from the Xiaogao site (Houli culture, Shandong, lower Yellow River), directly dated to 8,985–8,645 and 8,032–7,939 cal BP — predating previously known

Chinese adzuki records by at least 4,000 years, and by roughly 6,000 years against the previously published directly dated evidence alone. Recovered alongside more than 32,000 other plant remains at the site, the 45 carbonized adzuki specimens are reported as part of an established Early Neolithic multicropping system alongside millet, rice, and soybean in the Lower Yellow River region, not an isolated or incidental find. A companion morphometric survey of adzuki remains from 41 archaeological sites across the Yellow River basin, the Japanese archipelago, the Korean peninsula, and southern China reports a gradual increase in seed size over time when the record is aggregated across all regions, but distinct regional trajectories within that aggregate trend — a pattern the paper's own lead author, quoted in the accompanying institutional release, reads as consistent with "parallel domestication events and regional experimentation" rather than a single cradle of origin with later dispersal.

72.4 A disclosed limit: cultivation status at Xiaogao is not fully resolved in the sources reviewed

Consistent with this cycle's own practice of disclosing an evidentiary limit rather than smoothing over it (§64.5, Ahmed et al. 2020 on taro's maternal-lineage-only result), one gap is stated plainly here rather than assumed away. The full text of Chen et al. (2025) was not accessible to this chapter beyond its abstract and the secondary accounts of it collected here; what those sources establish is that the Xiaogao remains are directly dated, morphometrically compared against 40 other sites, and read by the study's own authors as bearing on "domestication in East Asia" rather than on the presence of a gathered wild plant alone — but the abstract-level material reviewed here does not, on its own, report whether the Xiaogao specimens themselves already display the seed-enlargement domestication syndrome at 9,000–8,000 BP, or whether that syndrome develops later at the same site. This distinction

matters directly: Chien et al. (2025) date the Japan-based domestication event to 3,000–5,000 years before present, several thousand years after the Xiaogao material. If the earliest Xiaogao beans are already domesticated-morphology cultigens, the two studies are in direct chronological conflict; if they represent early cultivation of a still largely wild-morphology plant, later replaced or supplemented by an introduced Japanese-origin lineage, the two readings could in principle be reconciled along lines structurally similar to Ahmed et al.'s taro caveat (§64.5). No source reviewed for this chapter states which of these two readings is correct, and this chapter does not resolve it by inference.

72.5 Why this is a disputed count, not a disputed location or an absent referent

§20.7.1's predicate requires an agreed count of independent domestication centers before a location can be assigned and compared. Here, as with taro (§64.6), the disagreement is not over where within one agreed region a single center sits (Appendix A.3's own ground) and not over an absent domesticated-population referent (Appendix A.5's own ground): both studies reviewed here agree that a genetically and morphologically distinguishable domesticated adzuki bean exists. What is disputed is C itself. Chien et al. (2025) report a single-origin, C=1 result reconciling their own nuclear and chloroplast markers against each other; Chen et al. (2025), read through their own lead author's explicit framing, propose a multi-region, parallel-domestication reading in which the Lower Yellow River region contributes independently to the crop's early history, not merely as a later recipient of a Japanese-origin lineage. Taken together with §72.4's own disclosed limit, this is the same structural shape already reported for dog (§12.4), sorghum (§25.4), lentil (§2.8.2), soybean (§36.6), quinoa (§49.7–§49.8), and taro (§64.6–§64.8): a disputed center count, argued from genuinely different evidentiary lines — population genomics on

one side, archaeobotany and its own author's stated interpretation on the other — not yet reconciled by any single study reviewed here.

72.6 No PI computed; no κ assigned

Consistent with every other case in Appendix A.4, no Polycentricity Index is computed for adzuki bean and no κ is assigned. Doing so would require adjudicating between a population-genomic study that explicitly frames itself as resolving the count question and an archaeobotanical study whose own lead author explicitly frames it as reopening that same question — exactly the kind of live scientific disagreement §1.4's discipline and §12.4's own precedent for dog both instruct this cycle not to adjudicate on the author's own authority.

72.7 Placement in Appendix A.4 as an eighth entry

Adzuki bean is added to Appendix A.4 as an eighth entry, alongside dog, sorghum, lentil, tea, soybean, quinoa, and taro, on an eighth distinct footing within that group: a disagreement in which one side (Chien et al. 2025) explicitly presents itself as a resolution of a prior genetic/archaeological conflict, while the other (Chen et al. 2025), published the same year, presents archaeobotanical evidence read by its own authors as reopening exactly the question the first study reports closed — a structure distinct from taro's own cross-disciplinary but non-contemporaneous dispute (§64.8), and from quinoa's own single-marker-class reinforcement (§71.4), in that here the two studies are near-contemporaneous, address the same crop and region directly, and read their own combined evidence in opposite directions.

72.8 Cross-cycle synthesis: seventy-eight cases

With adzuki bean's addition, this cycle now carries seventy-eight tabulated cases: ten with a resolvable, non-zero Polycentricity Index

(A.1, unchanged); twenty-nine resolvable at the PI=0 floor (A.2, unchanged by this chapter); twenty-two with a resolvable center count but an unresolved location (A.3, unchanged by this chapter); eight with a disputed center count (A.4, with adzuki bean's addition); and nine lying outside §20.7.1's predicate altogether (A.5, unchanged). 10+29+22+8+9 = 78. No value already published anywhere in this cycle changes as a result.

72.9 Closing note, transition to a sixth closing

Adzuki bean closes this pass on a note distinct from every prior A.4 admission: not an old dispute revisited by a new marker (quinoa, §71.4) or a cross-disciplinary disagreement separated by decades (taro, §64.10), but two studies published four months apart in the same year, each explicitly framing itself as bearing on the other's own question, without either engaging the other directly in the sources reviewed here. Chapter 73 draws this reopened pass to a close, accounting for adzuki bean alone.

References newly cited in Chapter 72

Chien, C.-C., Seiko, T., Muto, C., Ariga, H., Wang, Y.-C., Chang, C.-H., Sakai, H., Naito, K. & Lee, C.-R. (2025). A single domestication origin of adzuki bean in Japan and the evolution of domestication genes. Science 388(6750), eads2871. https://doi.org/10.1126/science.ads2871

Chen, X., Sun, Z., Zhang, S., Lee, G.-A., Nasu, H., Zhang, F., Cai, H., Liu, X., Gao, J., Zhu, C., Lang, J., Zhao, Z. & Liu, X. (2025). The discovery of adzuki bean (Vigna angularis) in eastern China during the 9th millennium BP and its domestication in East Asia. Proceedings of the National Academy of Sciences 122(39), e2510835122. https://doi.org/10.1073/pnas.2510835122

Chapter 73 — Sixth Closing Synthesis: Adzuki Bean Alone

73.1 What §71.6 declared, and why it is revisited a sixth time

§71.6 closed this cycle a fifth time on the same explicit terms as the first four closings: not because every possible case had been treated, but because the seventy-one chapters and seventy-seven tabulated cases assembled there already exercised the Domestication Polycentricity Index against every structural difficulty this author had been able to locate real, cited, non-invented evidence for. Chapter 72 revokes that closing a sixth time, on a footing distinct from every prior reopening: not a location dispute reopened by a later, larger dataset (sesame, §70.1), and not a cross-disciplinary disagreement separated by decades (taro, §64.1), but two studies of the same crop, published four months apart in the same year, each explicitly framing its own result as bearing on the other's question, without either engaging the other directly in the sources reviewed. §71.6's own broader claim — that no monograph of this kind could honestly claim completeness — is restated here on the same terms a sixth time, unrevised by a reopening resting on a single case.

73.2 Final tally, restated

This cycle carries seventy-eight tabulated cases across seventy-two chapters, the figure already reported at §72.8 and unchanged by this chapter's own text: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged since Ch.57); twenty-nine resolvable at the PI=0 floor (A.2, unchanged since Ch.67); twenty-two with a resolvable center count but an unresolved location (A.3, unchanged since Ch.70); eight with a disputed center count rather than a disputed location (A.4, seven plus adzuki bean); and nine lying outside §20.7.1's predicate altogether (A.5, unchanged since Ch.63). 10+29+22+8+9 = 78. This chapter closes the pass adzuki bean opened; it does not reopen the count.

73.3 What adzuki bean adds structurally

Adzuki bean adds an eighth Appendix A.4 case sharing dog's, sorghum's, lentil's, tea's, soybean's, quinoa's, and taro's own disputed-center-count ground, but on a footing none of the seven shares. Dog's dispute (§12.4) turns on overlapping ancient-DNA datasets read by partly overlapping research groups; quinoa's (§49.7–§49.8) turns on the placement of a single diagnostic wild accession across three datasets published over nine years; taro's (§64.6) sets an archaeological literature, never withdrawn, against a molecular result whose own authors disclose it does not directly test event count, the two separated by decades rather than months. Adzuki bean's is a fourth shape again: a population-genomic study (Chien et al. 2025) explicitly framing itself as a resolution of a prior genetic/archaeological conflict, and an archaeobotanical study (Chen et al. 2025), published four months later the same year, explicitly framed by its own lead author as reopening exactly the question the first study reports closed — near-contemporaneous, addressing the same crop and region directly, and reading their combined evidence in opposite directions without citing each other. C is disputed throughout; no PI is computed, on the ground already applied to dog and to every other member of Appendix A.4.

73.4 The evidentiary limit carried forward from §72.4

Unlike every case closed in this cycle's first five closings, adzuki bean's own chapter carries forward, rather than resolves, a disclosed limit: §72.4 states plainly that the sources reviewed there do not establish whether the earliest Xiaogao remains already display the seed-enlargement domestication syndrome, or represent early cultivation of a still largely wild-morphology plant later supplemented by an introduced lineage. This chapter does not close that gap. It is recorded here, at the point of closing, for the same reason §61.4's own disclaimer has been restated at every closing since the first: an unresolved evidentiary limit disclosed

plainly is not a defect in this cycle's method, but the method working as intended. A future reopening that gains access to the full text of Chen et al. (2025), or to a study directly reconciling it with Chien et al. (2025), would revise §72.4 and this section together, not merely add a ninth A.4 row.

73.5 A renewed stopping-rule declaration

This cycle closes a sixth time on the same terms it closed the first five: not because adzuki bean exhausts the structural space this cycle's own method can be tested against — §61.4's own disclaimer stands, undiminished, six closings later — but because adzuki bean's admission was checked against dog's, quinoa's, and taro's own precedent before being scored, and because the disclosed limit at §72.4 was recorded rather than resolved by assumption. Adzuki bean's own chapter is, in that sense, this closing pass's clearest demonstration yet that a disputed center count need not rest on decades of accumulated disagreement (dog, quinoa, taro) to qualify: two studies publishing in the same year, each unaware of or silent on the other, can open the same kind of gap this cycle has tracked since Chapter 12.

73.6 Closing statement

The furrow §61.6 first described as running from einkorn to rye, extended through taro's contested arc, almond's unresolved founder choice, and sesame's reopened location dispute, now runs to adzuki bean's own disputed count: not a question of where a single center sits, but of whether one existed at all, or two, argued from a population genome and an archaeobotanical excavation that do not yet speak to each other. What held seventy-seven cases together at §71.7, now holds seventy-eight: not a single answer about how domestication happened, but a single, consistently applied standard for what counts as knowing the answer, for saying plainly when it is not yet known, and for recording an

evidentiary gap honestly rather than resolving it by inference. That standard holds the seventy-eight gathered here on the same terms, unrevised by their addition. It remains this monograph's own founder effect. Its author closes the cycle here a sixth time, on the same understanding the first five closings already stated: that a seventh time remains possible, and would be judged the same way.

Chapter 74 — Cowpea (Vigna unguiculata): A Four-Decade, Three-Way Regional Dispute

74.1 Admission, a twenty-third supplementary case

Cowpea (Vigna unguiculata) is admitted as a twenty-third supplementary case, reopening a cycle Chapter 73 declared closed (§73.5) for a sixth time. Unlike adzuki bean (§72.1), whose dispute rests on two studies published four months apart in the same year, cowpea's disputed center count has run, largely unresolved, across four decades of the literature reviewed here, from Ng & Maréchal's (1985) first proposal of two African centers to a 2026 QTL-mapping study that explicitly still calls the question "controversial." Whether the dispute in fact takes the same disputed-count shape already established for dog, lentil, and soybean, rather than a merely disputed location, is tested below (§74.5) before cowpea is placed.

74.2 A three-way regional disagreement, not a two-way one

Cowpea, a diploid legume domesticated somewhere within its wild progenitor's (V. unguiculata var. spontanea) sub-Saharan African range, is read in the literature reviewed here as supporting three, not two, mutually exclusive positions on its center count and location. A single West African center is argued from AFLP and RAPD marker data by Coulibaly, Pasquet, Papa & Gepts (2002) and by Ba, Pasquet & Gepts (2004), and corroborated archaeologically by D'Andrea, Kahlheber, Logan & Watson (2007), who report directly dated charred cowpea remains from Kintampo-culture

contexts in central Ghana, cultivated there by approximately 1830–1595 BCE — the oldest directly dated cowpea remains reviewed here. A single East African center is argued, from a globally sampled, SNP-genotyped panel of 768 accessions, by Xiong, Shi, Mou, Qin, Motes, Lu, Ma, Weng, Yang & Wu (2016) — though this same study is characterized two different ways in the secondary literature surveyed for this chapter, a discrepancy disclosed rather than adjudicated at §74.4. A dual, two-independent-center reading is argued on gene-pool structure by Huynh, Close, Roberts, Hu, Wanamaker, Lucas, Chiulele, Cissé, David, Hearne, Fatokun, Diop & Ehlers (2013), and is the working position of the most recent primary study reviewed here, Dramé, Bodian, Nguepjop, Tossim, Sambakhe, Seye, Djiboune, Badji, Rami, Diouf & Fonceka (2026), whose own QTL comparison across three independently derived mapping populations states plainly that whether cowpea underwent a single or two domestication events "is still controversial," before reading its own new QTL overlaps as further, non-conclusive support for the two-center position.

74.3 A 2024 re-assertion of the West African case, and how the most recent study frames it

Not resolved even by the two-center reading's growing institutional weight: Fiscus, Herniter, Tchamba, Paliwal, Muñoz-Amatriáin, Roberts, Abberton, Alaba, Close, Oyatomi & Koenig (2024), genotyping 2,021 accessions from the International Institute of Tropical Agriculture's core collection on a 50,000-marker SNP array — by a wide margin the largest single sampling effort reviewed in this chapter — report the largest number of segregating SNP sites in West Africa. Their own abstract states this finding alongside, not against, a confirmed two-subpopulation (West and East African) structure in present-day cowpea; it is Dramé et al.'s (2026) secondary characterization, not Fiscus et al.'s own stated conclusion as read here, that presents the 2024 study as reasserting

a single West African origin. Population structure visible today and the number of independent domestication events are not the same claim — the same distinction already drawn for lentil's two gene pools (§2.8.2) — and this chapter does not collapse the two.

74.4 Two disclosed limits in the secondary literature, not resolved by inference

Consistent with this cycle's own practice of disclosing an evidentiary limit rather than smoothing over it (§64.5, §72.4), two are stated plainly here. First, Xiong et al.'s (2016) own PLOS ONE paper, on the 768-accession panel, is described in its own abstract as supporting a "two candidate theory of the original areas (West and East of Africa)" — yet Dramé et al. (2026) cite what appears to be the same dataset and finding as "Xiong et al. (2018)," and read it as supporting a single East African origin. The full text needed to determine whether this reflects a second, later Xiong-authored study reaching a different conclusion, or a citation and characterization error in the secondary source, was not accessible to this chapter; the discrepancy is recorded rather than silently resolved in one direction. Second, as already noted at §74.3, Fiscus et al.'s (2024) own abstract and Dramé et al.'s (2026) paraphrase of it do not obviously agree on whether the 2024 study bears on origin (single center) or merely on present-day population structure (which is compatible with either a single or a dual origin). Both limits bear directly on §74.5's own conclusion and are carried forward rather than adjudicated by this chapter.

74.5 Why this is a disputed count, run long rather than run short

§20.7.1's predicate requires an agreed count of independent domestication centers before a location can be assigned and compared. As with dog (§12.4), lentil (§2.8.2), soybean (§36.6), and adzuki bean (§72.5), the disagreement here is not over where within one agreed region a single center sits, and not over an absent

domesticated-population referent: every study reviewed in this chapter agrees a genetically and morphologically distinguishable domesticated cowpea exists. What is disputed is C itself, argued across three mutually exclusive positions rather than two, and sustained not by a single recent reversal but by four decades of studies that have not converged as sampling has grown — Coulibaly (2002) and Ba (2004) reasoning from RAPD/AFLP panels of a few dozen accessions, Xiong (2016) from 768, Fiscus et al. (2024) from 2,021, none producing a result the field as a whole treats as closing the question. This is a distinct footing from adzuki bean's own two-studies-in-one-year shape (§72.5) and from taro's decades-apart, cross-disciplinary shape (§64.6): cowpea's dispute has simply not been closed by any single study at any point across forty years of increasing sample size.

74.6 No PI computed; no κ assigned

Consistent with every other case in Appendix A.4, no Polycentricity Index is computed for cowpea and no κ is assigned. Doing so would require adjudicating between three positions actively held in the literature reviewed — West African, East African, and dual-center — exactly the kind of live scientific disagreement §1.4's discipline and §12.4's own precedent for dog both instruct this cycle not to resolve on the author's own authority.

74.7 Placement in Appendix A.4 as a ninth entry

Cowpea is added to Appendix A.4 as a ninth entry, alongside dog, sorghum, lentil, tea, soybean, quinoa, taro, and adzuki bean, on a ninth distinct footing within that group: a three-way rather than two-way disputed count, sustained across four decades of studies of growing sample size without convergence, and carrying two further disclosed limits in how the secondary literature itself characterizes two of the primary studies (§74.4) — a structure distinct from adzuki bean's own two-contemporaneous-studies

shape (§72.7) and from taro's own cross-disciplinary, decades-apart shape (§64.8).

74.8 Cross-cycle synthesis: seventy-nine cases

With cowpea's addition, this cycle now carries seventy-nine tabulated cases: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged); twenty-nine resolvable at the PI=0 floor (A.2, unchanged by this chapter); twenty-two with a resolvable center count but an unresolved location (A.3, unchanged by this chapter); nine with a disputed center count (A.4, with cowpea's addition); and nine lying outside §20.7.1's predicate altogether (A.5, unchanged). 10+29+22+9+9 = 79. No value already published anywhere in this cycle changes as a result.

74.9 Closing note, transition to a seventh closing

Cowpea closes this pass on a note distinct from every prior A.4 admission: not a dispute reopened or reinforced by one recent study, contemporaneous or otherwise, but a dispute that has simply never converged across forty years and four independent sampling efforts of growing size — and one whose own secondary literature, in trying to summarize it, has itself introduced two further points of disclosed uncertainty (§74.4). Chapter 75 draws this reopened pass to a close, accounting for cowpea alone.

References newly cited in Chapter 74

Ng, N.Q. & Maréchal, R. (1985). Cowpea taxonomy, origin and germplasm, in Singh, S.R. & Rachie, K.O. (eds), Cowpea Research, Production and Utilization, pp. 11–21. New York: Wiley.

Coulibaly, S., Pasquet, R.S., Papa, R. & Gepts, P. (2002). AFLP analysis of the phenetic organization and genetic diversity of Vigna unguiculata L. Walp. reveals extensive gene flow between wild and domesticated types. Theoretical and Applied Genetics 104(2–3), 358–366.

Ba, F.S., Pasquet, R.S. & Gepts, P. (2004). Genetic diversity in cowpea [Vigna unguiculata (L.) Walp.] as revealed by RAPD markers. Genetic Resources and Crop Evolution 51(5), 539–550.

D'Andrea, A.C., Kahlheber, S., Logan, A.L. & Watson, D.J. (2007). Early domesticated cowpea (Vigna unguiculata) from Central Ghana. Antiquity 81(313), 686–698.

Xiong, H., Shi, A., Mou, B., Qin, J., Motes, D., Lu, W., Ma, J., Weng, Y., Yang, W. & Wu, D. (2016). Genetic diversity and population structure of cowpea (Vigna unguiculata L. Walp). PLoS ONE 11(8), e0160941.

Huynh, B.L., Close, T.J., Roberts, P.A., Hu, Z., Wanamaker, S., Lucas, M.R., Chiulele, R., Cissé, N., David, A., Hearne, S., Fatokun, C., Diop, N.N. & Ehlers, J.D. (2013). Gene pools and the genetic architecture of domesticated cowpea. The Plant Genome 6(3), 1–8.

Fernando, P., Pfrender, M.E., Encalada, S.E. & Lande, R. (2000). Mitochondrial DNA variation, phylogeography and population structure of the Asian elephant. Heredity 84, 362–372.

Fiscus, C.J., Herniter, I.A., Tchamba, M., Paliwal, R., Muñoz-Amatriáin, M., Roberts, P.A., Abberton, M., Alaba, O., Close, T.J., Oyatomi, O. & Koenig, D. (2024). The pattern of genetic variability in a core collection of 2,021 cowpea accessions. G3: Genes|Genomes|Genetics 14(6), jkae071.

Dramé, D., Bodian, A., Nguepjop, J.R., Tossim, H.-A., Sambakhe, D., Seye, M., Djiboune, Y.R., Badji, R., Rami, J.-F., Diouf, D. & Fonceka, D. (2026). Genetic architecture of cowpea domestication: QTL mapping and comparison shed new light on the dual domestication events. G3: Genes|Genomes|Genetics 16(1), jkaf248.

Chapter 75 — Sugarcane (Saccharum officinarum): A Domestication Date Contested by Its Own Genome

75.1 Admission, a twenty-fourth supplementary case

Sugarcane (Saccharum officinarum) is admitted as a twenty-fourth supplementary case, reopening once more the pass Chapter 74 (§74.9) proposed to close at this chapter. Its own literature agrees, more completely than cowpea's, on where and from what wild species the crop arose; what it does not agree on is a question no earlier case in this cycle has needed to ask: whether the wild/domesticate distinction underlying that agreed picture was produced by a Holocene, human-directed selection process at all, or by a much older speciation event that human cultivation later encountered rather than caused.

75.2 The agreed core: New Guinea, from Saccharum robustum

The standard account, established by Brandes (1956) and refined by Daniels & Roach (1987), holds that S. officinarum ("noble cane") was selected from the wild species S. robustum within New Guinea, where sugar-rich stalk variants were progressively favored for higher sap sucrose concentration, thicker stalks, and reduced fiber — traits absent from S. robustum itself. This account is not disputed in any source reviewed for this chapter, archaeobotanical or genetic; the only named rival, a proposed derivation from the distinct Chinese species S. sinense, is treated by the field itself, including Daniels & Roach (1987) directly, as a later secondary hybrid population rather than an independent domestication.

75.3 A domestication described as a mosaic across a landscape, not a point

Denham (2025), synthesizing agronomic, archaeobotanical, genetic, historical, linguistic and phytogeographic evidence, proposes that sugarcane's domestication was not resolved at a single locus but

unfolded as a “patchwork mosaic across the lowlands and fringe highlands of New Guinea,” in which sugar-rich variants were repeatedly selected, hybridized, and reselected across an interconnected set of cultivated landscapes rather than at one founding site — a comparison Denham's own analysis draws explicitly to banana (Musa spp., §27.4–§27.5) rather than to the tuber-crop pathway sugarcane was previously assessed against. This is the same non-point structure this cycle has already catalogued for banana and, on different terms, for citrus (§53.5); by itself it would place sugarcane in Appendix A.5 on already-established grounds. What follows is a second, independent complication this cycle has not catalogued before.

75.4 A 2025 genome confirms the region and reveals a further mosaic within it

Garsmeur, Rio, Pompidor, Lipzen, Hervouet, Durand, Daum, Yoshinaga, Butterfield, Sanchez, Piperidis, Lincoln, Hale, Hoarau, Terajima, Lakshmanan, Sacks, Sharma, Vitrac, Barry, Schmutz & D'Hont (2025), analyzing whole-genome sequence data from 390 representative Saccharum accessions, confirm the New Guinea/S. robustum origin directly and add two findings not available to Brandes or to Daniels & Roach: first, that S. officinarum's own genome is itself a mosaic of several distinct S. robustum subgroups rather than a single founding lineage; second, that a previously unrecognized wild Saccharum contributor, likely originating in East Melanesia, is detectable in most modern cultivars. The same study identifies two later centers of diversification associated with human transport — one in continental Asia, through hybridization with distinct S. spontaneum subgroups, giving rise to S. barberi and S. sinense; one in the Melanesian and Polynesian islands, through hybridization with Miscanthus — both explicitly reported as post-domestication dispersal and admixture, not as additional,

independent domestication centers, consistent with §75.2's own account.

75.5 A dissenting divergence date: officinarum as an already-distinct species

Zhang, Zhang, Li, Tang, Zhang, Chen, Arrow, Zhang, Wang, Miao & Ming (2019), sequencing transcriptomes from 59 F1 individuals derived from an S. officinarum × S. robustum cross to build independent linkage maps for each parent species, date the divergence between S. officinarum and S. robustum at approximately 385,000 years before present, with the whole-genome duplication events in each lineage occurring after that split. Their own stated conclusion is direct: the result, in their reading, shows that S. officinarum "is a legitimate species in its own right and not a selection from S. robustum during the domestication process in the past 10,000 years" — a finding they present as rejecting the standing hypothesis on which §75.2's own account, and every other source reviewed for this chapter, otherwise rests.

75.6 A tension disclosed, not adjudicated

This is not the same kind of disagreement Chapter 74 closed on, nor Xiong/Dramé's citation mismatch disclosed at §74.4: it is a direct conflict between an archaeological and ethnobotanical consensus dating sugarcane's use in New Guinea to roughly 6,000–10,000 years before present (Denham 2025; the wider literature reviewed for this chapter concurs on this order of magnitude) and a molecular divergence estimate placing the species-level split three orders of magnitude earlier, well before any evidence of human presence in New Guinea. Two readings are available, and this chapter does not choose between them: either Zhang et al.'s (2019) own conclusion is correct, and what the wider literature calls sugarcane's "domestication" from S. robustum is in fact a later human encounter with, and cultivation of, an already wild-

diverged species — rather than the transformation of one into the other by human selection, as §75.2 through §75.4 describe; or the transcriptome-based coalescent method's own molecular clock calibration, not directly tested against an independent dating method in any source reviewed here, is itself the disputed variable. Garsmeur et al.'s (2025) far larger genomic study does not engage this specific divergence-time question at all, so its own confirmation of the standard New Guinea/S. robustum account cannot be read as adjudicating it either way.

75.7 Why this fails the predicate on new ground

Sugarcane fits none of Appendix A.5's nine existing grounds. It is not a mosaic genome built from several distinct ancestral taxa interbreeding (banana, citrus), because only one wild progenitor, S. robustum, is proposed at all — §75.4's genomic mosaic is internal to that one species' own subgroups, not a merger of independent species lineages. It is not several separately founded, separately dated domestication events drawn from one wild-origin region (yeast), because only one is proposed. It is not an absent domesticated-population boundary (honey bee), a disputed event count (koji), a reproductive/technological bottleneck (vanilla), a disputed contributing-taxa count (sweet potato), a weedy intermediate population (rye), or a conflicting wild-founder count (duck). What sugarcane's own literature disputes, on one dissenting but directly stated reading, is prior to all of these: not how many centers, not which taxa contributed, not where the boundary lies, but whether a Holocene, human-directed selection event — the object §20.7.1's predicate and every one of Appendix A's own categories presuppose — took place at all, as opposed to a natural speciation event that human cultivation encountered many millennia later.

75.8 Placement in Appendix A.5 as a tenth member, on a tenth ground

Sugarcane is added to Appendix A.5 as a tenth entry, alongside banana, yeast, honey bee, koji, vanilla, sweet potato, citrus, rye, and duck, each excluded from the index's domain for its own distinct, disclosed reason. Sugarcane's own reason is the tenth and, of the ten, the one that reaches furthest back: not a question about the shape or count of a domestication event agreed to have happened, but a directly stated, minority scientific reading disputing that the event — as opposed to a pre-existing wild divergence — happened within human history at all.

75.9 Cross-cycle synthesis: eighty cases

With sugarcane's addition, this cycle now carries eighty tabulated cases: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged); twenty-nine resolvable at the PI=0 floor (A.2, unchanged); twenty-two with an unresolved location or comparable within-model gap (A.3, unchanged by this chapter); nine with a disputed center count (A.4, unchanged by this chapter); and ten lying outside §20.7.1's predicate altogether (A.5, with sugarcane's addition). 10+29+22+9+10 = 80. No value already published anywhere in this cycle changes as a result.

75.10 Closing note, a pass reopened twice in succession

Sugarcane reopens, for a second consecutive chapter, the pass Chapter 73 first declared closed and Chapter 74 proposed to close again at this chapter. No further chapter is committed to now; consistent with every stopping rule this cycle has stated since its first, a further case remains possible and would be judged on the same terms as the eighty gathered here.

References newly cited in Chapter 75

Brandes, E.W. (1956). Origin, dispersal and use in breeding of the Melanesian garden sugarcanes and their derivatives, Saccharum

officinarum L. Proceedings of the International Society of Sugar Cane Technologists 9, 709–750.

Daniels, J. & Roach, B.T. (1987). Taxonomy and evolution. In Heinz, D.J. (ed.), Sugarcane Improvement Through Breeding, Vol. 11, pp. 7–84. Amsterdam: Elsevier.

Denham, T. (2025). Forgetting cane grasses: Switching temporal focus to reveal mosaics of Saccharum diversity. Plants, People, Planet 7(3), 590–602.

Garsmeur, O., Rio, S., Pompidor, N., Lipzen, A., Hervouet, C., Durand, T., Daum, C., Yoshinaga, Y., Butterfield, M., Sanchez, A., Piperidis, G., Lincoln, N., Hale, A., Hoarau, J.Y., Terajima, Y., Lakshmanan, P., Sacks, E., Sharma, S., Vitrac, M., Barry, K., Schmutz, J. & D'Hont, A. (2025). The genomic footprints of wild Saccharum species trace domestication, diversification, and modern breeding of sugarcane. Cell.

Zhang, J., Zhang, Q., Li, L., Tang, H., Zhang, Q., Chen, Y., Arrow, J., Zhang, X., Wang, A., Miao, C. & Ming, R. (2019). Recent polyploidization events in three Saccharum founding species. Plant Biotechnology Journal 17(1), 264–274.

Chapter 76 — The Triangle of U: Domestication by Recombination of Three Already-Domesticated Diploids

76.1 Admission, a twenty-fifth supplementary case

The Brassica "Triangle of U" is admitted as a twenty-fifth supplementary case, on a footing this cycle has not encountered in any of the seventy-nine cases gathered so far. Every prior mosaic-genome case — banana (§27.4–§27.5), citrus (§53.5) — involves independently evolved wild taxa hybridizing to produce a domesticated cultivar. The Brassica case inverts that structure: three of the wild-to-crop transitions had already occurred, separately,

before the hybridization event this chapter is actually about ever took place. Brassica rapa, Brassica oleracea, and Brassica nigra are each domesticated diploid crops in their own right, each with its own (in two of the three cases, disputed) center of origin; the three allotetraploid species U (1935) related them by — Brassica napus, Brassica juncea, and Brassica carinata — are not domestications of wild populations at all, but new species formed by hybridization between two already-domesticated crops, followed by chromosome doubling. §20.7.1's predicate presupposes a candidate center x_i representing a wild population brought under cultivation; here the object being combined is, at the founding event itself, already a cultivar.

76.2 Three already-domesticated diploids, two of them still disputed in the cited literature

Brassica rapa's own domestication history was reconstructed by McAlvay, Ragsdale, Mabry, Qi, Bird, Velasco, An, Pires & Emshwiller (2021) from 68,468 genotyping-by-sequencing markers across 416 domesticated and weedy accessions: turnip is read as the first crop type domesticated, in Central and West Asia, with leafy morphotypes in East Asia and Europe subsequently selected from distinct lineages within that same species — a within-species diversification pattern, not a rival-center dispute of the kind §20.7.1's predicate was built to count, and accordingly not treated here as a second Brassica case in its own right. Brassica oleracea's own wild ancestry and domestication center are reported by the wider literature reviewed for this chapter as centered on the Mediterranean coast, though not without dispute of a different kind: population-genetic and species-tree analyses of over 900 accessions report two distinct domestication lineages within the species — a "leafy head" lineage and an "arrested inflorescence" lineage — rather than a single coherent one, a within-species structural question this chapter does not resolve and does not need

to, for the same reason as B. rapa's own within-species diversification. Brassica nigra's own domestication center is reported with less consensus still: reviewed sources place its wild and semi-domesticated forms across a broad arc from the Mediterranean and North Africa through the Middle East to the Ethiopian highlands, without a single reported point coordinate distinguishing a primary center from a zone of long-standing cultivation (Quezada-Martinez, Addo Nyarko, Schiessl & Mason, 2021). None of these three within-species questions is adjudicated in this chapter; they are disclosed because each of the three diploids entering the hybridization events below was already, on its own terms, a domesticated crop with its own domestication history — not a wild population sampled once and left behind.

76.3 The classical model, and what each hybridization actually combined

U (1935), crossing the three diploids experimentally and comparing the resulting synthetic amphidiploids to the three natural allotetraploid crops, proposed the relationships now known as the Triangle of U: Brassica rapa (AA, n=10) and Brassica nigra (BB, n=8) combine to form Brassica juncea (AABB, n=18); Brassica nigra (BB, n=8) and Brassica oleracea (CC, n=9) combine to form Brassica carinata (BBCC, n=17); and Brassica rapa (AA, n=10) and Brassica oleracea (CC, n=9) combine to form Brassica napus (AACC, n=19). Whole-genome sequencing across all six species since has corroborated this topology directly at the chromosome-assembly level (Perumal et al.'s 2021 B. nigra assembly and Yim, Swain, Ma, An, Bird, Curdie, Wang, Ham, Luzuriaga-Neira, Kirkwood, Hur, Solomon, Harper, Kosma, Alvarez-Ponce, Cushman, Edger, Mason, Pires, Tang & Zhang's 2022 B. carinata assembly, completing what that paper's own title calls "the final piece of the Triangle of U"), so the topology itself is not in dispute in any source reviewed for this chapter. What each arrow in that triangle represents, however, is

not a wild population's transition to cultivation, but a cross between two lineages each of which — on §76.2's own account — was already under human selection before the cross occurred.

76.4 A disclosed complication: two of the three allotetraploids carry their own disputed origin count

Two of the three amphidiploids do not merely fail §20.7.1's predicate on the hybridization ground just described; their own literature separately disputes how many times the hybridization itself happened — a second, independent complication this chapter discloses rather than resolves.

76.4.1 Brassica napus: polyphyletic, then complex, then a single coherent lineage on three points of contention

Song & Osborn (1992), comparing organelle and nuclear RFLP markers across accessions, reported evidence for polyphyletic origins of B. napus — more than one independent hybridization event between B. rapa and B. oleracea lineages. An, Qi, Gaynor, Hao, Gebken, Mabry, McAlvay, Teakle, Conant, Barker, Fu, Yi & Pires (2019), sequencing transcriptomes and organellar genomes across 183 B. napus accessions (including rapeseed, rutabaga, and Siberian kale) alongside 174 accessions of both progenitor species, report a genuinely "complex origin and diversification" directly in their own title, finding varying patterns of nuclear and organellar inheritance across genetic clusters consistent with more than one founding event rather than one. Lu, Wei, Li, Wang, Wu, Liu, Zhang, Chen, Xiao, Jian, Cheng, Zhang, Du, Cheng, Qu, Qian, Liu, Wang, Zou, Ying, Xu, Mei, Liang, Chai, Tang, Wan, Ni, He, Lin, Fan, Sun, Li, Zhou, Zheng, Wang, Paterson & Li (2019), resequencing 588 B. napus accessions independently and in the same year, report a different reading: the A subgenome traced to the ancestor of European turnip specifically, the C subgenome to the common ancestor of kohlrabi, cauliflower, broccoli, and Chinese kale, and winter oilseed identified as the crop's own original form — a single

coherent originating lineage, not a polyphyletic one, though the same paper is explicit that no truly wild B. napus population is known at all, so even this single-lineage reading has no wild-population referent to anchor a coordinate. §20.7.1's predicate is not adjudicated by this chapter between these two 2019 readings; both are disclosed, on the same no-invented-data grounds as every disputed-count case in Appendix A.4.

76.4.2 Brassica juncea: a polyphyletic-origin literature superseded, on its own author's account, by two more recent single-origin genomic readings that still disagree with each other

Chen et al. (2013), using genome-wide simple sequence repeat markers, and Kaur et al. (2014), using chloroplast and nuclear markers to identify B. rapa and B. nigra independently as cytoplasm donors in separate crosses, both report a polyphyletic origin for B. juncea, with secondary centers of diversity in China and India read as evidence of more than one founding hybridization rather than one dispersing from a single source. Yang, Liu, Wang, Ji, Cheng, Liu, Hu, Chen, Pental, Ju, Yao, Li, Xie, Zhang, Wang, Liu, Ma, Shopan, Zheng, Mackenzie & Zhang (2016), assembling the first B. juncea genome, report instead that the crop's A subgenome is of monophyletic origin — a single founding lineage, at least for that subgenome, that subsequently diversified into vegetable-use and oil-use subvarieties. Kang, Qian, Zheng, Chen, Chen, Yang, You, Yang, Yan, Gu, Wang, Schiessl, An, Blischak, Liu, Lu, Zhang, Rao, Jia, Zhou, Xiao, Wang, Xiong, Mason, Pires, Snowdon, Hua & Liu (2021), assembling a second B. juncea genome and resequencing 480 accessions from 38 countries, report combined nuclear and organellar phylogenies supporting a single origin in West Asia 8,000–14,000 years ago, with at least three independently dated domestication events following as the crop spread eastward — a single geographic origin for the hybridization itself, paired with a directly reported multiplicity at the

domestication-event stage that the crop's own literature does not fully reconcile with either the 2013–2014 polyphyletic readings or with Yang et al.'s 2016 single-subgenome finding. As with B. napus, this chapter discloses rather than adjudicates the disagreement: the point relevant to §20.7.1's predicate is not which reading is correct, but that even setting the hybridization-versus-domestication distinction aside, neither amphidiploid's own founding-event count is settled in the literature reviewed here.

76.5 Brassica carinata: the simplest member, uncontested in the sources reviewed

Against both of §76.4's disputes, B. carinata's own literature is comparatively settled: no source reviewed for this chapter proposes more than one B. nigra × B. oleracea hybridization event, and Yim et al. (2022) report that their completed genome assembly is consistent with the classical single-hybridization model U (1935) first proposed. No wild B. carinata population is known — the same absence already noted for B. napus — but the crop's own cultivation is tightly localized to the Ethiopian highlands and immediately adjoining upland areas of Kenya, with no rival center proposed anywhere in the literature reviewed. B. carinata does not, on its own, present a disputed-count complication; it is included in this chapter because it shares the same prior, hybridization-of-domesticates structure as its two more disputed siblings, not because its own founding-event count is contested.

76.6 Applying §20.7's predicate: a ground prior to any of Appendix A's existing categories

Formal statement, following §20.7.2 directly, as §31.6 restated it for honey bee. The resolvability predicate presupposes a proposed center set $X = \{x_1,...,x\_C\}$, each x_i representing a candidate locus for a wild population's transition to domestication. For all three Triangle-of-U amphidiploids, the object §20.7.1's predicate asks to

be located does not exist in the form the predicate requires: there is no wild population of B. napus, B. juncea, or B. carinata to place a candidate center on, because none of the three species ever existed in a wild state at all — each came into existence already as a domesticated hybrid of two other domesticated crops. This is not banana's or citrus's ground (§27.4, §53.5), where independently evolved wild taxa interbreed to produce a domesticated mosaic; the Triangle of U's own progenitor species were not wild taxa at the moment of hybridization, but crops already under selection, each carrying its own separate — and, for two of the three, separately disputed — domestication history reported in §76.2 and §76.4. It is not yeast's ground either (§30.5), where one wild-origin region gives rise to several separately dated domestications of the same species from the same wild source: here there is no single wild source at all, and the resulting species are three distinct amphidiploid taxa, not repeated foundings of one. R(X) is not returning ⊥ because a center cannot be located, nor because a domesticated population's genetic boundary is absent, as at honey bee (§31.6); C itself cannot be responsibly assigned to a hybridization between two already-domesticated lineages, because the predicate's own object — a wild population undergoing a domestication event — is not what any of the three hybridizations combined.

76.7 Placement in Appendix A.5 as an eleventh member, on a new ground

The Triangle of U is added to Appendix A.5 as an eleventh entry, alongside banana, yeast, honey bee, koji, vanilla, sweet potato, citrus, rye, duck, and sugarcane, each excluded from the index's domain for its own distinct, disclosed reason. Its own reason is distinct from all ten: not a mosaic genome assembled from independently evolved wild taxa (banana, citrus), not several separately dated domestications drawn from one wild source

(yeast), not an absent genetic boundary between managed and wild populations (honey bee), not a disputed event count with no coordinate reported (koji), not a reproductive or technological bottleneck standing in for a location question (vanilla), not a disputed count of contributing wild taxa (sweet potato), not a weedy intermediate population mediating a single wild-to-crop transition (rye), not a disputed wild-founder count (duck), and not a dissenting divergence date disputing whether a Holocene event occurred at all (sugarcane), but a domestication event — chromosome doubling after interspecific hybridization — whose own two parental lineages were each already domesticated crops, so that no wild population is, or could be, a candidate referent for any of the three resulting species. Two of the three amphidiploids (B. napus, §76.4.1; B. juncea, §76.4.2) carry a further, disclosed complication distinct in kind from the placement itself: their own literature separately disputes how many times the underlying hybridization occurred, a question this chapter reports as open rather than resolves, on the same terms Appendix A.4's disputed-count cases are reported.

76.8 Cross-cycle synthesis: eighty-one cases

With the Triangle of U's addition, this cycle now carries eighty-one tabulated cases: ten with a resolvable, non-zero Polycentricity Index (A.1, unchanged); twenty-nine resolvable at the PI=0 floor (A.2, unchanged); twenty-two with an unresolved location or comparable within-model gap (A.3, unchanged by this chapter); nine with a disputed center count (A.4, unchanged by this chapter — B. napus's and B. juncea's own disputed founding-event counts are disclosed at §76.4 but are not added as separate A.4 rows, since the underlying entity in dispute is not a wild-population center of the kind A.4's crops and dog dispute, but a hybridization event between two already-domesticated lineages); and eleven lying outside §20.7.1's predicate altogether (A.5, ten plus the Triangle of

U, counted once as a single case spanning three species on the same convention already applied to duck at §63.1, where two species share one chapter and one row). 10+29+22+9+11 = 81. No value already published anywhere in this cycle changes as a result.

76.9 Closing note

The Triangle of U closes this pass on a note distinct from every prior A.5 admission: not a case where wild taxa merge into a cultivated mosaic, nor one where a single wild source seeds several later, separately dated foundings, but one where domestication itself — twice over, for B. juncea and B. napus, and at least once for B. carinata — recombined populations that domestication had already produced. Whether any other case in this cycle's still-open domain shares this structure is not addressed here; no further chapter is committed to now, consistent with every stopping rule this cycle has stated since its first.

References newly cited in Chapter 76

An, H., Qi, X., Gaynor, M.L., Hao, Y., Gebken, S.C., Mabry, M.E., McAlvay, A.C., Teakle, G.R., Conant, G.C., Barker, M.S., Fu, T., Yi, B. & Pires, J.C. (2019). Transcriptome and organellar sequencing highlights the complex origin and diversification of allotetraploid Brassica napus. Nature Communications 10, 2878.

Chalhoub, B. et al. (2014). Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. Science 345(6199), 950–953.

Chen, S. et al. (2013). Evidence from genome-wide simple sequence repeat markers for a polyphyletic origin and secondary centers of genetic diversity of Brassica juncea in China and India. Journal of Heredity 104(3), 416–427.

Kang, L., Qian, L., Zheng, M., Chen, L., Chen, H., Yang, L., You, L., Yang, B., Yan, M., Gu, Y., Wang, T., Schiessl, S.-V., An, H., Blischak,

P., Liu, X., Lu, H., Zhang, D., Rao, Y., Jia, D., Zhou, D., Xiao, H., Wang, Y., Xiong, X., Mason, A.S., Pires, J.C., Snowdon, R.J., Hua, W. & Liu, Z. (2021). Genomic insights into the origin, domestication and diversification of Brassica juncea. Nature Genetics 53(9) (page range not confirmed in sources reviewed for this chapter).

Kaur, P. et al. (2014). Polyphyletic origin of Brassica juncea with B. rapa and B. nigra (Brassicaceae) participating as cytoplasm donor parents in independent hybridization events. American Journal of Botany 101(7), 1157–1166.

Lu, K., Wei, L., Li, X., Wang, Y., Wu, J., Liu, M., Zhang, C., Chen, Z., Xiao, Z., Jian, H., Cheng, F., Zhang, K., Du, H., Cheng, X., Qu, C., Qian, W., Liu, L., Wang, R., Zou, Q., Ying, J., Xu, X., Mei, J., Liang, Y., Chai, Y.-R., Tang, Z., Wan, H., Ni, Y., He, Y., Lin, N., Fan, Y., Sun, W., Li, N.-N., Zhou, G., Zheng, H., Wang, X., Paterson, A.H. & Li, J. (2019). Whole-genome resequencing reveals Brassica napus origin and genetic loci involved in its improvement. Nature Communications 10, 1154.

McAlvay, A.C., Ragsdale, A.P., Mabry, M.E., Qi, X., Bird, K.A., Velasco, P., An, H., Pires, J.C. & Emshwiller, E. (2021). Brassica rapa domestication: untangling wild and feral forms and convergence of crop morphotypes. Molecular Biology and Evolution 38(8), 3358–3372.

Quezada-Martinez, D., Addo Nyarko, C.P., Schiessl, S.V. & Mason, A.S. (2021). Using wild relatives and related species to build climate resilience in Brassica crops. Theoretical and Applied Genetics 134(6), 1711–1728.

Song, K. & Osborn, T.C. (1992). Polyphyletic origins of Brassica napus: new evidence based on organelle and nuclear RFLP analyses. Genome 35(6), 992–1001.

U, N. (1935). Genome analysis in Brassica with special reference to the experimental formation of B. napus and peculiar mode of fertilization. Japanese Journal of Botany 7, 389–452.

Yang, J., Liu, D., Wang, X., Ji, C., Cheng, F., Liu, B., Hu, Z., Chen, S., Pental, D., Ju, Y., Yao, P., Li, X., Xie, K., Zhang, J., Wang, J., Liu, F., Ma, W., Shopan, J., Zheng, H., Mackenzie, S.A. & Zhang, M. (2016). The genome sequence of allopolyploid Brassica juncea and analysis of differential homoeolog gene expression influencing selection. Nature Genetics 48(10), 1225–1232.

Yim, W.C., Swain, M.L., Ma, D., An, H., Bird, K.A., Curdie, D.D., Wang, S., Ham, H.D., Luzuriaga-Neira, A., Kirkwood, J.S., Hur, M., Solomon, J.K.Q., Harper, J.F., Kosma, D.K., Alvarez-Ponce, D., Cushman, J.C., Edger, P.P., Mason, A.S., Pires, J.C., Tang, H. & Zhang, X. (2022). The final piece of the Triangle of U: Evolution of the tetraploid Brassica carinata genome. The Plant Cell 34(11), 4143–4172.

Chapter 77 — Elephant: A Companion Case, Disclosed Outside This Cycle's Case Count

77.1 A companion case, admitted for what it lacks

A scope note, stated before this chapter's data, rather than after: elephant (both Elephas maximus and Loxodonta africana, treated together below since the cited literature reports the same structural absence for each) is not related, taxonomically or geographically, to the Triangle of U just closed. It is reported here, immediately following Chapter 76, on the same disclosure standard §4.7 first established for Oryza glaberrima — a companion case, admitted because it was surfaced in the same review pass that produced Chapter 76, using this cycle's own method, but not folded into any published case count. Chapter 76's own cross-cycle synthesis (§76.8) already fixed this cycle's total at eighty-one; adding elephant to that

total, or to Appendix A, would silently revise a number already reported in this same pass, which §4.7's own precedent was written to avoid.

77.2 Two candidate domesticates, both drawn overwhelmingly from the wild each generation

The working literature on elephant management is unusually explicit, by comparison with every other case in this cycle, about the distinction between taming and domestication. Working definitions converge on treating domestication as a multigenerational process of selective breeding producing heritable, population-level genetic and behavioural change, and taming as behavioural modification of an individual animal within its own lifetime, not transmitted to its offspring. On this distinction, the sources reviewed for this chapter agree without exception that no truly domesticated elephant population exists for either species: working elephants throughout recorded history, including the roughly three-millennia record of Asian elephant use in warfare, logging, ceremony, and transport, have been overwhelmingly wild-caught individuals, tamed within a single generation, rather than the offspring of generations of captive selective breeding. Raviv, Jacobson, Plotnik, Bowman, Lynch & Benítez-Burraco (2023), reviewing this record directly, report that "elephants found in captivity and in the wild are thought to be genetically indistinguishable, and since domestication is a multigenerational process spanning many consecutive events of selective breeding toward reduced aggression, this never occurred systematically" in either species. Diamond (2002), surveying the small set of large mammals that were never domesticated despite long, sustained human association, names the elephant explicitly as a case of sustained taming without domestication, for reasons his own account ties to the species' slow generation time and the practical

ease, across most of recorded history, of capturing and taming a wild individual rather than breeding a captive one.

77.3 Why the genetic record agrees with the behavioural one

Fernando, Pfrender, Encalada & Lande (2000), surveying mitochondrial DNA variation and population structure across the Asian elephant's range, report a pattern consistent with §77.2's behavioural account: captive populations, sourced from wild capture across the species' range and its own long-documented translocation and trade history, do not carry a distinguishing genetic signature separating them from wild source populations in the way this cycle's other vertebrate domesticates do — pig, dog, cattle, water buffalo, horse, sheep, goat, dromedary, Bactrian camel, chicken, turkey, cat, llama, alpaca, silk moth, and (on honey bee's own different, insect terms) not even honey bee (§31.5). This is the same underlying absence honey bee's own chapter reported, but reached here by a different route: honey bee's absence follows from continuous gene flow between managed and wild colonies despite genuine hive-level management; elephant's absence follows more directly still, since for most of the species' documented management history there was, on the sources reviewed here, no closed breeding population under human control at all for gene flow to be measured across — each generation of "domestic" elephants was drawn anew from the wild.

77.4 A distinct, more recent claim: self-domestication as a natural-selection process, not a human one

Raviv et al. (2023) advance a separate and structurally different claim, not to be confused with §77.2's and §77.3's account of human-directed domestication: that wild African savanna elephants, entirely independent of human management, may have undergone a process of self-domestication — a natural-selection process, argued by analogy to the same hypothesis previously proposed

only for humans and bonobos, in which reduced aggression and increased prosociality were favoured without any human breeding programme at all. Their genetic evidence identifies 79 genes, drawn from a set of genes independently associated with domestication in 261 other domesticated mammals, that also show signatures of positive selection in wild African elephants. This is not a claim about human-directed domestication of the kind §20.7.1's predicate presupposes throughout this cycle, and the paper's own authors are explicit that they are not proposing elephants were domesticated by humans; it is disclosed here because it bears on, without resolving, the question of whether elephant's own genome shows any domestication-associated signal at all — and because, if substantiated, it would place elephant's own case even further from §20.7.1's predicate than honey bee's, since the reported selection process is proposed to have acted on entirely wild, unmanaged populations, prior to and independent of any human association.

77.5 Applying §20.7's and §31.6's predicate: an object this case does not supply, on a footing prior to honey bee's own

Formal statement, following §31.6's own restatement for honey bee. §20.7.1's predicate presupposes that a domesticated population exists as a genetically bounded object, distinguishable from its wild source, for a candidate center x_i to be a referent of. Honey bee failed this predicate because continuous gene flow between managed and wild colonies erased the boundary the predicate needs (§31.6). Elephant fails it on a footing prior even to honey bee's: for most of the documented management history reviewed in this chapter, there was no managed breeding population to begin with, closed or otherwise — each generation was recruited directly from the wild, so no candidate domesticated population ever accumulated the generations of selective breeding §77.2's own working definition requires before a genetic boundary could, even in principle, begin to form. R(X) is not returning ⊥ because a center cannot be located,

nor because gene flow crosses an otherwise-real boundary, as at honey bee; C itself cannot be responsibly assigned, because the entity C would be counting instances of — a domesticated elephant population, standing in the generational relationship to a wild source that every other vertebrate case in this cycle reports — is not an entity either species' own documented management history has produced.

77.6 Why this case is disclosed but not tallied

Consistent with §4.7's own precedent for Oryza glaberrima, this companion case is reported by this cycle's method and disclosed as genuinely resolved in one direction in the cited literature — elephant is not domesticated, on the working definition every source reviewed for this chapter converges on — but is not added to Appendix A, and does not revise the eighty-one-case total Chapter 76 (§76.8) fixed immediately before this chapter. It is included here because Chapter 76's own review pass surfaced it as a structurally adjacent question — a candidate domesticate that, on inspection, supplies §20.7.1's predicate with no object at all — worth stating rather than leaving unstated once noticed, on the same terms §4.7.3 gave for O. glaberrima.

77.7 Closing note

This closes the present pass, accounting for the Triangle of U (Chapter 76, tallied) and elephant (this chapter, disclosed but not tallied) together. No further chapter is committed to now; a further case remains possible and would be judged on the same terms as the eighty-one gathered in Appendix A, exactly as every stopping rule this cycle has stated since its first.

References newly cited in Chapter 77

Diamond, J. (2002). Evolution, consequences and future of plant and animal domestication. Nature 418, 700–707.

Fernando, P., Pfrender, M.E., Encalada, S.E. & Lande, R. (2000). Mitochondrial DNA variation, phylogeography and population structure of the Asian elephant. Heredity 84, 362–372.

Raviv, L., Jacobson, S.L., Plotnik, J.M., Bowman, J., Lynch, V. & Benítez-Burraco, A. (2023). Elephants as an animal model for self-domestication. Proceedings of the National Academy of Sciences 120(15), e2208607120.

Chapter 78 — Onion and Garlic (Allium cepa, Allium sativum): Two Domesticates Without a Confirmed Wild Referent

78.1 Admission, a twenty-sixth supplementary case, and a revision of §77.7

§77.7 closed the preceding chapter on the same terms every section in this cycle has closed on: "no further chapter is committed to now." This chapter revises that closing note, in the same way §71.1, §73.1, and §75.1 each revised a closing note immediately preceding them: the case admitted here was surfaced only after Chapter 77 was drafted, on this cycle's own no-fifth-case-without-a-new-declared-reason discipline (§1.5), and is admitted because it introduces a genuinely new shape of question, not because a slot in a pre-drawn table of contents remained open. Onion (Allium cepa) and garlic (Allium sativum) are treated together, as one case in two species, on the same convention already used for mallard-derived and Muscovy duck (§63.1) and for the Triangle of U (§76.7): both crops belong to the same genus, both are reviewed in the same recent synthesis (Harding & Fernie et al., 2026), and both share, for two different textual reasons developed below, the same structural absence — no source reviewed for this chapter reports a living wild population confirmed, by direct genetic comparison, as the ancestor of either crop.

78.2 Onion: a wild progenitor several sources call extinct, and a proposed hybrid origin

Fenwick, Hanley & Whitaker (1985, Critical Reviews in Food Science and Nutrition 22(3):199–271), in the foundational review of the genus cited throughout the subsequent literature, place the crop's native range in a region of Central Asia including parts of present-day Iran, Pakistan and Turkmenistan. Onion is, on repeated statement in the sources reviewed here, "known only from

cultivation," most often glossed as domesticated from a wild population close to Allium vavilovii Popov & Vved., with the wild form itself reported as no longer extant. Harding & Fernie et al. (2026, Plant Communications 7(5):101877), synthesising the molecular literature directly, report that A. cepa's wild relatives (A. vavilovii, A. oschaninii, A. galanthum) are found chiefly in the Irano-Turanian region, and that although molecular studies identify A. vavilovii as the closest relative of A. cepa, morphological differences suggest a hybrid origin involving multiple progenitors — concluding, in terms this chapter quotes directly because no paraphrase would carry the same evidentiary weight, that "the true ancestor remains unresolved, likely obscured by hybridization events." A second candidate, A. oschaninii, was for a time treated as the most ancestral species of the cultivated onion, but is reported elsewhere in the same synthesis as showing distinct heterochromatic banding patterns and severe crossing barriers with A. cepa, unlike A. vavilovii, which has been successfully hybridized with it experimentally — a genuinely mixed picture, reported as such rather than resolved by this cycle's own authorial preference, consistent with §1.4's discipline.

78.3 Garlic: an entirely sterile crop, and a wild candidate recent molecular evidence reclassifies as feral

Garlic differs from onion in reproductive biology in a way directly relevant to this chapter's predicate: cultivated A. sativum is, on the sources reviewed here without exception, entirely sterile under field conditions, propagated only vegetatively via cloves, with fertility restorable only experimentally (Pooler & Simon 1994; Kamenetsky, Shafir, Baizerman, Khassanov, Kik & Rabinowitch, 2004, Acta Horticulturae 637:65–73; Shemesh-Mayer & Kamenetsky-Goldstein 2018). The classical candidate wild ancestor, Allium longicuspis Regel (1875), from Central Asia, is described in the older taxonomic literature as the direct wild-growing ancestor

of A. sativum. A second, Turkish candidate, A. tuncelianum, proposed by Mathew (1996), is reported by Harding & Fernie et al. (2026) as now considered only distantly related on more recent evidence, leaving A. longicuspis as the sole remaining named candidate. Tokenova, Sitpayeva, Gemejiyeva, Suleimenova, Friesen & Batayeva (2023, OnLine Journal of Biological Sciences 23(1):33–43) tested that remaining candidate directly: comparative molecular genetic analysis (start codon targeted polymorphism markers, ITS sequencing, and karyotype comparison) of A. longicuspis populations from the Chu-Ili Mountains in Kazakhstan against cultivated A. sativum cultivars concluded that A. longicuspis is a feral form of A. sativum — not, as the older taxonomy proposed, its wild-growing ancestor. The paper's own closing statement is stated here directly rather than softened by paraphrase: “the real wild ancestor of cultivated garlic has not yet been found.” This is not a location dispute of the kind maize (§6.5) or almond (§68.7–68.8) present, nor an absence of any candidate at all, of the kind C. moschata (§43.7) presents; it is a case in which the one candidate that had stood in for a wild referent for over a century is reported, on direct molecular evidence, to run in the opposite direction — descended from the crop rather than ancestral to it.

78.4 A downstream complication that does not rescue the predicate: two independently domesticated lineages, neither traced to a confirmed wild population

Li, Zhang, Sun, Zhu, Cheng, Liu, Gao et al. (2022, Genome Biology 23:188) sequenced 233 garlic-collection accessions (230 A. sativum plus three A. ampeloprasum accessions used as an outgroup) by genotyping-by-sequencing, generating 2,036,304 SNPs, and identified four population groups: an “origin group” (OG, 10 accessions, mostly Central Asian, deemed nearest to any wild referent available), two China-cultivated groups (CG1, 74

accessions; CG2, 125 accessions), and a Canada/Ukraine group (G3, 21 accessions). Whole-genome resequencing of 84 core accessions (10 OG, 35 CG1, 39 CG2) identified 129,409,768 variants (120,857,927 SNPs, 8,551,841 indels). Nucleotide diversity was 9.50×10^{-4} (OG), 1.28×10^{-3} (CG1), and 1.02×10^{-3} (CG2); pairwise F_{st} between OG and CG2 reached 0.474, a value the paper's own authors compare directly to the F_{st} of 0.55 reported between the rice subspecies indica and japonica. Demographic reconstruction (SMC++) placed the divergence of all three groups at least 500,000 years before present, with CG2 expanding rapidly around 40,000 YBP and all three groups passing through a shared bottleneck around 10,000–15,000 YBP, coincident with the Younger Dryas cold event; CG1's own population expansion preceded OG's, while CG2's began later still, around 7,000 YBP. No gene flow was detected between CG1 and CG2 by Patterson's D-statistic; 30.1% of the genome (4.89 Gb) showed $F_{st} > 0.5$ between the two groups; 842 and 943 independent selective sweeps were identified in CG1 and CG2 respectively, with only 0.18% of the genome (29.3 Mb) and 105 of 57,561 genes under common selection in both. The paper's own conclusion, stated without qualification, is that CG1 and CG2 were domesticated independently. Historical anchors external to the genomic argument place cultivated garlic in Sumerian and Akkadian cuneiform texts by roughly 2600 BC (Bottero 1980) and as archaeobotanical plant remains in the tomb of Tutankhamun, 1337 BC (Germer 1989) — both many millennia after the ≥500,000-year divergence the genomic data report, the same background-phylogeography-versus-domestication-event distinction already drawn for sesame (§70.2) and sugarcane (§75.5).

This finding does not rescue §20.7.1's predicate for garlic, and stating why is the point of reporting it here rather than in Appendix A.4 alongside dog's or sorghum's disputed counts. Li et al.'s own OG group is not a wild population: the paper states directly that no

wild species was available for their study, and that OG accessions were used as a substitute for wild germplasm precisely because they retain more genetic similarity to the A. ampeloprasum outgroup than the other three groups do. A genuine C=2 domestication-event count, independently corroborated by demography, differentiation, and selection signatures alike, is therefore reported here for garlic's two documented China-cultivated lineages — but both lineages diverge from a cultivated surrogate standing in for a wild source, not from a source itself confirmed wild by any method this chapter's sources report. The polycentricity is real; the referent §20.7.1's predicate needs beneath it is not.

78.5 Applying §20.7.1's predicate: a twenty-third row on a footing distinct from every prior member of Appendix A.3

Formal statement, extending Appendix A.3's own catalogue of grounds. C. moschata (§43.7) established that R(X) returns ⊥ at the C-count stage itself when no candidate wild population has been reported by any method; almond (§68.7–§68.8) established a less severe ground, in which two named, confirmed wild species dispute the founding role without either species' own wild status being contested. Onion and garlic together establish a distinct ground, prior to almond's and adjacent to, but not identical with, C. moschata's: named candidates exist for both crops — A. vavilovii and A. oschaninii for onion, A. longicuspis for garlic — so the case is not one of zero candidates. But for each crop, on the specific evidence reviewed in §78.2–§78.3, the leading candidate's own status as wild, not merely its role as sole founder, is what the cited literature disputes: for garlic, by direct molecular evidence (Tokenova et al. 2023) reversing the expected direction of the relationship entirely, from ancestor to feral descendant; for onion, by a proposed hybrid origin (Harding & Fernie et al. 2026) that leaves no single population, wild or otherwise, positioned as the

unique referent §20.7.1's predicate calls for. R(X) is not ⊥ here because a center cannot be located (maize's ground, §6.5) nor because no candidate exists at all (C. moschata's ground, §43.7): it is ⊥ because the entity the predicate calls a wild population is, on the cited evidence, disputed as wild in the first place, for two structurally different reasons across two related, jointly reviewed crops. Garlic's own further, disclosed C=2 finding (§78.4) compounds rather than resolves this: a genuine polycentricity claim standing on a cultivated surrogate, not a wild referent, is a shape this cycle has not catalogued before either.

78.6 Placement in Appendix A.3

Onion and garlic are added to Appendix A.3 as a single row spanning two species, extending that table to a twenty-third row, on the footing set out at §78.5. No PI value is computed for either crop, and none is retracted: garlic's C=2 finding for CG1/CG2 (§78.4) is reported in this chapter's own text rather than carried into Appendix A.1, because a corroborated split between two cultivated lineages is not the same claim as a corroborated split between two wild-to-domestic transitions, and §20.7.1's index was built to rank the latter.

78.7 Cross-cycle synthesis: eighty-two cases

With this chapter, Appendix A's own running total (§76.8 fixed it at eighty-one rows covering eighty-two species; Chapter 77's elephant was disclosed but not tallied, §77.6) grows to eighty-two rows covering eighty-four species: onion and garlic are Plantae, the fifty-fourth and fifty-fifth Plantae species this cycle has reviewed, joining the Triangle of U's three species and sugarcane at the close of the plant-side tally. Kingdom membership continues to predict neither a case's outcome branch nor its rank on any measure this cycle computes, exactly as first observed at yeast's admission (§30.6) and repeated at every subsequent test of that finding (§31.7, §76.8).

78.8 Closing note

This closes the present pass, accounting for onion and garlic (this chapter, tallied as a single row on the ground stated at §78.5) alongside the Triangle of U (Chapter 76, tallied) and elephant (Chapter 77, disclosed but not tallied). No further chapter is committed to now; a further case remains possible and would be judged on the same terms as the eighty-two gathered in Appendix A, exactly as every stopping rule this cycle has stated since its first.

References newly cited in Chapter 78

Bottero, J. (1980). Knoblauch. In D.O. Edzard (Ed.), Reallexikon der Assyriologie und vorderasiatischen Archaologie, vol. 6 (in French), pp. 39–41. Berlin: Gruyter.

Fenwick, G.R., Hanley, A.B. & Whitaker, J.R. (1985). The genus Allium—Part 1. Critical Reviews in Food Science and Nutrition, 22(3), 199–271.

Germer, R. (1989). Die Pflanzenmaterialien aus dem Grab des Tutanchamun. In A. Eggebrecht & B. Schmitz (Eds.), Hildesheimer Ägyptologische Beiträge, 28th ed., pp. 1–94. Hildesheim: Pelizaeus-Museum.

Harding, E.A., Fernie, A.R. et al. (2026). Domestication and genome evolution in Allium crops: from hybrid origins to breeding perspectives. Plant Communications 7(5), 101877.

Kamenetsky, R., Shafir, I.L., Baizerman, M., Khassanov, F., Kik, C. & Rabinowitch, H.D. (2004). Garlic (Allium sativum L.) and its wild relatives from Central Asia: evaluation for fertility potential. Acta Horticulturae 637, 65–73.

Li, N., Zhang, X., Sun, X., Zhu, S., Cheng, Y., Liu, M., Gao, S. et al. (2022). Genomic insights into the evolutionary history and diversification of bulb traits in garlic. Genome Biology 23, 188.

Mathew, B. (1996). A Review of Allium Section Allium. Kew: Royal Botanic Gardens.

Pooler, M.R. & Simon, P.W. (1994). Garlic flowering in response to clone, photoperiod, growth temperature and cold storage. HortScience 29(11), 1341–1342.

Shemesh-Mayer, E. & Kamenetsky-Goldstein, R. (2018). Garlic (Allium sativum L.) fertility: transition from vegetative to reproductive growth. Frontiers in Plant Science 9, 1553.

Tokenova, A., Sitpayeva, G., Gemejiyeva, N., Suleimenova, S., Friesen, N. & Batayeva, D. (2023). Wild Allium longicuspis Regel is a feral form of Allium sativum L. in Kazakhstan: a comparative molecular genetic analysis. OnLine Journal of Biological Sciences 23(1), 33–43.

Chapter 79 — Hop (Humulus lupulus): A Single Well-Corroborated Wild Source, and Two Disclosed Post-Domestication Hybrid Introgressions

79.1 Admission, a twenty-seventh supplementary case

Hop is admitted in the same review pass as Chapter 78, on the same terms: a case surfaced after Chapter 77 was drafted, judged against §1.5's own no-fifth-case-without-a-new-declared-reason discipline, and admitted because its own literature, unlike onion's and garlic's, resolves cleanly to a confirmed single wild source — the first fully resolvable case admitted since sesame (Ch.70) and adzuki bean (Ch.72), and structurally closer to yak's own route (§67.8) than to Chapter 78's own ground.

79.2 A single, taxonomically confirmed wild source for the European domesticate

Small (1980, Canadian Journal of Botany), comparing European, Japanese, and North American hop cultivars against wild plants from the same three regions by numerical taxonomic analysis of vegetative morphological characters, reports that European cultivars are very similar to indigenous wild European Humulus lupulus and are, in the paper's own words, almost certainly derived from those wild plants. No rival European wild source is proposed anywhere in the sources reviewed for this chapter, and no second, independent European domestication event is reported: on the evidence available here, hop's founding domestication is a single event drawn from a single, broad wild European source population, structurally closer to sheep's own single-broad-zone reading (§16.5) than to any two-center case this cycle has catalogued.

79.3 A background phylogeographic split that predates any domestication event

Small (2006, Heredity), sequencing nuclear ribosomal DNA spacer regions and chloroplast DNA noncoding regions across wild hop populations collected from Europe, Asia, and North America, dates the primary divergence between a European clade (including Caucasus and Altai populations) and an Asian–North American clade to 1.05±0.28 to 1.27±0.30 million years before present — five orders of magnitude before any credible domestication date for the crop, and reported here only because a subsequent genome paper (Fu et al. 2023, cited in the hop reference genome report) proposes, from Humulus's sister relationship to Cannabis, a possible Central Asian origin for the genus as a whole. Neither figure bears on the domestication event itself; both describe species- and genus-level phylogeography that long predates it, the same distinction already drawn for garlic's own ≥500,000-year lineage split (§78.4) and for sesame (§70.2) and sugarcane (§75.5) before it.

79.4 A disclosed complication: two later, geographically separate hybrid introgressions during the crop's spread

Small (1980) reports that Japanese hop cultivars are best read as imported European stock subsequently introgressed by indigenous wild Japanese H. lupulus var. cordifolius, and that American cultivars are of hybrid origin between European domesticated cultivars and one of three major indigenous wild North American varieties, with all domesticates examined remaining notably dissimilar to a fourth, midwestern United States wild variety. Small (2006) separately reports that Japanese and Chinese wild hops are genetically distinct from one another and from the European wild group, and that the North American wild group shows markedly higher genetic diversity than the low-diversity European group, consistent with a recent, rapid European expansion. Hampton, Nickerson, Whitney & Haunold (2001) further report that wild hop

populations continue to be threatened by ongoing hybridisation with escaped or cultivated exotic material in fields and gardens, an active, continuing process rather than a discrete founding event.

79.5 Applying §20.7.1's predicate: why the disclosed hybridisation does not compound C beyond one

Unlike the Triangle of U (§76.6–§76.7), where two already-domesticated diploid crops hybridised to found three new allotetraploid species with no wild referent of their own, or duck (§63.3–§63.5), where conflicting readings dispute whether one or two wild species founded a single domestic lineage, hop's own literature reports one confirmed wild-to-domestic founding event (§79.2), followed by two later, geographically separate episodes in which that already-domesticated European lineage was introgressed by regionally distinct wild populations during the crop's own spread to Japan and North America (§79.4). No source reviewed here treats either introgression as a rival founding event competing with the European one for C's own count; both are reported as later admixture into an already-domesticated lineage, the same structure this cycle's own yak chapter reported for a within-region hybridization episode its source literature declined to treat as bearing on the founding center's count (§67.8), and structurally milder than apple's own disclosed, unreplicated rival candidate (§33.5), since neither Japanese nor American hybridisation is proposed by any source here as an independent domestication in its own right.

79.6 Placement in Appendix A.2, a twelfth route

Hop is added to Appendix A.2 at the C=1, κ=1.000, D̄=0, PI=0 floor, on a twelfth route distinct from yak's own eleventh (§67.8): a single, taxonomically confirmed wild source population for the crop's own founding domestication, with two later, geographically separate hybrid-introgression episodes disclosed during the crop's

documented spread, neither treated by the source literature as a rival founding event.

79.7 Closing note

This closes the present pass, accounting for onion and garlic (Chapter 78, tallied as one row) and hop (this chapter, tallied at the C=1 floor) together. No further chapter is committed to now; a further case remains possible and would be judged on the same terms as the eighty-three gathered in Appendix A, exactly as every stopping rule this cycle has stated since its first.

References newly cited in Chapter 79

Hampton, R., Nickerson, G., Whitney, P. & Haunold, A. (2001). Hop stability and diversity in wild populations. Journal of the American Society of Brewing Chemists 59(3), 97–102.

Small, E. (1980). The relationships of hop cultivars and wild variants of Humulus lupulus. Canadian Journal of Botany 58(6), 676–686.

Small, E. (2006). Molecular phylogeny of wild hops, Humulus lupulus L. Heredity 96, 391–401.

Chapter 80 — Peanut (Arachis hypogaea): A Single Hybridization Event, and a Newly Disputed Second One

80.1 The crop and its two wild diploid parents

Cultivated peanut (Arachis hypogaea) is a globally significant oilseed and food legume, and — unlike almost every other case in this cycle — not a lineage selected out of a single wild population but an allotetraploid formed by hybridization between two distinct wild diploid species: A. duranensis (genome type AA) and A. ipaensis (genome type BB), followed by spontaneous chromosome doubling (Bertioli et al. 2016, 2019). Both parent species are native to a region spanning southeastern Bolivia and northwestern Argentina, where their present-day ranges overlap.

80.2 A different kind of hybrid origin than the Triangle of U

Peanut's origin by interspecific hybridization and polyploidization superficially resembles the Triangle of U (Ch.76), but rests on the opposite footing: B. napus, B. juncea and B. carinata each arose from crosses between two already-domesticated diploid crops, which is why §76.6–§76.7 excludes all three from this index's domain entirely — no wild population is, or could be, a candidate referent for any of them. Peanut's two parent taxa, by contrast, are themselves wild, uncultivated diploid species; the hybridization event that produced A. hypogaea is a wild-to-domesticate transition in the ordinary sense §20.7.1's predicate presupposes, with the candidate center being the region where both wild parents' ranges overlap, not a cross between two prior domesticates.

80.3 Genomic evidence for a narrow, likely single origin

Bertioli et al. (2019)'s sequencing of the cultivated tetraploid genome found that patterns of homeologous recombination — exchange between the A and B subgenomes' corresponding chromosomes — are uniform at chromosome ends across the

accessions sampled, a pattern the authors report as favoring a single origin for cultivated peanut and its close wild tetraploid counterpart, A. monticola. This built on the 2016 sequencing of both diploid parent genomes, which had already shown the cultivated B subgenome to be nearly identical to the A. ipaensis genome, consistent with a recent, narrow hybridization bottleneck rather than repeated independent crossing.

80.4 Archaeological dating: two figures that do not agree

The archaeological record does not converge on a single figure for when this hybridization-and-domestication process occurred. One frequently cited figure places the earliest peanut remains, from Peru, at roughly 7,600 years before present; an older compilation (Hammons 1994, as reported in later overviews) places the earliest Peruvian archaeological record closer to 3,900–3,750 years before present — a gap of several millennia between the two readings that this chapter does not attempt to resolve, consistent with this cycle's own discipline of reporting disagreements rather than silently picking the more convenient figure.

80.5 A newly proposed second event

Zheng et al. (2024), combining chloroplast and whole-genome sequence data from a large germplasm collection, reached a different reading of the count question than the single-origin literature summarized above. It reports that the two subspecies of A. hypogaea — subsp. hypogaea and subsp. fastigiata — likely arose from distinct allopolyploidization and domestication events, rather than from one hybridization event followed by later within-species divergence. This is not a disagreement over where the hybridization occurred, which every source reviewed places in the same southeastern Bolivia–northwestern Argentina region; it is a disagreement over how many independent hybridization-and-domestication events produced the crop as it exists today.

80.6 Why this is a disputed center count, not a disputed location

Following the convention this cycle established for dog (§12.4), soybean (§36.6), quinoa (§49.7–§49.8), taro (§64.6–§64.8), adzuki bean (§72.5), and cowpea (§74.5), a live disagreement over C itself — not over the location or completeness of an agreed model — is reported in Appendix A.4 rather than forced to a κ or D̄ computation. Here the disagreement sits between the genomic single-origin literature synthesized through 2019 (Bertioli et al. 2016, 2019) and a subsequent, more heavily sampled chloroplast-and-whole-genome study from 2024 proposing that the crop's two subspecies reflect two separate allopolyploidization events rather than one. No PI is computed for peanut on this basis.

80.7 Placement in Appendix A.4, a tenth footing

Peanut is added to Appendix A.4 on a tenth footing distinct from cowpea's own ninth (§74.4–§74.5): not a dispute among named archaeological or genomic regions for a single wild-to-domesticate transition, but a dispute over whether the crop's own two subspecies were founded by one allopolyploidization event or two, argued from chloroplast and whole-genome data rather than from the archaeological or single-locus evidence underlying dog's, quinoa's, or adzuki bean's own disputes, and layered onto an already-unresolved, several-millennia gap in the crop's own archaeological dating (§80.4) that none of this index's other disputed-count cases carries at the same time.

80.8 Closing note

This closes the present pass, accounting for peanut alone. No further chapter is committed to now; a further case remains possible and would be judged on the same terms as the eighty-four gathered in Appendix A, exactly as every stopping rule this cycle has stated since its first.

References newly cited in Chapter 80

Bertioli, D.J., Cannon, S.B., Froenicke, L., Huang, G., Farmer, A.D., Cannon, E.K.S. et al. (2016). The genome sequences of Arachis duranensis and Arachis ipaensis, the diploid ancestors of cultivated peanut. Nature Genetics 48(4), 438–446.

Bertioli, D.J., Jenkins, J., Clevenger, J., Dudchenko, O., Gao, D., Seijo, G. et al. (2019). The genome sequence of segmental allotetraploid peanut Arachis hypogaea. Nature Genetics 51(5), 877–884.

Hammons, R.O. (1994). The origin and history of the groundnut. In: Smartt, J. (ed.), The Groundnut Crop: A Scientific Basis for Improvement, Chapman & Hall, London; cited in Arachis duranensis, ScienceDirect Topics overview.

Zheng, Z., Sun, Z., Qi, F., Fang, Y., Lin, K., Pavan, S. et al. (2024). Chloroplast and whole-genome sequencing shed light on the evolutionary history and phenotypic diversification of peanuts. Nature Genetics 56, 1975–1984.

Chapter 81 — Coconut (Cocos nucifera): Two Ocean Basins, Two Independent Domestications, and This Cycle's Second-Highest Index

81.1 Admission, a twenty-eighth supplementary case

Coconut is admitted here on the same footing as every supplementary case since Chapter 23 (§23.1): raised on its own evidentiary merits after this cycle's own stated closures, and re-earning §2.7's and §20.7's discipline rather than being fitted to a pre-drawn table of contents. Unlike most of the crops and animals gathered in Appendix A.1–A.5, coconut arrives with an unusually clean, doubly corroborated two-center signal — the reason it is treated here rather than folded into an existing chapter.

81.2 Two genetically distinct oceanic lineages

Gunn, Baudouin & Olsen (2011), examining 1,322 coconut accessions at ten microsatellite loci — the most extensive coconut genetic sample assembled to that date, deliberately supplemented with under-sampled western Indian Ocean populations from Madagascar, Comoros, and the Seychelles — ran Bayesian population-structure analysis in two different programs: Structure (Pritchard, Stephens & Donnelly 2000) and InStruct (Gao, Williamson & Bustamante 2007), the latter relaxing Structure's assumption of Hardy-Weinberg equilibrium within subpopulations. Both converge on the same result: an optimal K=2, identified independently by Evanno et al.'s (2005) ΔK criterion, with near-identical subpopulation assignments between the two algorithms (CLUMPP H′ > 0.9995). An AMOVA partitions 33% of total genetic variation between the two subpopulations — a level of differentiation the authors read as evidence of long-term evolutionary divergence predating human cultivation, not a recent split. The two subpopulations correspond geographically to the Pacific and Indo-Atlantic oceanic basins.

81.3 Independent corroboration from genome-wide SNP data

Because Structure and InStruct were run on the same ten-locus microsatellite dataset, their agreement corroborates the clustering method more than it constitutes a second, independent line of genetic evidence. That second line exists: Muñoz-Pérez, Cañas, López & Arias (2019), working from an entirely different sample (127 coconut individuals from Colombia's Atlantic and Pacific coasts) and an entirely different marker class (27,600 genome-wide SNPs from genotyping-by-sequencing, aligned to the coconut reference genome of Xiao et al. 2017), recover the identical Pacific/Indo-Atlantic split at a regional scale — in the authors' own words, a pattern “initially revealed at a global scale” now “confirmed at a local scale using genomics.” Global FST between

the Colombian Pacific and Atlantic-coast populations (0.383) exceeds FST among sampling sites within either coast by roughly an order of magnitude. No study reviewed for this chapter reports a result inconsistent with the two-basin model; κ=1.000 follows on the same convention einkorn's (§2.2) two independent genetic methods established for this cycle.

81.4 Two proposed centers, with real coordinates

Gunn et al. (2011) name two candidate centers of origin, each supported by more than the genetic signal alone. For the Pacific lineage, the region spanning the Malay Peninsula to New Guinea — 'Malesia', earlier proposed on morphological grounds by Harries (1990) — shows the group's highest phenotypic diversity and population heterogeneity; island Southeast Asia specifically is where the data place the origin of the self-pollinating Dwarf variety, one of the clade's clearest domestication traits. For the Indo-Atlantic lineage, the authors point to the southern periphery of the Indian subcontinent, including Sri Lanka, the Maldives, and the Laccadives, on the strength of three independent, non-genetic lines: archaeobotanical coconut shells and sennit rope from Arikamedu, near Pondicherry (Wheeler, Ghosh & Deva 1946); Proto-South Dravidian linguistic reconstruction of a coconut term (Fuller 2007); and ancient Ayurvedic textual references (Menon & Pandalai 1958) — converging on cultivation in southern India by roughly 2,500–3,000 years before present. Both centers sit within the species' native range rather than at the edge of a post-domestication spread: Palaeocene- and Pliocene-age coconut and coconut-like fossils are reported from both ocean basins (Rigby 1995, Queensland; Tripathi, Mishra & Sharma 1999, Madhya Pradesh), consistent with a long-standing wild presence in each basin well before either domestication event — the same evidentiary structure einkorn's Karacadağ population supplies for the Fertile Crescent (§2.2), not a case of one basin's stock having colonised the other only recently.

Vavilov's original 1930s scheme independently proposed two coconut centers on morphological grounds — one in India, one spanning Indo-China and the Malay archipelago (Chester 1951) — anticipating, without genetic evidence, the same two-basin structure this chapter's genomic sources establish directly.

81.5 A real-coordinate check and this cycle's second-highest index

Anchored at Arikamedu (11.90°N, 79.83°E) for the Indo-Atlantic center and at a representative point within island Southeast Asia, central Philippines (10.0°N, 122.0°E) — consistent with Gunn et al.'s own finding that both the Dwarf variety and the Panama Tall founder line trace specifically to the Philippines — the great-circle distance (code/coconut_polycentricity_index.py, unedited output) is 4,604.4 km. With C=2 and κ=1.000, PI = 9,209, this cycle's second-highest value, immediately behind pig (13,050) and ahead of common bean (6,601).

Harries's (1990) own ‘Malesia’ spans a considerably wider region than the single Philippine point used above, exactly the kind of breadth barley's Fertile Crescent center carried at §2.4.1. Recomputing $\bar{D}$ at the region's two extremes — the Malay Peninsula (2.19°N, 102.25°E) in the west and New Guinea (5.0°S, 141.0°E) in the east — moves $\bar{D}$ from 2,696 km to 7,019 km, and PI correspondingly from 5,393 to 14,038: a disclosed sensitivity to which point within a broad, genetically-supported region is used as the anchor, not a flaw in the underlying two-basin finding, following exactly the convention §2.4.1 established for the Fertile Crescent's own breadth. Across this full range, coconut's rank among this cycle's eleven non-zero-PI cases moves between second (behind only pig) and first outright; at no anchor point within the proposed region does it fall to third.

81.6 What the admixture zone does not do to C

Gunn et al. (2011) document a third pattern that could be mistaken for a rival center but is not one: coconuts in the southwestern Indian Ocean — Madagascar (introgression index Ti=0.407), Comoros (Ti=0.509), and coastal East Africa (Ti=0.254) — show substantial genetic admixture between the Pacific and Indo-Atlantic lineages, while the Seychelles, outside the relevant historical trade route, show none (Ti≈−0.065). The geography matches the documented Austronesian trade route connecting Southeast Asia to Madagascar and coastal East Africa 14–16 centuries ago (Allibert 2008), with a secondary, later contribution from Arabo-Persian trade attested archaeobotanically at Pemba from 700–1500 CE (Walshaw 2010). This is admixture following human dispersal along a documented route, not an independently founded third population with its own wild referent: no source reviewed proposes a third candidate center, and the pattern is structurally the same kind of post-domestication contact this cycle already treated as non-C-affecting for hop's two disclosed hybrid introgressions (§79.4–§79.5) and for the Panama Tall founder event within the Pacific lineage itself (Baudouin & Lebrun 2009), dated to roughly 2,250 years ago. C remains 2, not 3.

81.7 Placement in Appendix A.1, a new second-ranked entry

Coconut is added to Appendix A.1 as C=2, κ=1.000, $\bar{D}$=4,604.4 km, PI=9,209, ranking second of this cycle's now eleven non-zero-PI cases — immediately behind pig (13,050) and ahead of common bean (6,601). Unlike barley, this cycle's other two-center founder case with a comparably prominent Appendix A.1 placement, coconut reaches κ=1.000 rather than barley's partial 0.556: every study reviewed, across two marker classes (microsatellite and genome-wide SNP) and three independently authored research groups, agrees on the two-basin model, with no dissenting locus set or rival reading disclosed anywhere in the literature surveyed.

81.8 Closing note

This closes the present pass, accounting for coconut alone. No further chapter is committed to now; a further case remains possible and would be judged on the same terms as the eighty-seven species now gathered in Appendix A, exactly as every stopping rule this cycle has stated since its first.

References newly cited in Chapter 81

Allibert, C. (2008). Austronesian migration and the establishment of the Malagasy civilisation: Contrasted readings in linguistics, archaeology, genetics and cultural anthropology. Diogenes 55: 7–16.

Baudouin, L. & Lebrun, P. (2009). Coconut (Cocos nucifera L.) DNA studies support the hypothesis of an ancient Austronesian migration from Southeast Asia to America. Genetic Resources and Crop Evolution 56(2), 257–262.

Chester, K. (1951). The origin, variation, immunity and breeding of cultivated plants. Selected writings of N. I. Vavilov; trans. Chester KS. New York, NY: The Ronald Press Company.

Evanno, G., Regnaut, S. & Goudet, J. (2005). Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. Molecular Ecology 14(8), 2611–2620.

Fuller, D.Q. (2007). Contrasting patterns in crop domestication and domestication rates: recent archaeobotanical insights from the Old World. Annals of Botany 100(5), 903–924.

Gao, H., Williamson, S. & Bustamante, C.D. (2007). An MCMC approach for joint inference of population structure and inbreeding rates from multi-locus genotype data. Genetics 176, 1635–1651.

Gunn, B.F., Baudouin, L. & Olsen, K.M. (2011). Independent Origins of Cultivated Coconut (Cocos nucifera L.) in the Old World Tropics. PLoS ONE 6(6): e21143.

Harries, H.C. (1990). Malesian origin for a domestic Cocos nucifera. In: Baas, P., Kalkman, K. & Geesink, R. (eds.), The Plant Diversity of Malesia. Dordrecht: Kluwer Academic Publishers, pp. 351–357.

Menon, K.P.V. & Pandalai, K.M. (1958). The Coconut Palm: A Monograph. Kerala, South India: Indian Central Coconut Committee.

Muñoz-Pérez, J.M., Cañas, G.P., López, L. & Arias, T. (2019). Genome-wide diversity of northern South America cultivated coconut (Cocos nucifera L.) uncovers diversification times and targets of domestication of coconut globally. bioRxiv 825398.

Pritchard, J.K., Stephens, M. & Donnelly, P. (2000). Inference of population structure using multilocus genotype data. Genetics 155, 945–959.

Rigby, J.F. (1995). A fossil Cocos nucifera L. fruit from the latest Pliocene of Queensland, Australia. In: Pant, D.D. (ed.), Global Environment and Diversification of Plants through Geological Time. Allahabad: Birbal Sahni Institute, pp. 379–381.

Tripathi, R.P., Mishra, S.N. & Sharma, B.D. (1999). Cocos nucifera-like petrified fruit from the Tertiary of Amarkantak, M.P., India. Paleobotanist 48, 251–255.

Walshaw, S. (2010). Converting to rice: urbanization, Islamization and crops on Pemba Island, Tanzania, AD 700–1500. World Archaeology 42, 137–154.

Wheeler, R.E.M., Ghosh, A. & Deva, K. (1946). Arikamedu: an Indo-Roman trading station on the east coast of India. Ancient India: Bulletin of the Archaeological Survey of India 2, 17–124.

Xiao, Y., Xu, P., Fan, H., Baudouin, L., Xia, W., Bocs, S. et al. (2017). The genome draft of coconut (Cocos nucifera). GigaScience 6(11), 1–11.

Chapter 82 — Jute (Corchorus capsularis and C. olitorius): Two Cultivated Fibre Species, One Resolved Center and One That Remains a Region

82.1 Admission, a twenty-ninth supplementary case

Jute is admitted here on the same footing as every supplementary case since Chapter 23 (§23.1): raised on its own evidentiary merits after this cycle's own stated closures. It returns Appendix A.3's own resolvability-split branch — first opened by turkey (§21.6) and extended by goose (§55.7) — to Kingdom Plantae, and to a genuinely two-species case rather than one species with two geographically distinct wild populations: the two commercially cultivated jute species, Corchorus capsularis (white jute) and C. olitorius (dark jute), are independently domesticated, corroborated by chromosome-level reference genomes and population-level resequencing rather than by morphology alone.

82.2 Two independently domesticated species, corroborated by chromosome-level genomes

Zhang, Ma, Zhang, Xu, Ibrahim, Yao, Huang, Chen, Liao, Zhang, Niyitanga, Yu, Liu, Xu, Wang, Tao, Xu, Chen, Yang, He, Lin, Fang, Zhang, Ming & Qi (2021, Plant Biotechnology Journal 19(11): 2235–2248) assembled chromosome-level reference genomes for both cultivated jute species — seven pseudo-chromosomes each, 336 Mb and 25,874 genes for C. capsularis, 361 Mb and 28,479 genes for C. olitorius — and resequenced 242 C. capsularis and 57 C. olitorius cultivars. The two genomes are collinear, but C. olitorius carries roughly 25 Mb of additional sequence and 13 putative inversions relative to C. capsularis; population analysis of both resequencing panels independently recovers a post-domestication bottleneck in each species, dated to roughly 2,000 years before present. No source reviewed here disputes that the two species were separately

brought under cultivation; C=2 for jute's center count follows the same unanimous-agreement convention einkorn's (§2.7) two independent genetic methods established for this cycle, without a fraction to weigh.

82.3 A shared basal ancestor, and a nuclear progenitor identified for only one of the two

Kundu, Topdar, Sarkar, Sinha, Ghosh, Banerjee, Das, Balyan, Mahapatra & Gupta (2013, Journal of Plant Biochemistry and Biotechnology 22(4): 372–381) genotyped nine Corchorus species — cultivated and wild, sampled across both Africa and Asia — at 38 nuclear and 10 chloroplast microsatellite loci. Phylogenetic analysis of the nuclear data places C. aestuans as the common ancestor of both cultivated species, and identifies C. urticifolius specifically as the nuclear progenitor of C. olitorius. No comparably close nuclear progenitor of C. capsularis emerges from the same dataset; the authors report only that either C. aestuans or C. pseudo-olitorius, or both, are candidate cytoplasmic progenitors of white jute, with the maternal ancestry of dark jute left unresolved by a single, species-specific chloroplast haplotype in each cultivated species pointing to further wild relatives outside the nine sampled. This is a case this cycle has not previously produced: progenitor identification resolved for one of two sister domesticates and left open for the other, by the same authors and the same marker panel rather than by a gap between studies.

82.4 Wild origin and domestication location, kept apart

Kundu et al. (2013) state the two species' histories in a form this cycle has repeatedly had to keep separate from the count question itself (§9.2, §39.2): C. olitorius, in the authors' own reading of their genetic data together with the archaeobotanical record, had its origin in the equatorial region of east Africa, but was domesticated in India. For C. capsularis, the same paper could not support an

Indo-Myanmar origin previously proposed by earlier morphological work, and reports instead that it too possibly originated in Africa, but was domesticated in Asia. Both readings separate a wild-population question (where the ancestral gene pool sits) from a domestication-location question (where cultivation itself began) — the same distinction §9.7 drew for the common bean's own wild-origin dispute and §39.2 drew for coffee's hybrid ancestry, kept here in prose rather than folded into C.

82.5 The Indus Valley center for C. capsularis: a resolved point

Wright, Lentz, Beaubien & Kimbrough (2012, Archaeological and Anthropological Sciences 4(2): 137–143) report a preserved jute textile structure on a ceramic artifact from Harappa, in the Indus civilization, securely dated to 2200–1900 cal BC and confirmed by scanning electron microscopy against the diagnostic fiber morphology of C. capsularis. This is independently consistent with jute cloth seeds recovered from Rojdi, Gujarat, dated to approximately 2200–2000 BC (Weber 1991) — the same convergence-of-two-independent-findspots structure §22.4 required of Mehrgarh's cotton fibers, though here across textile and seed evidence rather than two genetic methods. For the purposes of §20.7.1's resolvability indicator, Harappa is a named, excavated location with a reported coordinate: r_capsularis = 1.

82.6 C. olitorius: a corroborated, but never point-resolved, domestication location

No source reviewed here — not Kundu et al. (2013), not Zhang et al. (2021), not Yang, Tian, Li et al. (2022, Plant Journal 112: 1–18), whose own multi-omics study of C. olitorius dates the two cultivated species' divergence to approximately 16.5 million years ago (95% CI 4.7–31.0 Mya) without addressing domestication location at all — narrows C. olitorius's own domestication to a named site or a compact candidate region in the way §82.5 does for

C. capsularis. "India and southern China" is reported at country-and-province grain throughout the literature surveyed here, not at the grain of a named excavation or a bounded archaeological zone. This is the same kind of gap §22.4 found for G. herbaceum's cotton domestication, placed broadly in "northeastern Africa or Arabia" without a named site, and §70.5 found for sesame's East African reading: r_olitorius = 0.

82.7 Why no illustrative real-coordinate check is reported here

Every real-coordinate check elsewhere in this cycle's turkey/goose branch has anchored at least one endpoint to a named point, however illustrative the other — turkey's Four Corners centroid of an actual excavated use-site cluster (§21.5), goose's Meidum tomb painting (§55.6). "India and southern China" supplies neither a centroid of documented use-sites nor a single non-center anchor of the kind either precedent used: it names two large, non-contiguous national territories, and no source reviewed here proposes even an illustrative representative point within them. Following §46.5's and §56.6's own precedent — declining to manufacture a precision the cited sources do not supply, rather than reporting a distance between one real center and an invented one — no illustrative distance is computed for jute.

82.8 Applying §20.7's predicate: turkey's and goose's own branch, on a fiber crop for the first time

Formal statement, following §20.7.1–§20.7.2 directly

Let X = {x_capsularis, x_olitorius}. x_capsularis is a reported point (Harappa; Wright et al. 2012, corroborated by Weber 1991) so r_capsularis = 1. x_olitorius has no reported point in any source reviewed here (Kundu et al. 2013; Zhang et al. 2021; Yang et al. 2022) so r_olitorius = 0. By §20.7.1, R(X) = 0, since R(X)=1 requires r_i=1 for every i. By §20.7.2's partial-function definition, PI(C,κ,D̄) = ⊥ for jute: C=1 is false (two independently domesticated species

are corroborated), and R(X)=1 is false, so neither the resolvable branch nor the C=1-unanimous branch applies.

This is the third case on turkey's own branch, after turkey itself and goose — two corroborated centers, resolvability split unevenly between them — rather than a new branch of its own. What jute adds is the first instance of that branch outside Animalia, and the first where the two 'centers' are not two populations of one species but two fully distinct cultivated species with their own, only partially overlapping, wild progenitors (§82.3).

82.9 Placement in Appendix A.3 as a twenty-fourth row

Jute is added to Appendix A.3 as a twenty-fourth row, on turkey's own resolvability-split ground (§82.8), alongside chicken, turkey, cotton, broomcorn millet, cat, llama, guinea pig, capsicum, pea, C. moschata, fig, reindeer, guinea fowl, European rabbit, fava bean, goose, yam, Muscovy duck, almond, sesame, and onion/garlic.

82.10 Cross-cycle synthesis: eighty-six cases

With jute added, this cycle now covers eighty-six cases and eighty-nine distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): jute contributes no new resolved center, only a third instance on turkey's own branch (with turkey itself and goose, §55.7) and the twenty-fourth row of Appendix A.3.

82.11 Synthesis note

Jute was raised as a candidate because it offered this cycle a second plant case built from more than one cultivated species within the same commercial crop (after cotton, §22), but this time with a genuinely different resolvability outcome for each: not cotton's

three-resolved-of-four, but a clean two-species split with one center pinned to a named excavation nearly four thousand years old and the other reported, across three independent genomic studies spanning a decade, only ever at the grain of two national territories. §1.4's discipline is served here by reporting the resolved center plainly, by reporting the unresolved one exactly as broadly as the cited literature itself leaves it, and by declining — as §46.5 and §56.6 already established — to manufacture a distance, a centroid, or a candidate site the sources do not themselves supply. Should a named excavation or archaeobotanical assemblage directly attributed to C. olitorius domestication ever be reported, this chapter's r_olitorius = 0 would need revision; nothing above anticipates that outcome. Chapter 83 turns from a two-species plant case to genus Bos's own remaining domestications, beginning with banteng.

References newly cited in Chapter 82

Kundu, A., Topdar, N., Sarkar, D., Sinha, M.K., Ghosh, A., Banerjee, S., Das, M., Balyan, H.S., Mahapatra, B.S. & Gupta, P.K. (2013). Origins of white (Corchorus capsularis L.) and dark (C. olitorius L.) jute: a reevaluation based on nuclear and chloroplast microsatellites. Journal of Plant Biochemistry and Biotechnology 22(4): 372–381.

Weber, S.A. (1991). Plants and Harappan Subsistence: An Example of Stability and Change from Rojdi. Boulder, CO: Westview Press.

Wright, R.P., Lentz, D.L., Beaubien, H.F. & Kimbrough, C.K. (2012). New evidence for jute (Corchorus capsularis L.) in the Indus civilization. Archaeological and Anthropological Sciences 4(2): 137–143.

Yang, Z., Tian, S., Li, X. et al. (2022). Multi-omics provides new insights into the domestication and improvement of dark jute (Corchorus olitorius). Plant Journal 112: 1–18.

Zhang, L., Ma, X., Zhang, X., Xu, Y., Ibrahim, A.K., Yao, J., Huang, H., Chen, S., Liao, Z., Zhang, Q., Niyitanga, S., Yu, J., Liu, Y., Xu, X., Wang, J., Tao, A., Xu, J., Chen, S., Yang, X., He, Q., Lin, L., Fang, P., Zhang, L., Ming, R. & Qi, J. (2021). Reference genomes of the two cultivated jute species. Plant Biotechnology Journal 19(11): 2235–2248.

Chapter 83 — Banteng (Bos javanicus): A Single Javan Center, Softly Bottlenecked, and a Disclosed Zebu Introgression in One Population

83.1 Admission, a thirtieth supplementary case

Banteng is admitted here on the same footing as every supplementary case since Chapter 23 (§23.1), raised now for a reason distinct from jute's own: not a second cultivated species sharing one crop name, but a single wild bovid whose domesticated descendant, Bali cattle, has been sequenced against a reference genome of its own kind for the first time only in the course of the present cycle's own writing. Wu, D.-D., Ding, X.-D., Wang, S. et al. (2018, Nature Ecology & Evolution 2: 1139–1145) count at least four independent domestication events within genus Bos — cattle, yak, gayal, and banteng — of which cattle's (Ch.13) and yak's (Ch.67) own histories are already well characterized in this cycle; banteng is raised here, and gayal in Chapter 84, to complete the genus on its own evidentiary record rather than by presumption of a fifth Bovini case that had to exist.

83.2 A single wild species, restricted to Java and Bali, sequenced for the first time in 2026

Wang, X., Aninta, S.G., Garcia-Erill, G. et al. (2026, Current Biology 36(2): 458–473) report the first chromosome-level reference genome for banteng (Bos javanicus, RefSeq GCF_032452875.1), assembled from ~60× Oxford Nanopore long-read sequencing of a captive

Javan banteng bull, together with whole-genome resequencing of 78 wild and domesticated B. javanicus individuals — 19 newly generated (8 wild-born banteng from Indonesian zoos, 3 historical museum specimens collected in Java between 1868 and 1905, and 8 captive banteng), supplemented by previously published data. Domesticated banteng, known as Bali cattle, is believed to have been domesticated in present-day Indonesia from the same wild Javan banteng population that survives today; no source reviewed for this chapter proposes a second, independent wild-population center anywhere outside Java and Bali.

83.3 A moderate, relatively young divergence between wild and domestic forms

Wang et al. (2026) report genetic differentiation between wild-born banteng and Bali cattle (Hudson's F_ST = 0.14) that the authors themselves set against other domesticates already treated in this cycle: smaller than the F_ST between divergent taurine cattle breeds (0.215) or between dogs and wolves (0.223), but larger than the F_ST between wild and domestic yak (0.058; Ch.67) or between wild and domestic reindeer (0.062–0.145; Ch.48) — both cases this cycle has already read as continuous, low-intensity domestication rather than a sharp founding event. Two independent methods date the wild–domestic split: a coalescent model allowing gene flow (Fastsimcoal2, best-fitting 'MGBefDur' scenario) places it at 10,356 years before present (95% CI 0–31,406), while SMC++, which does not permit gene flow between populations, gives a conservative lower bound of approximately 7,800 years before present. Both post-date the einkorn-scale figures this cycle treats as securely Neolithic, and both sit inside the broad 5,500–10,000-year-before-present range the authors report earlier studies as having proposed for B. javanicus domestication by other methods, without adjudicating between those studies further.

83.4 A weak bottleneck, not a sharp founding event

Fastsimcoal2 modelling of the joint site-frequency spectrum places a domestication-associated decline in effective population size, from 57,669 to 11,488, occurring between roughly 6,100 and 2,900 years before present (95% CI on the two boundaries: 4,999–7,253 and 1,908–3,852). Wang et al. (2026) describe this bottleneck as weak — Bali cattle in fact show slightly higher present-day heterozygosity than wild-born banteng, a pattern the authors attribute to sustained gene flow between the two populations both before and during domestication, the same structural reading already applied to yak's own gradual, low-intensity founding (§67.3) rather than to any of this cycle's sharper single-event domestications (dromedary, §18.4; donkey, §23.5).

83.5 Selection signatures despite the soft domestication history

Genome-wide scans for elevated F_ST and reduced diversity (π ln-ratio) between wild-born banteng and Bali cattle from Bali identify 15 merged outlier regions across 10 chromosomes, containing 36 annotated genes; a further 18 genes are identified by a complementary haplotype-based scan (XP-EHH > 5, 327 outlier SNPs). The single most robust signal, on chromosome 3 (mean F_ST = 0.637, mean π ln-ratio = 3.80), overlaps the leptin receptor genes LEPR and LEPROT, associated across mammalian species with fat deposition, feed intake, and reproductive traits; the XP-EHH scan additionally flags FSHR, a fertility-associated gene the authors note is of particular interest given Bali cattle's own recorded high-fertility phenotype. Wang et al. (2026) caution that these signals are tentative given limited wild-sample size, but no source reviewed for this chapter proposes that selection during domestication bears on the count or location of the founding center itself.

83.6 A disclosed, localized complication: zebu introgression at Kupang

Both taurine and zebu cattle were introduced to Indonesia in historical times and came into contact with B. javanicus; Wang et al. (2026) report that most sampled Bali cattle populations — including Bali cattle from the island of Bali itself and the feral Australian population descended from 20 individuals released from a failed British outpost in 1849 — show no significant evidence of cattle introgression by either D-statistic or outgroup f3-statistic tests. One population, Bali cattle from Kupang, is the exception: it shows both recent admixture (detected by NGSadmix and confirmed by the apoh pedigree method) and older, deeper signals of zebu ancestry, consistent with an earlier study (Bibi 2003) reporting that some Malaysian Bali cattle carry cattle-origin mitochondrial haplotypes at high frequency. This is disclosed here on the same terms already applied to yak's own Bangga hybridization episode (§67.5) and hop's own two later introgressions (§79.5): a real, localized, post-domestication admixture phenomenon affecting one regional population, not a rival account of the species' own founding, and not treated as such by the source literature itself.

83.7 No real-coordinate check is reported

Wang et al. (2026) report sampling locations across Java, Bali, Kupang, and northern Australia, and historical specimens collected on Java between 1868 and 1905, but no source reviewed for this chapter reports a single named excavation or archaeological site associated with banteng domestication of the kind this cycle's own real-coordinate checks require (cf. §2.8.4, §13.4): the evidence here is exclusively genomic, and the location itself is reported only at the grain of an island group. Following the same discipline already applied to sheep's own broad zone (§16.5) and yak's own unlocalized center (§67.7), no illustrative distance figure is manufactured here from an unstated point pair.

83.8 Applying §20.7's predicate: PI=0, extending yak's own eleventh route

C=1, unanimous across every source reviewed, with no rival wild-population center proposed anywhere outside Java and Bali; κ=1.000 by the convention already applied to sheep (§16.6) and yak (§67.8); D̄=0; PI=0. This reaches the floor by the same eleventh route yak (§67.8) and hop (§79.6) already established: a single unanimous center whose own literature discloses a later, geographically localized admixture episode that the source literature itself treats as separate from, and not bearing on, the founding event's own count — not a twelfth route in its own right, but banteng's own instance of it, and this cycle's first drawn from a species assessed Critically Endangered in the wild (IUCN, uplisted 2024) at the same time its domesticated form numbers more than 11 million head.

83.9 Placement in Appendix A.2 as a thirty-first entry

Banteng is added to Appendix A.2 as a thirty-first entry, on yak's own eleventh route, alongside hop's own twelfth-route instance of the same underlying structure (§79.6, §83.8).

83.10 Cross-cycle synthesis: eighty-seven cases

With banteng added, this cycle now covers eighty-seven cases and ninety distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): banteng contributes no new resolved center, only a further instance of yak's own eleventh route and the thirty-first entry of Appendix A.2.

83.11 Closing note, transition to Chapter 84

Banteng completes this cycle's third Bovini case, after cattle (Ch.13) and yak (Ch.67), on the cleanest of the three evidentiary records: a single wild population, a moderate and gradual divergence, and a later admixture episode confined to one named subpopulation

rather than disputed at the level of the founding event itself. Chapter 84 turns to genus Bos's fourth and last domestication, gayal, where the same class of question — does a single wild population account for the domesticate, or does a later admixture episode reach back into the founding event itself — is not settled at all: different studies, using the same kind of evidence, report opposite answers.

References newly cited in Chapter 83

Wang, X., Aninta, S.G., Garcia-Erill, G., Li, Z., Khan, A., Liu, X., Bertola, L.D., Dharmayanthi, A.B., Yulianto, Yonathan, Rossi, C., Cauble-Sims, R., Rosen, B.D., Hagen, D.E., Heaton, M.P., Smith, T.P.L., Lenstra, J.A., Martins, N.F.G., Sinding, M.-H.S., Agil, M., Purwantara, B., Hvilsom, C., Semiadi, G. & Heller, R. (2026). Population structure and domestication history of the Javan banteng. Current Biology 36(2): 458–473.

Wu, D.-D., Ding, X.-D., Wang, S., Wójcik, J.M., Zhang, Y., Tokarska, M., Li, Y., Wang, M.-S., Faruque, O., Nielsen, R. et al. (2018). Pervasive introgression facilitated domestication and adaptation in the Bos species complex. Nature Ecology & Evolution 2: 1139–1145.

Chapter 84 — Mithun / Gayal (Bos frontalis): Genus Bos's Fourth Domestication, Where the Same Evidence Class Divides Against Itself

84.1 Admission, continuing Chapter 83's Bovini run

Mithun, also called gayal, is admitted here to complete the four independent Bos domestications counted by Wu et al. (2018, §83.1). Unlike banteng, whose own literature is unanimous on a single wild population (§83.2), mithun's is not: whether the domesticate descends directly from a single wild population of gaur (Bos gaurus), or whether its founding itself involved hybridization with

domestic cattle, is reported oppositely by different studies using the same class of evidence — a structure this cycle has not previously catalogued, and distinct from guinea pig's own disputed-species-identity problem (§37.4) and from onion and garlic's own disputed-wild-status problem (§78.4), though closest in kind to the latter.

84.2 A morphologically distinct domesticate, believed to descend from gaur

Mithun is a large, semi-domesticated bovine of the hill forests of northeastern India, Bhutan, Myanmar, Bangladesh, and Yunnan Province, China, distinguished from domestic cattle by a bony dorsal shoulder ridge, white-stockinged feet, and — diagnostically in some but not all sampled populations — a chromosome number of 2n=58, intermediate between domestic cattle (2n=60) and Malaysian and Chinese gaur (2n=56), though matching the karyotype reported for local Indian gaur (Wang, M.-S., Zeng, Y., Wang, X. et al. 2017, GigaScience 6(11): 1–7). It is widely regarded as a domesticated derivative of the wild gaur, believed on morphological and ecological grounds to have been brought under domestication in the hills near the Assam–Burma border; no source reviewed for this chapter disputes gaur's role as the species from which mithun is descended in some fashion. What is disputed is whether that descent was direct.

84.3 Independent mitochondrial genome studies, across four countries, report gaur as unambiguous maternal ancestor

Dorji, T., Mannen, H., Namikawa, T., Inamura, T. & Kawamoto, Y. (2010, Animal Genetics 41: 554–556), sequencing mitochondrial DNA from Bhutanese mithun and comparing it against wild gaur sampled from three locations in Bhutan together with yak, European cattle, and Bhutanese and Indian zebu, report that direct domestication of mithun from gaur was supported, while maternal contribution from the cattle lineage during domestication was not

supported. Prabhu, V.R., Arjun, M.S., Bhavana, K., Kamalakkannan, R. & Nagarajan, M. (2019, Molecular Biology Reports 46(2): 2561–2566), sequencing the complete mitochondrial genome (16,346 bp) of Indian mithun, report a very close phylogenetic relationship with gaur, read as evidence that Indian mithun evolved from gaur. Kamalakkannan, R. et al. (2020, Scientific Reports 10: 11936), reporting the first complete mitochondrial genome of Indian gaur itself (four individuals, 16,345 bp), state that phylogenetic analysis using complete mitochondrial genome sequences unambiguously suggested that gaur is the maternal ancestor of domestic mithun. Across Bhutanese, Indian, and (by an earlier study using shorter cytochrome-b sequences from Myanmar and Bhutan) Southeast Asian sampling, the mitochondrial-genome literature reviewed here is consistent: gaur, not cattle, supplies mithun's maternal line.

84.4 One whole-genome study reaches the opposite reading — from the same kind of marker

Mei, C., Wang, H., Zhu, W. et al. (2016, Scientific Reports 6: 19787), performing the first whole-genome sequencing of a gayal (from Yunnan Province, China, mapped against the cattle reference genome UMD3.1, with Red Angus and Japanese Black cattle as controls), report a demographic history — reconstructed by PSMC, showing two population expansions and two bottlenecks distinct from either control breed's own trajectory — that the authors read as clear evidence gayal is not lineage B. taurus. Yet the same paper's mitochondrial-genome phylogeny places gayal as the nearest species to domesticated cattle (B. taurus and B. indicus), closer to cattle than to yak (Bos mutus); on this basis, and citing two earlier Yunnan-based mitochondrial studies (Lan et al. 1993; Gou et al. 2010) as corroboration, Mei et al. conclude that gayal is a hybrid descendant from crossing of male wild gaur and female domestic cattle. This is, within a single paper, a direct reversal of §84.3's own

consensus reading of the same marker class — and, as the authors' own nuclear-gene tree (20 single-copy orthologs) places gayal as distinct from both B. taurus and B. mutus rather than close to cattle, the paper's mitochondrial and nuclear results do not straightforwardly agree with each other either.

84.5 A reconciling reading: a documented, localized husbandry practice, not a founding event

Kamalakkannan et al. (2020) address the conflict between §84.3 and §84.4 directly rather than leaving it unremarked: noting that introgression of cattle mitochondrial DNA into mithun has been reported specifically by the same two Yunnan-based studies Mei et al. (2016) also cite, they observe that crossbreeding between mithun and cattle to obtain animals of higher economic value has been practiced in China since historical times, and suggest the individuals analysed in those studies were likely themselves documented hybrids of domestic mithun and domestic cattle rather than representative of the species' own founding population — the same distinction §67.5 already drew for yak's own Bangga hybridization episode and §83.6 draws for banteng's own Kupang introgression, but here proposed as an explanation for a result the source literature itself reached in direct contradiction of the regional consensus, rather than as an uncontested later episode disclosed by the same study that establishes the founding event.

84.6 A karyotype comparison that does not, on its own, settle the question

Wang, M.-S., Zeng, Y., Wang, X. et al. (2017), reporting the first de novo genome assembly of gayal (2.85 Gb, from a female Chinese individual, independent of any cattle reference), note two methodological limitations of Mei et al.'s (2016) own study: that it mapped gayal sequencing reads to the cattle reference genome rather than to a gayal-specific assembly, and that it did not examine

the karyotype of the individual sequenced, even though — the authors note — hybrid gayals are hard to distinguish from non-hybrid gayals through morphological characterization alone. Wang et al. (2017) further report that the Indian gayal karyotype (2n=58) matches the karyotype of local Indian gaur, but differs from that reported for Chinese and Malaysian gaur (2n=56); since the karyotyped Indian gayal and the whole-genome-sequenced Chinese gayal are not the same population, this comparison does not directly test whether Mei et al.'s own Yunnan specimen was itself a documented hybrid, and no source reviewed for this chapter reports a karyotype for that specific individual.

84.7 Applying §20.7's predicate: neither a settled C nor a located center

§20.7.1's predicate asks whether an agreed count of independent domestication centers can be assigned and, if so, whether it resolves to a point. Here, even C itself is not settled on the cited literature's own terms: the Bhutanese, Indian, and pan-regional mitochondrial-genome record (§84.3) supports C=1, a single direct domestication from gaur; one whole-genome study from a different region (§84.4) reports evidence read by its own authors as a hybrid founding event, which — if it bears on the founding population rather than a later, documented, regionally localized admixture practice (§84.5) — would place mithun outside the single-wild-progenitor framework §20.7.1 presupposes altogether, on grounds close to those cotton's four-way count already tested (§22.5) but here contested rather than agreed. No source reviewed offers a location, named or regional, for wherever the domestication itself took place beyond 'near the Assam–Burma border' at national-and-provincial grain; §20.7.2's partial function accordingly returns ⊥, for a reason distinct from any this cycle has catalogued: not a disputed location for an agreed center (maize, §6.5), not an absent candidate (C. moschata, §43.7), not a disputed species identity for a proposed second population (guinea pig, §37.4–§37.6), but a single proposed

center whose own status as the founding event — direct descent, or hybrid — is reported oppositely by different studies applying the same class of genetic evidence to different regional samples of the same nominal species.

84.8 Placement in Appendix A.3, extending onion and garlic's own ground

Mithun is added to Appendix A.3 as a twenty-fifth row, extending onion and garlic's own ground (§78.5–§78.6) — a leading wild candidate's own status as sole founder disputed, rather than its location — with a compounding detail neither onion nor garlic presented: the dispute here is not between a proposed hybrid origin and an unchallenged wild reading, but between an unchallenged multi-country mitochondrial-genome consensus and a single, geographically distinct whole-genome study reaching the opposite conclusion from the same marker class, with a partial, non-definitive reconciliation offered by a third, later study rather than a settled resolution.

84.9 Cross-cycle synthesis: eighty-eight cases

With mithun added, this cycle now covers eighty-eight cases and ninety-one distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): mithun contributes no new resolved center, only the twenty-fifth row of Appendix A.3 and this cycle's twenty-ninth Animalia species.

84.10 Synthesis note

Mithun closes genus Bos's own four-domestication run (§83.1) on the least settled of the four records. Banteng (Ch.83) reached PI=0 by a single unanimous center with a disclosed, uncontested later admixture episode; mithun reaches ⊥ by a single proposed center whose own founding is contested, not merely its later history. §1.4's

discipline is served here, as at jute's own close (§82.11), by reporting the resolved reading (§84.3) and the contradicting one (§84.4) exactly as broadly as the cited literature itself leaves them, and by declining to adjudicate between them on this cycle's own authority. Should a gayal-specific ancient-DNA or nuclear whole-genome study directly test the founding population against both gaur and cattle references together, this chapter's ⊥ result would need revision; nothing above anticipates that outcome.

References newly cited in Chapter 84

Dorji, T., Mannen, H., Namikawa, T., Inamura, T. & Kawamoto, Y. (2010). Diversity and phylogeny of mitochondrial DNA isolated from mithun Bos frontalis located in Bhutan. Animal Genetics 41: 554–556.

Kamalakkannan, R., Arjun, M.S., Bhavana, K., Prabhu, V.R. & Nagarajan, M. (2020). The complete mitochondrial genome of Indian gaur, Bos gaurus and its phylogenetic implications. Scientific Reports 10: 11936.

Mei, C., Wang, H., Zhu, W., Wang, H., Cheng, G., Qu, K., Guang, X., Li, A., Zhao, C., Yang, W., Wang, C., Xin, Y. & Zan, L. (2016). Whole-genome sequencing of the endangered bovine species Gayal (Bos frontalis) provides new insights into its genetic features. Scientific Reports 6: 19787.

Prabhu, V.R., Arjun, M.S., Bhavana, K., Kamalakkannan, R. & Nagarajan, M. (2019). Complete mitochondrial genome of Indian mithun, Bos frontalis and its phylogenetic implications. Molecular Biology Reports 46(2): 2561–2566.

Wang, M.-S., Zeng, Y., Wang, X., Nie, W.-H., Wang, J.-H., Su, W.-T., Otecko, N.O., Xiong, Z.-J., Wang, S., Qu, K.-X., Yan, S.-Q., Yang, M.-M., Wang, W., Dong, Y., Wu, D.-D. & Zhang, Y.-P. (2017). Draft genome of the gayal, Bos frontalis. GigaScience 6(11): 1–7.

Chapter 85 --- Mango (*Mangifera indica*): Two Corroborated Gene Pools, and a Domestication History Its Own Authors Call Complex Rather Than Resolved

85.1 Admission, extending the disputed-count group (Appendix A.4)

Mango is admitted here on the same footing as lentil (§2.8.2) and soybean (§36.6): not a case where a proposed second center was raised and refuted (§8.3's second route), nor one where a location is disputed for an otherwise agreed single center (maize, §6.5), but one where the cited genomic literature itself reports a population structure that its own authors decline to read as settled evidence of two independently founded centers. Mango (*Mangifera indica*) is a major tropical fruit crop, cultivated across South and Southeast Asia for approximately four thousand years, and its own domestication history is a genuine test of this cycle's discipline: two independent genomic studies agree on a structural finding, and disagree — or, more precisely, decline to resolve — on what that finding means for the center count.

85.2 The traditional single-origin account

The traditional account, repeated across horticultural and archaeobotanical literature, holds that mango was domesticated once, in India, roughly four thousand years ago, from a wild ancestor in the foothills of the Himalaya, and was introduced into Southeast Asia only later, well after domestication was complete. On this account C=1 is not itself in dispute — only whether the genomic record actually supports it.

85.3 Population genomics: two independently corroborated gene pools

Warschefsky & von Wettberg (2019, *New Phytologist* 222(4): 2023–2037), using restriction-site-associated DNA (RAD) sequencing to generate genome-wide SNP data from 106 mango cultivars sampled across seven geographical regions (plus 52 samples of

closely related species), report that cultivated mango resolves into two primary genetic gene pools, corresponding to Indian and Southeast Asian germplasm, with a third, less well-defined group representing Caribbean and South American cultivars. Critically, they report no significant genetic bottleneck associated with mango's introduction into new regions of the world — the opposite of what the traditional single-origin-then-spread account would predict — and find that Southeast Asian cultivars carry genetic diversity (measured by percentage of polymorphic sites and number of private alleles) not present in the Indian gene pool, read by the authors as evidence this diversity did not simply originate in India and travel eastward.

Wang, Luo, Huang, Gao, Zhu, Dang et al. (2020, *Genome Biology* 21: 60), reporting a chromosome-scale reference genome assembly of mango together with genome resequencing of a cultivar panel, independently report the same two-group structure: commercial varieties cluster with Indian germplasm and show allelic admixture, while indigenous varieties from Southeast Asia form a second, distinct group; landraces indigenous to China form their own clades, some showing admixture between the two main groups. This is the same bipartite genetic structure Warschefsky & von Wettberg report, reached by an independent sequencing method (whole-genome resequencing against a de novo reference, rather than RAD-seq SNP calling) and an independently assembled sample panel.

85.4 What the source literature does, and does not, conclude from two gene pools

Neither paper frames its own two-gene-pool finding as proof of two independently founded domestication centers. Warschefsky & von Wettberg state that their results suggest mango's domestication history has been "more complex" than previously assumed, and may follow one or two other patterns documented in perennial fruit

crops generally: multiple domestications, or interspecific hybridization with congeneric wild *Mangifera* species — phrased as a disjunction of possibilities, not a conclusion. This is the same structure lentil's own two gene pools (§2.8.2) presented: a genuine, independently corroborated population split that its own source literature does not itself frame as a claim of C=2, and that this cycle's discipline (§1.4) accordingly declines to convert into one on the reporting cycle's own authority. Neither study offers a second candidate wild population, a second archaeobotanical assemblage, or a second independently dated domestication event located in Southeast Asia — only a genetic gene pool, of debated origin, layered onto a single named traditional center.

85.5 Applying the predicate: why no C is assigned, and no PI computed

§20.7.1's predicate asks whether an agreed count of independent domestication centers can be assigned before any location question is reached. Here it cannot: the cited literature reports a corroborated genetic structure (two gene pools, independently found by two methods) without agreeing among its own authors on whether that structure reflects two founding centers, one center followed by strong post-domestication population structuring, or an unresolved mixture of the two. Following lentil's and soybean's own precedent (§2.8.2, §36.6), no κ is assigned to either reading and no PI is computed, on the grounds that doing so would require adjudicating a live disagreement the cited authors themselves decline to settle, rather than reporting one, exactly the authorial overreach §1.4's discipline was written to prevent.

85.6 Placement in Appendix A.4, an eleventh entry

Mango is added to Appendix A.4 as an eleventh entry, on lentil's own ground (§2.8.2): a genuinely corroborated population split, reported by the cited literature's own authors as unresolved between a one-center and a multi-center reading, rather than

framed by that literature itself as a disputed center count in the adversarial sense dog (Ch.12), quinoa (Ch.49), or cowpea (Ch.74) present. The traditional four-thousand-year, India-only account and the two-gene-pool genomic record sit side by side in this appendix precisely as reported, with neither promoted to a settled verdict on this cycle's own authority.

85.7 Cross-cycle synthesis: eighty-nine cases

With mango added, this cycle now covers eighty-nine cases and ninety-two distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): mango contributes no new resolved center, only the eleventh row of Appendix A.4 and this cycle's sixty-first Plantae species.

References newly cited in Chapter 85

Wang, P., Luo, Y., Huang, J., Gao, S., Zhu, G., Dang, Z., Gai, J., Yang, M., Zhu, M., Zhang, H., Ye, X., Gao, A., Tan, X., Wang, S., Wu, S., Cahoon, E.B., Bai, B., Zhao, Z., Li, Q., Wei, J., Chen, H., Luo, R., Gong, D., Tang, K., Zhang, B., Ni, Z., Huang, G., Hu, S. & Chen, Y. (2020). The genome evolution and domestication of tropical fruit mango. Genome Biology 21(1): 60.

Warschefsky, E.J. & von Wettberg, E.J.B. (2019). Population genomic analysis of mango (Mangifera indica) suggests a complex history of domestication. New Phytologist 222(4): 2023–2037.

Chapter 86 --- Opium Poppy (*Papaver somniferum*): A Rival Hypothesis Directly Tested and Discarded

86.1 Admission, extending the tested-and-refuted route to PI = 0 (§8.3)

Opium poppy is admitted here on sunflower's own footing (§7.3, §8.3): not a case unanimous from the outset, but one where a

genuinely live rival hypothesis for the crop's origin was carried in the literature for years, was directly tested by a study designed for that purpose, and did not survive testing. Opium poppy (*Papaver somniferum*) is among the oldest medicinal plants under cultivation, and its own domestication history was, on the reviewed literature's own account, unresolved as recently as 2025.

86.2 Two competing hypotheses, stated before either is tested

Machado, Bonhomme, Soteras, Jeanty, Bouby, Evin, Fernandes Martins, Gonçalves, Antolín, Salavert & Oliveira (2025, Philosophical Transactions of the Royal Society B 380(1926): 20240198) state the dispute plainly: the traditional hypothesis holds that opium poppy was domesticated in the Western Mediterranean, where its putative wild ancestor, *Papaver setigerum*, is native and still grows wild today; a rival hypothesis, also current in the literature, holds instead that *somniferum* was introduced into Europe by early farmers from Southwest Asia — the Fertile Crescent — as a weed of cultivation, only later brought under deliberate cultivation itself.

86.3 Genotyping-by-sequencing and seed morphometrics together

To test these hypotheses directly, Machado et al. (2025) analysed 190 accessions across 15 *Papaver* species and subspecies, combining genotyping-by-sequencing (GBS) with geometric morphometric (GMM) analysis of seed shape. Their genetic analysis found that *setigerum* is the only taxon genetically close to *somniferum*, better described as a subspecies of it than as a separate species — and found no genetic signal placing any Southwest Asian or Fertile Crescent population closer to *somniferum* than *setigerum* itself. The authors report that phylogenetic analysis corroborates a single domestication wave, in the Western Mediterranean, and that on this basis the hypothesis of an origin in the Fertile Crescent, followed by introduction into Europe as a weed, can be discarded.

86.4 A within-somniferum structure disclosed, but not read as a second center

The same study reports two major genetic populations within cultivated *somniferum* itself, corresponding, to some extent, to differences in seed form. The authors read this structure as reflecting relatively recent selection for different end uses — varieties bred for high opiate content as against varieties grown for poppyseed — rather than as evidence of two independent domestication events; no second wild progenitor, no second archaeobotanical assemblage, and no second geographic center is proposed for either population. This is the same distinction §17.5 drew for goat's own disclosed "mosaic domestication" finding: a real population structure, explicitly not promoted to a second center by the source literature itself.

86.5 Applying the predicate: C = 1, κ = 1.000, $\bar{D}$ = 0

§20.7.1's predicate is met cleanly here, on sunflower's own "proposed, tested, and refuted" route (§8.3) rather than einkorn's "unanimous from the outset" route: a named rival hypothesis (Fertile Crescent introduction as a weed) was live in the literature, was directly tested by a purpose-built genomic and morphometric study, and was explicitly discarded by its authors. C=1 (Western Mediterranean, *setigerum* as wild progenitor), κ=1.000 (the rival center tested and refuted, not merely unraised), and $\bar{D}$=0 (a single center admits no between-center distance to average), giving PI=0 by the same floor-through-refutation route as sunflower and horse, not by pig's or coconut's two-center arithmetic.

86.6 Placement in Appendix A.2, a thirty-second entry

Opium poppy is added to Appendix A.2 as a thirty-second entry, on sunflower's and horse's own footing: a rival second-center hypothesis directly tested and discarded, rather than a center never contested at all. It is also added to Appendix F's own catalog of

proposed-and-rejected hypotheses, as the Fertile-Crescent-weed-introduction hypothesis is precisely the shape that appendix collects: a named rival claim, raised in the literature, tested by a specific study, and reported by that study's own authors as not surviving the test.

86.7 Cross-cycle synthesis: ninety cases

With opium poppy added, this cycle now covers ninety cases and ninety-three distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): opium poppy contributes a thirty-second Appendix A.2 row, at the same PI=0 value already carried by every other member of that group, and this cycle's sixty-second Plantae species.

References newly cited in Chapter 86

Machado, R.S.R., Bonhomme, V., Soteras, R., Jeanty, A., Bouby, L., Evin, A., Fernandes Martins, M.J., Gonçalves, S., Antolín, F., Salavert, A. & Oliveira, H.R. (2025). The origins and spread of the opium poppy (Papaver somniferum L.) revealed by genomics and seed morphometrics. Philosophical Transactions of the Royal Society B 380(1926): 20240198.

Chapter 87 --- Bottle Gourd (*Lagenaria siceraria*): A Transoceanic Rival Hypothesis Directly Tested and Discarded, and a Diffuse New World Domestication Left Unresolved

87.1 Admission, on guinea fowl's own dual footing (§50.8)

Bottle gourd is admitted here on the same dual footing as helmeted guinea fowl (Ch.50): a case whose own resolvable question — how the species reached the Americas — was directly tested and settled, earning it an Appendix F row, while a second, distinct question —

how many independent domestication events subsequently occurred once it arrived — remains genuinely unresolved, earning it a place in Appendix A.3 rather than A.2. Bottle gourd (*Lagenaria siceraria*) is native to Africa but was in use by humans across Africa, Asia, the Pacific, and the Americas in pre-Columbian times — the only species with this global a distribution before contact — valued not as food but for its hard, buoyant rind, prized as a container, float, and instrument casing.

87.2 The first tested hypothesis: a Paleoindian, Asian-origin introduction

Erickson, Smith, Clarke, Sandweiss & Tuross (2005, *Proceedings of the National Academy of Sciences* 102(51): 18315–18320) directly accelerator-mass-spectrometer-dated bottle gourd rind fragments from archaeological sites in Peru, Mexico, and the eastern United States, and sequenced ancient chloroplast DNA from ten of the oldest specimens (the earliest at roughly 10,000 calendar years before present). All ten archaeological specimens that yielded ancient DNA, dating from before European contact, matched the modern Asian reference genotype rather than the African one; the sole post-contact specimen tested matched the African genotype instead. On this basis, the authors concluded that domesticated, Asian-lineage bottle gourd was carried into the Americas by Paleoindian populations as they colonized the New World — alongside the dog — crossing Beringia well before any food crop or livestock species reached the hemisphere.

87.3 A second, larger ancient-DNA dataset directly tests, and reverses, that conclusion

Kistler, Montenegro, Smith, Gifford, Green, Newsom & Shapiro (2014, *Proceedings of the National Academy of Sciences* 111(8): 2937–2941) isolated roughly 86,000 base pairs of plastid genome sequence from a substantially larger and more geographically representative

sample of archaeological and modern bottle gourds than Erickson et al. (2005) had available, explicitly designed to re-test the 2005 study's Asian-introduction conclusion. Contrary to that earlier result, Kistler et al. report that every pre-Columbian bottle gourd specimen in their expanded dataset is most closely related to African, not Asian, gourds. Combining this result with ocean-current drift modelling, the authors show that wild African bottle gourds could plausibly have crossed the Atlantic by simple surface drift during the Late Pleistocene, with naturalized populations subsequently established in the Neotropics via dispersal by megafaunal mammals — a scenario requiring no human vector, and no crossing of the Arctic, at all.

87.4 Applying §8.3's floor-through-refutation route to the arrival question alone

On the specific, resolvable question of how bottle gourd reached the Americas, §8.3's already-established proposed-tested-and-refuted route applies cleanly: Erickson et al.'s Asian-introduction hypothesis was a named, directly tested claim, refuted by a larger and independently constructed ancient-DNA dataset explicitly designed to re-examine it, on the same footing as sunflower's, horse's, and helmeted guinea fowl's own refuted rivals (§7.3, §15.6, §50.7). This question alone would earn bottle gourd a floor value were it the only question this case raised.

87.5 A second, unresolved question: how many domestication events followed arrival

Kistler et al. (2014) do not stop at the route of arrival. They report that once naturalized in the Neotropics, wild African-derived bottle gourd populations "were domesticated in several distinct New World locales, most likely near established centers of food crop domestication," with early and nearly contemporaneous use of the species documented in South America, Mesoamerica, and eastern

North America alike. This is explicitly hedged language — “several,” “most likely” — not a corroborated count of independently founded centers with any location resolved to a point, and no coordinate, archaeological site, or genetic boundary is offered by the authors as marking a specific center in any of the three regions named.

87.6 Applying §20.7.1's predicate to the domestication-count question: distinct from yam's own ground

§20.7.1's predicate fails here for a reason distinct from yam's own (§56.7): yam supplied this cycle's first case with three or more independently corroborated centers of which none resolves to a point, each center nonetheless treated in its own source literature as a discrete, nameable event. Bottle gourd's own cited literature does not go even that far: “several distinct New World locales” is presented as a diffuse, weedy-growth-habit-enabled cultivation pattern rather than a specific, countable set of founding events, so that not only R(X) but C itself is left genuinely open by the source reviewed. No κ is assigned and no PI is computed.

87.7 Placement in Appendix A.3, a twenty-sixth row, and in Appendix F

Bottle gourd is added to Appendix A.3 as a twenty-sixth row, on a footing distinct from every prior member: not a disputed location for an agreed center (maize, almond, sesame), not an absent candidate (C. moschata), not a disputed species identity (guinea pig) or descent-versus-hybrid reading (mithun), but a diffuse, unresolved domestication pattern layered atop a resolved question of geographic and genetic origin. It is also added to Appendix F, on helmeted guinea fowl's own dual-placement footing (§50.8): the case's own point-resolvability failure in A.3 does not exclude it from also contributing a genuinely tested-and-refuted claim — Erickson et al.'s Asian-Paleoindian introduction hypothesis — to that table.

87.8 Cross-cycle synthesis: ninety-one cases

With bottle gourd added, this cycle now covers ninety-one cases and ninety-four distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): bottle gourd contributes a twenty-sixth Appendix A.3 row, a further Appendix F entry, and this cycle's sixty-third Plantae species.

References newly cited in Chapter 87

Erickson, D.L., Smith, B.D., Clarke, A.C., Sandweiss, D.H. & Tuross, N. (2005). An Asian origin for a 10,000-year-old domesticated plant in the Americas. Proceedings of the National Academy of Sciences 102(51): 18315–18320.

Kistler, L., Montenegro, Á., Smith, B.D., Gifford, J.A., Green, R.E., Newsom, L.A. & Shapiro, B. (2014). Transoceanic drift and the domestication of African bottle gourds in the Americas. Proceedings of the National Academy of Sciences 111(8): 2937–2941.

Chapter 88 --- Grain Amaranth (*Amaranthus cruentus*, *A. hypochondriacus*, *A. caudatus*): Three Regional Domestications from a Polyphyletic Wild Ancestor, None Resolved to a Point

88.1 Admission, extending yam's own ground (§56.7)

Grain amaranth is admitted here on yam's own ground (Ch.56): a genus with three independently corroborated, regionally distinct domestications, none of which the cited literature resolves to a point-coordinate under any method reviewed. The three grain amaranths — *Amaranthus cruentus*, *A. hypochondriacus*, and *A. caudatus* — are diploid, C4 pseudocereals of major nutritional and historical importance across the pre-Columbian Americas, and this cycle's second case, after yam, to reach Appendix A.3 on this

specific unresolved-multi-center ground rather than avocado's own three-for-three resolved one (§57.7).

88.2 Sauer's original hypothesis, and its genomic corroboration

Sauer (1967) originally proposed that the three grain amaranths descend from geographically distinct wild lineages of a single putative ancestor species, *A. hybridus*, domesticated independently in different regions of the Americas rather than from one single founding event subsequently dispersed. Clouse, Adhikary, Page, Ramaraj, Deyholos, Udall, Fairbanks, Jellen & Maughan (2016, *The Plant Genome* 9(1): 1–14), reporting a draft genome assembly of *A. hypochondriacus*, confirm *A. hybridus* as its wild progenitor. Stetter & Schmid (2017, *Molecular Phylogenetics and Evolution* 109: 80–92), genotyping 94 genebank accessions across 35 *Amaranthus* species by genotyping-by-sequencing, report that *A. hybridus* is itself polyphyletic: it resolves into genetically distinct North American and South American lineages, each more closely related to a different one of the three grain species than to each other — corroborating Sauer's original multi-lineage hypothesis with genome-wide molecular data rather than morphology alone.

88.3 Differential post-domestication gene flow across the three species

Gonçalves-Dias, Singh, Graf & Stetter (2023, *Molecular Biology and Evolution* 40(8): msad177), analysing genome-wide data across the grain amaranths and their sympatric wild relatives, report a geographically counterintuitive pattern of post-domestication gene flow: substantial introgression between the Mexican *A. hypochondriacus* and the South American *A. caudatus*, despite their present-day geographic separation, but only restricted gene flow between *A. hypochondriacus* and *A. cruentus*, despite the latter two co-occurring across much of Mesoamerica today. The authors read this pattern as consistent with three separately founded domestication events subsequently reshaped by uneven, region-

specific patterns of exchange with wild and semi-domesticated relatives, rather than as evidence against independent founding in the first place.

88.4 A disclosed complication: caudatus read as incompletely domesticated

Stetter, Müller & Schmid (2017, *Molecular Ecology* 26(3): 871–886) report genomic and phenotypic evidence that *A. caudatus*, specifically, may be an incompletely domesticated crop — its own domestication syndrome only partially fixed, plausibly because of weak selection or elevated gene flow from its sympatric, undomesticated relatives (*A. hybridus*, *A. quitensis*) that has counteracted fixation of key domestication traits. This complication, like yak's disclosed within-region refinement (§67.8) or mithun's disclosed hybrid-founding dispute (§84.7), is reported here without being elevated to a formal reduction of C: no source reviewed proposes that *caudatus* is not an independently founded lineage, only that its own domestication process may remain, in a documented sense, unfinished.

88.5 Applying §20.7.1's predicate: three corroborated centers, none point-resolved

§20.7.1's predicate is satisfied at the level of C — three independently corroborated regional domestications (Mesoamerica for *A. hypochondriacus*, a more southerly Mesoamerican region for *A. cruentus*, the Andes for *A. caudatus*), each traced to a genetically distinct lineage of a polyphyletic wild ancestor by more than one independent genomic study — but fails at the location stage: no source reviewed resolves any of the three founding events to a specific coordinate or archaeological site of the kind avocado's own three centers reached (§57.4–§57.7), or Capsicum's partially resolved five (§40.7). R(X)=0 for all three; no κ is assigned and no PI

is computed, on yam's own precedent rather than a newly invented one.

88.6 Placement in Appendix A.3, a twenty-seventh row spanning three species

Grain amaranth is added to Appendix A.3 as a twenty-seventh row, counted once as a single case spanning three species, on the same convention already applied to the Triangle of U (§76.7), onion and garlic (§78.5–§78.6), and jute (§82.5–§82.6): a domestication event repeated across sister taxa rather than dispersed within one. Unlike the Triangle of U, whose three species arose from hybridization between already-domesticated lineages, grain amaranth's three species each descend independently from wild *A. hybridus*, on yam's own multi-center ground rather than the Triangle of U's hybrid-founding one.

88.7 Cross-cycle synthesis: ninety-two cases

With grain amaranth added, this cycle now covers ninety-two cases and ninety-seven distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): grain amaranth contributes a twenty-seventh Appendix A.3 row and this cycle's sixty-fourth, sixty-fifth, and sixty-sixth Plantae species.

References newly cited in Chapter 88

Clouse, J.W., Adhikary, D., Page, J.T., Ramaraj, T., Deyholos, M.K., Udall, J.A., Fairbanks, D.J., Jellen, E.N. & Maughan, P.J. (2016). The Amaranth Genome: Genome, Transcriptome, and Physical Map Assembly. The Plant Genome 9(1): 1–14.

Gonçalves-Dias, J., Singh, A., Graf, C. & Stetter, M.G. (2023). Genetic incompatibilities and evolutionary rescue by wild relatives shaped grain amaranth domestication. Molecular Biology and Evolution 40(8): msad177.

Stetter, M.G. & Schmid, K.J. (2017). Analysis of phylogenetic relationships and genome size evolution of the Amaranthus genus using GBS indicates the ancestors of an ancient crop. Molecular Phylogenetics and Evolution 109: 80–92.

Stetter, M.G., Müller, T. & Schmid, K.J. (2017). Genomic and phenotypic evidence for an incomplete domestication of South American grain amaranth (Amaranthus caudatus). Molecular Ecology 26(3): 871–886.

Chapter 89 --- Buckwheat (*Fagopyrum esculentum*): A Single Southwest Chinese Origin, and an Archaeological Record That Only Looks Like a Rival

89.1 Admission, on flax's own §20.7.2 route (§42.6)

Buckwheat is admitted here on flax's own ground (Ch.42): a single, corroborated wild source, with no source reviewed proposing a genuine second independently founded center, reaching PI=0 via §20.7.2's second branch rather than §8.3's refuted-rival one. Common buckwheat (*Fagopyrum esculentum*) is a pseudocereal of the family Polygonaceae, domesticated in China and dispersed across Eurasia by the third millennium before present, and its own literature raises what at first looks like a location dispute between archaeobotany and genomics before resolving into something else.

89.2 The archaeobotanical record: earliest agricultural finds in the north

Hunt, Shang & Jones (2018, *Vegetation History and Archaeobotany* 27(3): 493–506), synthesizing the full macro- and microfossil record of buckwheat cultivation across China (26 records in total, most of them pollen finds), report that the earliest plausibly agricultural *Fagopyrum* occurs in northern China — the southern Loess Plateau and Chengdu Plain — from the mid-sixth millennium before

present, geographically well north of where the crop's wild progenitor is found today.

89.3 The genomic and biogeographic record: a southwestern, Tibet-margin origin

Fawcett, Takeshima, Kikuchi, Yazaki, Katsube-Tanaka, Dong, Li, Hunt, Jones, Lister, Ohsako, Ogiso-Tanaka, Fujii, Hara, Matsui, Mizuno, Nishimura, Nakazaki, Saito, Takeuchi, Ueno, Matsumoto, Norizuki, Shirasawa, Li, Hirakawa, Ota & Yasui (2023, *Nature Plants* 9(8): 1236–1251), reporting chromosome-scale genome assemblies of *F. esculentum* and its self-compatible wild relative *F. homotropicum* together with the resequencing of 104 wild and cultivated accessions, confirm that common buckwheat is an orphan crop domesticated in southwest China and report that southeast Tibet specifically was involved in its domestication — consistent with the wild progenitor's own documented range margin (*F. esculentum* ssp. *ancestrale*, concentrated in Yunnan).

89.4 Why this is not a disputed count, on Hunt et al.'s own reading

Hunt et al. (2018) do not propose a rival, independently founded northern Chinese domestication center to set against the genomically indicated southwestern one; they state instead that the archaeobotanical record "requires reconciliation with" the genetic evidence, and suggest common buckwheat "may have been domesticated at the range margins of its wild progenitor before its cultivation expanded in the north" — a single domestication event followed by geographically uneven archaeological visibility, not two events. No source reviewed proposes a second wild *Fagopyrum* population, a second archaeobotanical assemblage read as an independent origin, or a second genetically distinct cultivated lineage; the disagreement is about where the record is best preserved, not about how many times the crop was domesticated.

89.5 Applying §20.7.2's second branch: C=1, unanimous, PI=0

§20.7.2's second branch applies whenever C=1 and the single center is unanimously corroborated, with no proposed rival requiring §8.3's separate refutation route — flax's own route (§42.6). Buckwheat meets it cleanly: the wild progenitor lineage is agreed (*F. esculentum* ssp. *ancestrale*, a Yunnan-margin population), no second lineage or second center is proposed by any source reviewed, and the apparent archaeobotanical-genomic mismatch is explicitly read by the archaeobotanical source itself as a preservation and post-domestication-spread artefact rather than a rival center. C=1, κ=1.000, D̄=0, giving PI=0.

89.6 Placement in Appendix A.2, a thirty-third entry

Buckwheat is added to Appendix A.2 as a thirty-third entry, on flax's own unanimous-single-center footing rather than sunflower's refuted-rival one: a case that could, read carelessly, resemble sesame's own reopened location dispute (§70), but that resolves, on the cited literature's own terms, into a single center with an archaeologically displaced footprint rather than two competing centers.

89.7 Cross-cycle synthesis: ninety-three cases

With buckwheat added, this cycle now covers ninety-three cases and ninety-eight distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): buckwheat contributes a thirty-third Appendix A.2 row and this cycle's sixty-seventh Plantae species.

References newly cited in Chapter 89

Fawcett, J.A., Takeshima, R., Kikuchi, S., Yazaki, E., Katsube-Tanaka, T., Dong, Y., Li, M., Hunt, H.V., Jones, M.K., Lister, D.L., Ohsako, T., Ogiso-Tanaka, E., Fujii, K., Hara, T., Matsui, K., Mizuno,

N., Nishimura, K., Nakazaki, T., Saito, H., Takeuchi, N., Ueno, M., Matsumoto, D., Norizuki, M., Shirasawa, K., Li, C., Hirakawa, H., Ota, T. & Yasui, Y. (2023). Genome sequencing reveals the genetic architecture of heterostyly and domestication history of common buckwheat. Nature Plants 9(8): 1236–1251.

Hunt, H.V., Shang, X. & Jones, M.K. (2018). Buckwheat: a crop from outside the major Chinese domestication centres? A review of the archaeobotanical, palynological and genetic evidence. Vegetation History and Archaeobotany 27(3): 493–506.

Chapter 90 --- T’ef and Finger Millet (*Eragrostis tef, Eleusine coracana*): Two Independent Domestications from the Same African Highlands

90.1 Admission, on the two-millets' own footing (§26.1)

T’ef and finger millet are admitted together on foxtail and broomcorn millet's own footing (Ch.26): two species examined together in the same source because they share a landscape and a domestication region, not because their own domestication histories are evidentially linked. Both are cereal staples of the Northern Highlands of Ethiopia and Eritrea (NHE), a region whose own archaeobotanical record is acknowledged by the cited literature to be sparse and poorly preserved — making this a genuine test of genomics standing in for, rather than merely supplementing, an absent archaeological record.

90.2 A joint genomic study, two separately confirmed wild progenitors

Mekonnen, Gomes, Machado & Oliveira (2025, *Philosophical Transactions of the Royal Society B* 380(1926): 20240196), using DArTSeq genotyping across wild and cultivated accessions of both species, report that their data confirm *Eragrostis pilosa* and *Eleusine coracana* subsp. *africana* as the sole wild progenitors of t’ef and

finger millet respectively — two independent domestication events, from two different genera, both localized to the NHE, with no second wild-progenitor candidate proposed for either species anywhere in the literature reviewed.

90.3 T'ef: a single center, with a stated subsequent spread

The authors report that t'ef was initially domesticated in the NHE before spreading into southern Ethiopia and eastwards into southern Arabia — a single-origin, single-species result with a documented post-domestication dispersal pattern, on the same evidentiary shape already established for cassava (§59) and dromedary (§18): a resolved center, an unremarkable and undisputed subsequent spread.

90.4 Finger millet: a single center, with two disclosed spread routes

For finger millet, the same study reports a single domesticated lineage that subsequently followed two distinct dispersal routes out of the NHE: one eastward through the Red Sea into India, the other southward through Kenya and Uganda into southern Africa. Following the convention already established for goose's and hop's own disclosed post-domestication episodes (§55.6, §79.6–§79.7), two spread routes for an agreed single origin are reported here without being read as two centers: no source reviewed proposes an independent second domestication of finger millet along either route, only a single founding event whose descendants later travelled in two directions.

90.5 Applying §20.7.2's second branch to each species independently

Each species is assessed against §20.7.1's predicate on its own terms, following §26.1's own precedent for treating co-discussed but evidentially independent cases separately. T'ef: C=1 (NHE, *Eragrostis pilosa*), unanimous, no rival proposed — PI=0 via §20.7.2's second branch. Finger millet: C=1 (NHE, *Eleusine coracana* subsp.

africana), unanimous despite two disclosed spread routes, no rival domestication center proposed for either route — PI=0 via the same route. Both reach the floor for the same reason flax and buckwheat did: a single corroborated origin with nothing in the cited literature requiring §8.3's separate refutation step.

90.6 Placement in Appendix A.2, a thirty-fourth and thirty-fifth entry

T’ef and finger millet are added to Appendix A.2 as a thirty-fourth and thirty-fifth entry respectively, counted separately on foxtail and broomcorn millet's own precedent (§26.5) rather than jointly on the Triangle of U's or grain amaranth's (§88.6): two independently founded domestications, from different wild genera, reported together only because one 2025 study happened to examine both species from the same understudied region in a single analysis.

90.7 Cross-cycle synthesis: ninety-five cases

With t’ef and finger millet added, this cycle now covers ninety-five cases and one hundred distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): t’ef and finger millet contribute a thirty-fourth and thirty-fifth Appendix A.2 row and this cycle's sixty-eighth and sixty-ninth Plantae species.

References newly cited in Chapter 90

Mekonnen, D.Z., Gomes, A.I., Machado, R.S.R. & Oliveira, H.R. (2025). The genomics of t’ef and finger millet domestication and spread. Philosophical Transactions of the Royal Society B 380(1926): 20240196.

Chapter 91 --- Pearl Millet (*Pennisetum glaucum*): A Multi-Center Hypothesis Tested by Whole-Genome Sequencing and Narrowed to One

91.1 Admission, on sunflower's own §8.3 route (§7.3)

Pearl millet is admitted here on sunflower's own footing: not a case unanimous from the outset, but one where a genuinely live multi-center hypothesis was carried in the archaeobotanical and enzyme-marker literature for decades before a purpose-built whole-genome study tested it directly and narrowed it to one. Pearl millet (*Pennisetum glaucum*) is the most widely cultivated millet in the world today, a staple across the semi-arid Sahel and, since its prehistoric dispersal, of South Asia as well.

91.2 An older multi-center hypothesis, reviewed rather than invented here

Winchell, Brass, Manzo, Beldados, Perna, Murphy, Stevens & Fuller (2018, *African Archaeological Review* 35(4): 483–505), reviewing the Sudanese and wider West African evidence for early cereal cultivation, report that Tostain, Fuller, and Neumann have each, in earlier work, hypothesized that pearl millet's domestication may have involved more than one center west of Lake Chad — a hypothesis grounded in isozyme data and in the geographic spread of early archaeobotanical finds across a broad swath of the Sahel from southeastern Mauritania to northeastern Mali.

91.3 Archaeobotanical anchoring: the Tilemsi Valley

Manning, Pelling, Higham, Schwenniger & Fuller (2011, *Journal of Archaeological Science* 38(2): 312–322) directly dated domesticated pearl millet caryopses from the Lower Tilemsi Valley, Mali, to roughly 4,500 years before present — among the earliest secure evidence for domesticated pearl millet anywhere, anchoring one candidate node of the multi-center hypothesis in a specific, well-

dated archaeological sequence rather than leaving it a purely inferential geographic spread.

91.4 A whole-genome test, and a narrowing to one center

Burgarella, Cubry, Kane, Varshney, Mariac, Liu, Shi, Thudi, Couderc, Xu, Chitikineni, Scarcelli, Barnaud, Rhône, Dupuy, François, Berthouly-Salazar & Vigouroux (2018, *Nature Ecology & Evolution* 2(9): 1377–1380), using whole-genome sequencing data explicitly designed to adjudicate the decades-old debate over pearl millet's geographic origin, report that their results support a single center in western Sahara, with cultivated pearl millet's expansion across Africa dated to roughly 4,900 years ago. The authors describe their own result as reconciling the genetic and archaeological data for one of Africa's oldest crops — not as adding a rival claim beside the older multi-center hypothesis, but as testing it directly and resolving it to one.

91.5 Applying §8.3's route: a hypothesis narrowed, not merely unraised

This is §8.3's proposed-tested-and-refuted route in a variant form already seen for cotton's fourth center (§22.4) and buckwheat's own apparent conflict (§89.4): the earlier hypothesis was not a single named rival location easily set beside the winning one, but a genuine possibility of plurality ("more than one center west of Lake Chad") that a purpose-built whole-genome study tested directly and did not confirm. Burgarella et al.'s own explicit framing — reconciliation of genetic and archaeological data, not addition of a second candidate — is decisive: no source reviewed, after 2018, continues to treat pearl millet's origin as unresolved between multiple centers.

91.6 Applying §20.7.1's predicate: C=1, κ=1.000, D̄=0

C=1 (western Sahara/Sahel, wild *P. glaucum* subsp. *monodii*), κ=1.000 (the older multi-center possibility directly tested and not

confirmed, on §8.3's own refutation-route terms), $\bar{D}=0$ (a single center admits no between-center distance to average), giving PI=0 — the same floor value already reached by sunflower, horse, opium poppy, and bottle gourd's own arrival-question, by the same route.

91.7 Placement in Appendix A.2, a thirty-sixth entry

Pearl millet is added to Appendix A.2 as a thirty-sixth entry, on sunflower's and horse's own refuted-rival footing rather than flax's and buckwheat's unanimous-from-the-outset one: unlike buckwheat, where no source ever proposed a genuine second center, pearl millet's own literature carried a real multi-center possibility for decades before a purpose-built genomic test resolved it.

91.8 Cross-cycle synthesis: ninety-six cases

With pearl millet added, this cycle now covers ninety-six cases and one hundred and one distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): pearl millet contributes a thirty-sixth Appendix A.2 row and this cycle's seventieth Plantae species.

References newly cited in Chapter 91

Burgarella, C., Cubry, P., Kane, N.A., Varshney, R.K., Mariac, C., Liu, X., Shi, C., Thudi, M., Couderc, M., Xu, X., Chitikineni, A., Scarcelli, N., Barnaud, A., Rhône, B., Dupuy, C., François, O., Berthouly-Salazar, C. & Vigouroux, Y. (2018). A western Sahara centre of domestication inferred from pearl millet genomes. Nature Ecology & Evolution 2(9): 1377–1380.

Manning, K., Pelling, R., Higham, T., Schwenniger, J.-L. & Fuller, D.Q. (2011). 4500-year old domesticated pearl millet (Pennisetum glaucum) from the Tilemsi Valley, Mali: new insights into an

alternative cereal domestication pathway. Journal of Archaeological Science 38(2): 312–322.

Winchell, F., Brass, M., Manzo, A., Beldados, A., Perna, V., Murphy, C., Stevens, C. & Fuller, D.Q. (2018). On the Origins and Dissemination of Domesticated Sorghum and Pearl Millet across Africa and into India: a View from the Butana Group of the Far Eastern Sahel. African Archaeological Review 35(4): 483–505.

Chapter 92 --- Goldfish (*Carassius auratus*): This Cycle's Second Osteichthyes, and a Domestication Question Kept Apart From a Much Older Speciation One

92.1 Admission, on common carp's own footing (§58.1)

Goldfish is admitted here as this cycle's second Osteichthyes, after common carp (Ch.58), and on flax's own unanimous-single-center route (§42.6) rather than a refuted-rival one. Goldfish (*Carassius auratus*) is the first domesticated ornamental fish, bred in China for over a thousand years for its extraordinary morphological diversity, and its own literature carries a distinction this chapter keeps deliberately separate: a very old question about the species' own evolutionary origin, and a much younger one about its domestication.

92.2 A species-level complication, disclosed and set aside

Chen, Zhang, Tang, Huang, Wang, Wang, Shi, Xu, Lin, Li, Chi, Huang, Xia, Zhang, Guo, Wang, Ma, Tang, Zhou, Liu, Liu, Hua, Wang, Shen, Jiang, Lin, Chen, Wang, Dou, Liu, Pan, Qi, Wu, Fang, Zhou, Cen, He, Zhang, Xue, Lin, Zhang, Liu, Qu, Wang, Ye, Chen, Zhang, Ming, Van Montagu, Tang, Van de Peer, Chen & Zhang (2020, *Proceedings of the National Academy of Sciences* 117(47): 29775–29785), reporting a chromosome-scale goldfish genome assembly, find that the 50 goldfish chromosomes resolve into two clearly

distinguishable subgenomes, consistent with an ancient allotetraploid hybridization event in *C. auratus*'s own species history, with one subgenome shared with Barbinae. This is a question about how the species *Carassius auratus* itself came to exist, on the same footing as the Triangle of U's own hybrid speciation (§76) — evolutionarily prior to, and categorically distinct from, the domestication event this chapter actually assesses, and is disclosed here without being folded into this chapter's own predicate.

92.3 The domestication question: a single, twice-confirmed source population

On domestication specifically, Wang, Luo, Murphy, Wu, Zhu, Gao & Zhang (2013, *PLoS ONE* 8(3): e59571), sequencing mitochondrial control-region and cytochrome *b* markers from 234 goldfish and a large series of native *Carassius* specimens, report that goldfish haplotypes root within two sublineages found specifically in native southern Chinese *C. a. auratus*, with the closest relationship to populations from the lower Yangtze River — consistent with goldfish's own recorded early history as an artificially selected variant of Song-dynasty (960–1279 AD) crucian carp aquaculture in that same region. Chen et al. (2020), resequencing 185 representative goldfish variants against 16 wild crucian carp genomes, independently confirm a closer genomic relationship between common goldfish and crucian carp than between different goldfish breeds themselves, corroborating a single domesticated source population rather than several independently tamed regional stocks.

92.4 Applying §20.7.2's second branch: C=1, unanimous, PI=0

No source reviewed proposes an independent second domestication of goldfish from a different regional wild *Carassius* population; both the 2013 mitochondrial study and the 2020 whole-genome study converge on the same southern Chinese, lower-

Yangtze-associated source. C=1, κ=1.000, D̄=0, giving PI=0 via §20.7.2's second branch — flax's and buckwheat's own route, not sunflower's refuted-rival one, since no rival center was ever seriously proposed for goldfish specifically.

92.5 Placement in Appendix A.2, a thirty-seventh entry

Goldfish is added to Appendix A.2 as a thirty-seventh entry, on flax's and buckwheat's own unanimous-single-center footing, and joins common carp as this cycle's second confirmed Osteichthyes case — two fish, two independently corroborated single domestications, from the same broad East Asian aquaculture tradition but not from each other.

92.6 Cross-cycle synthesis: ninety-seven cases

With goldfish added, this cycle now covers ninety-seven cases and one hundred and two distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): goldfish contributes a thirty-seventh Appendix A.2 row and this cycle's thirtieth Animalia species.

References newly cited in Chapter 92

Chen, D. et al. (2020). The evolutionary origin and domestication history of goldfish (Carassius auratus). Proceedings of the National Academy of Sciences 117(47): 29775–29785.

Wang, S.-Y., Luo, J., Murphy, R.W., Wu, S.-F., Zhu, C.-L., Gao, Y. & Zhang, Y.-P. (2013). Origin of Chinese Goldfish and Sequential Loss of Genetic Diversity Accompanies New Breeds. PLoS ONE 8(3): e59571.

Chapter 93 --- Eggplant (*Solanum melongena*): Two Independently Argued Centers Against a Single Genomic Reading That Reclassifies One of Them as Feral

93.1 Admission, extending the disputed-count group (Appendix A.4)

Eggplant is admitted here on cowpea's and mango's own footing (§74.5, §85.5): not a disputed location for an agreed single center, and not an absent candidate, but a live disagreement over the center count itself, C=1 versus C=2, argued from three independently generated genomic datasets that do not converge as sampling has grown. Eggplant (*Solanum melongena*) is among Asia's most widely cultivated vegetable crops, and its own reviewed literature divides cleanly between an older and a newer reading, with the newer reading itself explicitly reclassifying the older reading's second center as something other than an independent domestication.

93.2 A phylogeographic case for two centers

Meyer, Karol, Little, Nee & Litt (2012, *Molecular Phylogenetics and Evolution* 63(3): 685–701), synthesizing nuclear ribosomal ITS sequence data and AFLP fingerprinting across 149 accessions of landraces and candidate wild progenitors sampled from India, China, and elsewhere in tropical Asia, report that eggplant's own AFLP data resolve into two genetically distinct clusters corresponding to Indian and to southern Chinese/Southeast Asian germplasm, each containing candidate wild accessions of its own, and read this structure as supporting a minimum of two independent domestication events — one in India, one in southern China or Southeast Asia — with a possible third, more localized event behind the morphologically distinct *S. melongena* subsp. *ovigerum* in Southeast Asia. Barchi, Aprea, Rabanus-Wallace, Toppino, Alonso, Portis, Lanteri, Gaccione, Omondi, van Zonneveld, Schafleitner, Ferrante, Börner, Stein, Díez, Lefebvre,

Salinier, Boyaci, Finkers, Brouwer, Bovy, Rotino, Prohens & Giuliano (2023, *The Plant Journal* 116(6): 1667–1680), genotyping more than 3,400 worldwide eggplant and wild-relative accessions from seven international genebanks on a targeted SNP panel — by a wide margin the largest single sampling effort reviewed in this chapter — independently report the same bipartite structure: eggplant accessions from the Indian subcontinent and from Southeast Asia form two well-separated clusters in both maximum-likelihood and principal component analyses, and the paper's own stated reading identifies India and Southeast Asia as two independent domestication centers.

93.3 A single-center reading, and a named mechanism for the second cluster

Page, Gibson, Meyer & Chapman (2019, *Molecular Biology and Evolution* 36(7): 1359–1372), genotyping-by-sequencing 95 accessions spanning four wild *Solanum* species and *S. melongena*, report instead strong support for a single origin in Southeast Asia, accompanied by a domestication bottleneck of 47% genetic-diversity loss. Critically, this study's own SNP data resolve the wild progenitor *S. insanum* into an eastern group (Malaysia, Thailand, Vietnam) and a western group (India, Madagascar, Sri Lanka), with cultivated eggplant derived from the eastern group specifically; the western, Indian population of *S. insanum* is read by the paper's own authors not as an independently domesticated lineage's wild sister, but as showing gene flow from already-domesticated eggplant back into wild-type populations — a feralization reading, not a second-center one. On this reading, the Indian cluster Meyer et al. (2012) and Barchi et al. (2023) both report is not a second wild-progenitor population at all, but a secondarily feralized descendant of the single Southeast Asian domesticate.

93.4 Why this is a disputed count, not a resolved single center with disputed feralization

§20.7.1's predicate requires an agreed count of independent domestication centers before a location can be assigned and compared. Here it cannot: two independently generated, methodologically distinct genomic datasets (AFLP/nrITS in 2012; targeted SNP genotyping of an order of magnitude larger sample in 2023) converge on a two-center reading, while a third, methodologically distinct dataset (genotyping-by-sequencing, 2019) converges on a one-center-plus-feralization reading of the very same Indian population both other studies treat as a second wild-progenitor cluster. This is not soybean's or quinoa's shape, where the disagreement turns on the placement of a single diagnostic accession or an unbounded complex reading (§36.6, §49.7); it is closer to dog's own structure (§12.4), where the same underlying population signal is read in two mutually exclusive ways by researchers working from comparable data — except that here the disagreement runs three studies deep rather than two, and the more recent, larger 2023 study reasserts the two-center reading against the intervening 2019 challenge rather than resolving it.

93.5 No PI computed; no κ assigned

Consistent with every other member of Appendix A.4, no Polycentricity Index is computed for eggplant and no κ is assigned. Doing so would require adjudicating between a two-center reading held by the two largest sampling efforts reviewed here and a one-center-plus-feralization reading held by an intermediate one, exactly the kind of live scientific disagreement §1.4's discipline and §12.4's own precedent for dog both instruct this cycle not to resolve on the author's own authority.

93.6 Placement in Appendix A.4, a twelfth entry

Eggplant is added to Appendix A.4 as a twelfth entry, on a footing distinct from every prior member: not two studies disagreeing about how many centers a single agreed population structure reflects (mango, §85.4–§85.5), but two studies proposing a wild-progenitor population's independence and a third proposing that the same population is not wild at all, but feral — a disagreement over the ontological status of the disputed second center, not merely over how to interpret it once its status is settled.

93.7 Cross-cycle synthesis: ninety-eight cases

With eggplant added, this cycle now covers ninety-eight cases and one hundred and three distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): eggplant contributes a twelfth Appendix A.4 row and this cycle's seventy-first Plantae species.

References newly cited in Chapter 93

Barchi, L., Aprea, G., Rabanus-Wallace, M.T., Toppino, L., Alonso, D., Portis, E., Lanteri, S., Gaccione, L., Omondi, E., van Zonneveld, M., Schafleitner, R., Ferrante, P., Börner, A., Stein, N., Díez, M.J., Lefebvre, V., Salinier, J., Boyaci, H.F., Finkers, R., Brouwer, M., Bovy, A.G., Rotino, G.L., Prohens, J. & Giuliano, G. (2023). Analysis of >3400 worldwide eggplant accessions reveals two independent domestication events and multiple migration-diversification routes. The Plant Journal 116(6): 1667–1680.

Meyer, R.S., Karol, K.G., Little, D.P., Nee, M.H. & Litt, A. (2012). Phylogeographic relationships among Asian eggplants and new perspectives on eggplant domestication. Molecular Phylogenetics and Evolution 63(3): 685–701.

Page, A., Gibson, J., Meyer, R.S. & Chapman, M.A. (2019). Eggplant Domestication: Pervasive Gene Flow, Feralization, and Transcriptomic Divergence. Molecular Biology and Evolution 36(7): 1359–1372.

Chapter 94 --- Cochineal (*Dactylopius coccus*): This Cycle's Third Invertebrate, and a Single Center Contested Between Two Continents

94.1 Admission, on maize's and sesame's own footing (§6.5, §70.5)

Cochineal is admitted here as this cycle's third invertebrate case, after honey bee (Ch.31) and silk moth (Ch.38), and on a structure neither of those two shares: not an absent genetic boundary (honey bee, §31) and not a clean single-center floor case (silk moth, §38.2), but a single-center dispute contested between two named, geographically distant candidate regions, on maize's and sesame's own ground (§6.5, §70.5) rather than a disputed center count. Cochineal (*Dactylopius coccus*) is the domesticated scale insect farmed for carminic acid, the source of the natural red dye known since pre-Columbian times across Mesoamerica and the Andes, and its own literature agrees on C=1 while disagreeing, across three independent lines of evidence spanning more than two decades, on which of two disjunct native ranges the species itself originated in.

94.2 The domestication background and its disjunct modern range

Native *Dactylopius coccus* is today restricted to two disjunct populations: one in the Mexican highlands, centered on Oaxaca but also present in Puebla, Tlaxcala, and the Valley of Mexico, and one in the Andean highlands of southern Peru. Both regions carry independent early evidence of use — cochineal-dyed textiles at Paracas, Peru, and cochineal farming at Toltec-period sites in Mexico — and the species' own disjunct distribution, with no known wild or feral population reported in the intervening region,

is itself the starting fact every source reviewed here treats as needing an explanation: either an original range spanning both regions later contracted at one end, or a single-region origin followed by deliberate pre-Columbian introduction to the other.

94.3 A morphological case for a South American origin

Rodríguez, Méndez & Niemeyer (2001, *Antiquity* 75(287): 73–77), reconstructing a phylogeny of the genus *Dactylopius* from morphological characters and setting it against the disjunct distribution of *D. coccus* specifically, argue that the genus's own South American species diversity and phylogenetic pattern support a South American origin for *D. coccus*, subsequently introduced into Mexico by pre-Columbian maritime trade routes along the Pacific coast.

94.4 A mitochondrial and climatic case for a Mexican origin

Van Dam, Portillo Martinez, Jeri Chavez & May (2015, *Annals of the Entomological Society of America* 108(3): 299–310), sequencing three mitochondrial gene regions (cytochrome oxidase I, tRNA-leucine, cytochrome oxidase II; 1,294 bp total) across a range-wide sample and independently modeling Holocene and Pleistocene climatic suitability for the species, report that both the mtDNA phylogeography and the climate-niche reconstruction converge on Oaxaca, Mexico, as *D. coccus*'s center of origin, directly opposed to Rodríguez et al.'s (2001) South American reading. The paper's own text notes that other, unpublished genetic work available at the time had been inconclusive, and flags its own finding as provisional pending further meta-genomic data to rule out confounding selective sweeps from bacterial endosymbionts.

94.5 A disclosed limit: the primary 2001 study not independently reachable

Rodríguez et al.'s (2001) own morphological-character phylogeny was not directly accessible for verification in the course of this chapter's research; its South American conclusion is carried here via its own consistent secondary characterization across the literature — including by Campana, Robles García & Tuross (2015), who describe it explicitly as an argument from morphological phylogenetic analysis — rather than independently re-examined against the primary text, on the same disclosed-limit discipline already applied to cowpea's own secondary-literature discrepancy (§74.4).

94.6 A modern genomic complication: a documented Andean lineage inside the Mexican commercial stock

Campana, Robles García & Tuross (2015, *Ecology and Evolution* 5(3): 607–617), whole-genome pool-sequencing bulk samples of Oaxacan small-scale-farm cochineal alongside Mexican and Peruvian commercial stock, report that present-day Mexican highland *D. coccus* itself comprises two genetically divergent populations: one unique to Mexico, and one more closely related to extant Andean cochineal — most plausibly explained by an undocumented introduction of Andean-type stock into Mexican commercial cultivation, plausibly during the 19th- or 20th-century collapse and subsequent reconstitution of Mexican cochineal farming the paper's own text separately documents. This finding does not itself adjudicate between §94.3's and §94.4's competing origin claims — it postdates the domestication event by centuries — but it discloses a limit on what any single modern Mexican sample, including farmed stock, can be assumed to represent: not every Mexican-collected accession is drawn from an undisturbed founding lineage.

94.7 A real-coordinate check on how far apart the two candidate regions are

Recomputed via great-circle distance between Oaxaca, Mexico (17.0732°N, 96.7266°W) and Ayacucho, Peru (13.1639°S, 74.2236°W) — the two regions named across the sources reviewed, not site-level excavation or collection points — the two candidate origins are approximately **4,173 km** apart, on maize's and Bactrian camel's own illustrative-only convention (§6.4, §19.5): a genuinely different continent, not a fine-grained disagreement about where within one broadly agreed region the center sits.

94.8 Applying §20.7's predicate: R(X)=0, a single center contested across two continents

C=1 is unanimous across every source reviewed — no study proposes more than one domestication event for *D. coccus* — but the location is not: Rodríguez et al.'s (2001) South American reading and Van Dam et al.'s (2015) Mexican reading stand opposed, unreconciled, with neither side independently corroborated a second time by an intervening study and neither withdrawn by its own proponents. R(X)=0 by §20.7.2's first branch, maize's and sesame's own ground (§6.5, §70.5), not a disputed count in dog's or eggplant's sense (§12.4, §93.4). No PI is computed.

94.9 Placement in Appendix A.3, a twenty-eighth entry

Cochineal is added to Appendix A.3 as a twenty-eighth entry, joining maize, Bactrian camel, broomcorn millet, almond, and sesame on the single-center-contested-only-in-location ground, and is this cycle's third invertebrate case overall after honey bee (Ch.31) and silk moth (Ch.38) — the first of the three to land in Appendix A.3 rather than at the A.2 floor or outside the index's domain, since honey bee lacks a genetic boundary altogether (§31) and silk moth's single center was never disputed (§38.2).

94.10 Cross-cycle synthesis: ninety-nine cases

With cochineal added, this cycle now covers ninety-nine cases and one hundred and four distinct species across fifteen sections and their supplementary chapters. No PI value already published anywhere in this monograph changes as a result (§20.7.4): cochineal contributes a twenty-eighth Appendix A.3 row and this cycle's thirty-first Animalia species.

References newly cited in Chapter 94

Campana, M.G., Robles García, N.M. & Tuross, N. (2015). America's red gold: multiple lineages of cultivated cochineal in Mexico. Ecology and Evolution 5(3): 607–617.

Rodríguez, L.C., Méndez, M.A. & Niemeyer, H.M. (2001). Direction of dispersion of cochineal (Dactylopius coccus Costa) within the Americas. Antiquity 75(287): 73–77.

Van Dam, A.R., Portillo Martinez, L., Jeri Chavez, A. & May, B.P. (2015). Range Wide Phylogeography of Dactylopius coccus (Hemiptera: Dactylopiidae). Annals of the Entomological Society of America 108(3): 299–310.

Chapter 95 --- Walnut (*Juglans regia*): A Single Center Whose Named Location Has Moved Three Times

95.1 Admission, a thirty-first supplementary case

Walnut is admitted here on the same footing as every supplementary case since Chapter 23 (§23.1): raised on its own evidentiary merits, and re-earning §2.7's and §20.7's discipline rather than being fitted to a pre-drawn table of contents. Common walnut (*Juglans regia*) is domesticated from a species whose wild range is uncontested — the tree occurs, wild or feral, in a broad arc from the Balkans and Anatolia through the Caucasus, Iran, Central Asia, the Himalaya, and southwestern China — but whose

domestication center within that range has been named differently by three separate bodies of literature spanning more than a decade, the most recent of them published only months before this cycle's own current chapters.

95.2 The traditional picture: an Irano-Anatolian center

The standard reference account (Zohary, Hopf & Weiss 2012) places walnut domestication in the Irano-Anatolian region of West Asia. This reading is reinforced by the population-genomic study of Ding, Cao, Zhang, Chen, Liu, Li et al. (2022, *Genome Biology*), whose whole-genome resequencing and demographic modelling of Persian walnut alongside its sister species, the southwest Chinese endemic *Juglans sigillata*, is read in the wider literature as most readily reconciled with a western source population for the species' own deepest genetic differentiation between an eastern and a western group. This is the reading carried into decades of horticultural and popular literature, and the one this cycle would have reported without further inquiry had the walnut literature stopped there.

95.3 A 2022 revision: southwestern China and the Himalaya-Tibet plateau

It does not stop there. Luo, Zhou, Cao, Yan, Chen, Wang, Woeste, Chen, Fei, An, Malvolti, Ma, Liu, Ebrahimi, Qiao, Ye, Li, Lu, Xu, Cao & Zhao (2022, *PLOS Genetics*), sequencing 309 walnut accessions — 98 wild Persian walnuts among them, drawn from around the world — report the core areas of genetic diversity of *J. regia* germplasm as southwestern China and southern Asia near the Qinghai-Tibet Plateau and the Himalaya, and read the uplift of the Himalaya itself as the main factor shaping the species' current population structure. This is not a minor refinement of the Irano-Anatolian picture; it names a different broad region, several

thousand kilometers to the east, as the center of the species' own standing diversity.

95.4 A 2026 bias-corrected reanalysis: South Asia, and an explicit rejection of both prior readings

A third reading has since appeared. Chen, Pang, Ding, Zhang, Yang, Liu, Nersesyan, Zhang, Renner, Zhang & Bai (2026, *Genome Biology*) argue that both the Irano-Anatolian and the Central Asian (Tian Shan) readings are artefacts of unbalanced sampling and unequal effective population size in prior STRUCTURE-based analyses, correctable by a parameterization strategy the authors propose and validate by simulation. Applying it to 298 wild and cultivated accessions, they report South Asia — specifically the western Himalaya and adjacent areas of Afghanistan, Pakistan, India and Nepal — as the source population, on six lines of evidence within their own dataset: lowest genetic drift, deepest placement in a neighbor-joining phylogeny, the highest count of private alleles, the lowest deleterious-mutation load, a stable rather than repeatedly bottlenecked demographic history, and the highest count of distinct chloroplast haplotypes of any sampled region. The paper states in its own text that its findings "clarify the long-standing debate on the geographic origin of walnut domestication," and states as plainly that this displaces rather than merely narrows the two earlier readings: Central Asia and West Asia are read here as intermediate stops on an eastward and westward dispersal route out of South Asia, not as independent centers.

95.5 A real-coordinate check among the three named regions

Following the convention this cycle has applied to every comparable location dispute (maize, §6.4; cochineal, §94.7), three representative points are anchored to the three regions named across this literature: a point within the Zagros/Iranian-plateau portion of the Irano-Anatolian region (36.5°N, 44.0°E), a point

within the Tian Shan range of Central Asia (42.0°N, 78.0°E), and a point within the western Himalaya/Kashmir portion of South Asia (34.0°N, 74.8°E). The pairwise great-circle distances (code/walnut_polycentricity_index.py, unedited output) are: West Asia–South Asia, 2,798.7 km; West Asia–Central Asia, 2,970.4 km; South Asia–Central Asia, 932.5 km. These are reported as illustrative-only figures, on maize's and cochineal's own convention: the dispute here is over which one region is correct, not over a corroborated plural count, so no D̄ and no PI follow from them.

95.6 Applying §20.7's predicate: R(X)=0, a single center under an active three-way location dispute

C=1 is not itself in question anywhere in the literature reviewed for this chapter: no source proposes more than one domestication event for *J. regia*. What is disputed, across three named regions and three non-overlapping bodies of evidence published in 2012, 2022 and 2026, is where that one center sits. The 2026 study is the most recent, the most methodologically explicit about correcting for known sources of bias in its predecessors, and the only one of the three to state in its own text that it supersedes the other two — but it is a single study, not yet independently corroborated by a second research group using a different dataset or method, on the same disclosed threshold this cycle applied to apple's unreplicated Iranian candidate (§33.4) and to cotton's individually-unresolved fourth center (§22.4). By §20.7.2's first branch, on the same ground already established for maize and cochineal (§6.5, §94.8), R(X)=0: no PI is computed.

95.7 Placement in Appendix A.3, a twenty-ninth entry

Walnut is added to Appendix A.3 as a twenty-ninth entry, joining maize, Bactrian camel, broomcorn millet, almond, sesame and cochineal on the single-center-contested-in-location ground. It is

the first case in this cycle whose own most recent source states explicitly that it displaces, rather than merely adds to, two named predecessors — a structure closest to cat's three-region reversal (§28) among cases already catalogued, though reached here entirely within the plant genomics literature rather than by an aDNA study overturning an mtDNA one.

References newly cited in Chapter 95

Zohary, D., Hopf, M. & Weiss, E. (2012). Domestication of Plants in the Old World, 4th edn. Oxford University Press, pp. 254–261.

Ding, Y.M., Cao, Y., Zhang, W.P., Chen, J., Liu, J., Li, P. et al. (2022). Population-genomic analyses reveal bottlenecks and asymmetric introgression from Persian into iron walnut during domestication. Genome Biology 23: 145.

Luo, X., Zhou, H., Cao, D., Yan, F., Chen, P., Wang, J., Woeste, K., Chen, X., Fei, Z., An, H., Malvolti, M., Ma, K., Liu, C., Ebrahimi, A., Qiao, C., Ye, H., Li, M., Lu, Z., Xu, J., Cao, S. & Zhao, P. (2022). Domestication and selection footprints in Persian walnuts (Juglans regia). PLOS Genetics 18: e1010513.

Chen, C.-J., Pang, X.-X., Ding, Y.-M., Zhang, W.-P., Yang, Y., Liu, J., Nersesyan, A., Zhang, B.-W., Renner, S.S., Zhang, D.-Y. & Bai, W.-N. (2026). Resolving sampling and population-size biases in domestication genomics supports a South Asian origin of walnuts. Genome Biology 27: 61.

Chapter 96 --- Melon (*Cucumis melo*): A Corroborated Two-Lineage Case, and This Cycle's Closing Count

96.1 Admission, a thirty-second supplementary case, and the cycle's stated target

Melon is admitted here as the thirty-second supplementary case since Chapter 23, and, as disclosed in advance of researching it, as

the case intended to close this cycle's running tally at one hundred and one rows in Appendix A — a number chosen for no evidentiary reason and stated here plainly as such: the count is a stopping point set by this cycle's own author, not a finding the cited literature independently produces. *Cucumis melo* (melon) is not to be confused with *Citrullus lanatus* (watermelon) and its own African wild relatives, already treated at length in Chapter 44; the two share a common name in English and nothing else relevant to this chapter.

96.2 Two ancient wild lineages, one Asian and one African

Sebastian, Schaefer, Telford & Renner (2010, *PNAS*), sequencing plastid and nuclear markers across roughly 100 *Cucumis* accessions from Africa, Australia and Asia, report that melon's closest wild relatives are Asian and Australian rather than African, and that melon itself is of Asian origin — a direct correction of the nineteenth-century assumption, based on the genus's African species richness, that melon must have originated in Africa. Endl, Achigan-Dako, Pandey, Monforte, Pico & Schaefer (2018, *American Journal of Botany*), building a denser dataset of seven DNA regions across roughly 90% of the genus's species, resolve modern melon cultivars into two wild lineages that diverged an estimated one to three million years ago — long before any human involvement — one restricted to Asia (*C. melo* subsp. *melo*) and the other, described in that paper as *C. melo* subsp. *meloides*, restricted to Africa. Chomicki & Renner's (2020, *New Phytologist*) review synthesizes this literature and states plainly that honey melon "was domesticated at least once in Asia and once in Africa."

96.3 Archaeobotanical corroboration on both continents

The genetic picture is independently corroborated by archaeobotany on each continent. On the Asian side, the oldest secure melon remains are dated to roughly 3000 BC in China

(Watson 1969, as reviewed) and to 2300–1600 BC at Indus Valley sites (Vishnu-Mittre 1974, as reviewed) — within the broader geographic sweep Zhao, Lian, Zhang, Fu, He, Ma et al.'s (2019, *Nature Genetics*) whole-genome resequencing of 1,175 accessions independently names when it reports evidence for domestication activity centered on India specifically. On the African side, the oldest African melon seeds are dated to 3700–3500 BC at Maadi, a Predynastic site in Lower Egypt (van Zeist & de Roller 1993; El Hadidi et al. 1996, as reviewed by Chomicki & Renner 2020) — a site with a real, published excavation coordinate, unlike most of the regional candidates this cycle has had to anchor only approximately.

96.4 A disclosed complication: Zhao et al.'s (2019) finer count within the Asian lineage

One additional finding is disclosed here rather than smoothed into the two-lineage picture above. Zhao et al. (2019), whose genome-wide resequencing is the most extensive single dataset reviewed for this chapter, report their own results as supporting three independent domestication events, not two: two within India specifically, and one in Africa. This is not a rival geography — every study reviewed for this chapter, including Zhao et al.'s own, agrees that the deepest split is between an Indian/Asian source and an African one — but it is a finer subdivision of the Asian side than Sebastian et al. (2010), Endl et al. (2018) or Chomicki & Renner's (2020) synthesis report, and it has not, as of the literature reviewed here, been independently corroborated by a second whole-genome dataset at that finer resolution. Following the same disclosed-but-unfolded threshold this cycle applied to apple's Iranian candidate (§33.4) and barley's Tibetan candidate (§2.4), this chapter reports Zhao et al.'s finer count in full rather than omitting it, and does not fold it into the C term below: the corroborated, doubly-independent-method structure this cycle requires for C is the two-

lineage Asia/Africa split, not the further Indian subdivision one study proposes.

96.5 A real-coordinate check and this cycle's third-highest index

Anchored at Maadi, Lower Egypt (29.96°N, 31.25°E) for the African center and at Harappa, in the Indus Valley (30.633°N, 72.868°E) — the region Vishnu-Mittre's (1974) archaeobotanical dating and Zhao et al.'s (2019) genomic reading both independently point to — the great-circle distance (code/melon_polycentricity_index.py, unedited output) is 3,973.1 km. With C=2 and κ=1.000 (three independent lines of evidence — two genetic, Sebastian et al. 2010 and Endl et al. 2018, and one archaeobotanical — converging on the same Asia/Africa split with no dissenting reading anywhere in the literature reviewed), PI = 7,946, this cycle's third-highest value, behind pig (13,050) and coconut (9,209), and ahead of common bean (6,601). Recomputing $\bar{D}$ at a narrower Indus Valley anchor, Mohenjo-daro (27.325°N, 68.138°E), in place of Harappa, moves $\bar{D}$ to 3,596.4 km and PI to 7,193 — reported here as a sensitivity check only, on the same terms as coconut's own Malesia-anchor sensitivity (§81.5).

96.6 Placement in Appendix A.1, and this cycle's closing tally

Melon is added to Appendix A.1 as its twelfth entry, joining coconut, common bean, and the other corroborated multi-center cases this cycle has assembled since barley (§2.4). With walnut (Ch.95, Appendix A.3, twenty-ninth entry) and melon (Appendix A.1, twelfth entry) both added, Appendix A now totals one hundred and one rows covering one hundred and six distinct species across seventeen sections and their supplementary chapters. Walnut contributes this cycle's seventy-second Plantae species; melon contributes its seventy-third. By kingdom, seventy-three of the one hundred and six species are now Plantae, thirty-one are Animalia, and two — yeast and koji — are Fungi,

unchanged. No PI value already published anywhere in this monograph changes as a result of either addition (§20.7.4). This closes the cycle at the round number stated in advance at §96.1 — a stopping point chosen by this cycle's author, not a finding the evidence itself produced, and disclosed as such rather than left to look like a coincidence.

References newly cited in Chapter 96

Sebastian, P., Schaefer, H., Telford, I.R. & Renner, S.S. (2010). Cucumber (Cucumis sativus) and melon (C. melo) have numerous wild relatives in Asia and Australia, and the sister species of melon is from Australia. Proceedings of the National Academy of Sciences USA 107: 14269–14273.

Endl, J., Achigan-Dako, E.G., Pandey, A.K., Monforte, A.J., Pico, B. & Schaefer, H. (2018). Repeated domestication of melon (Cucumis melo) in Africa and Asia and a new close relative from India. American Journal of Botany 105: 1662–1671.

Chomicki, G. & Renner, S.S. (2020). Origin and domestication of Cucurbitaceae crops: insights from phylogenies, genomics and archaeology. New Phytologist 226: 1240–1255.

Zhao, G., Lian, Q., Zhang, Z., Fu, Q., He, Y., Ma, S. et al. (2019). A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. Nature Genetics 51: 1607–1615.

Van Zeist, W. & de Roller, G.J. (1993). Plant remains from Maadi, a Predynastic site in Lower Egypt. Vegetation History and Archaeobotany 2: 1–14.

Appendix A — Master Synthesis Table (All Cases, Consolidated)

This appendix consolidates, in one place, every C, κ, $\bar{D}$, and PI value already derived in the main text and carried forward through the cycle's own progressive synthesis tables (§8.2; §13.7; §14.7; §15.7; §17.6; §19.8; §20.8; §22.7; §23.6). No value below is computed for the first time here: every row reproduces a number already published at the chapter and section cited in the final column, under the same no-invented-data discipline declared in §1.4. The three groupings below (A.1–A.3) follow the cycle's own three-way division of outcomes (§8.3, §20.7.2), and A.4 reports the one case — dog — that this division does not accommodate at all, because its open question is the center count itself, not a location or a fractional split within an agreed model.

A.1 Resolvable cases with a non-zero Polycentricity Index, ranked

Case	C	κ	$\bar{D}$ (km)	PI	Source
Pig (core model)	2	1.000	6,525	13,050	Ch.11, §11.4
Coconut (Cocos nucifera)	2	1.000	4,604.4	9,209	Ch.81, §81.5
Melon (Cucumis melo)	2	1.000	3,973.1	7,946	Ch.96, §96.5
Common bean	2	0.902	3,658	6,601	Ch.9, §9.5
Water buffalo (core model)	2	1.000	2,914.7	5,829	Ch.14, §14.4

Case	C	κ	D̄ (km)	PI	Source
Cattle (core model)	2	1.000	2,758.7	5,517	Ch.13, §13.4
Squash (C. pepo)	2	1.000	2,282	4,565	Ch.7, §7.2
Barley	2	0.556	3,046	3,384	Ch.2, §2.8.3
Avocado (Persea americana)	3	1.000	867.9	2,604	Ch.57, §57.7
Rice (C=2 model)	2	0.200	1,761	704	Ch.4, §4.5
Grapevine	2	0.897	305	547	Ch.10, §10.4
Goat (core model)	2	0.014	693.1	19.4	Ch.17, §17.4

The ~670× span between pig (13,050) and goat (19.4) already noted at Fig. C.16 is visible directly here: PI tracks κ at least as strongly as it tracks D̄ across this group, exactly as §8.2 first observed for the seven-case run. Coconut (Ch.81, §81.5), added in the present pass, reaches PI=9,209 and ranks second of the twelve entries, immediately behind pig (13,050) and ahead of melon (7,946) — the same two-independent-basin structure as barley's own two-center model, but with two orthogonal genetic lines (Bayesian clustering on microsatellites, corroborated independently by genome-wide SNP data) agreeing unanimously rather than barley's own partial 10-of-18-locus support, giving coconut κ=1.000 against barley's 0.556; a sensitivity check across the full breadth of the region proposed as its Pacific-side center moves its own PI between 5,393 and 14,038 (§81.5), never dropping it below second place. Melon (Ch.96, §96.5), added in the present pass, reaches PI=7,946 and ranks third of the twelve entries,

immediately behind coconut (9,209) and ahead of common bean (6,601) — the same doubly-independent-method structure this cycle applied throughout its supplementary run, with two genetic studies (Sebastian et al. 2010, Endl et al. 2018) and one archaeobotanical record converging unanimously on the same Asia/Africa split, giving melon κ=1.000; a sensitivity check moving the Indus Valley anchor from Harappa to Mohenjo-daro moves its own PI between 7,193 and 7,946 (§96.5), never displacing it from third place. Avocado (Ch.57, §57.7), added in the present synthesis pass, reaches PI=2,604 and ranks ninth of the twelve entries, immediately behind barley (3,384) and ahead of the rice C=2 model (704) — this cycle's first three-center case to clear R(X)=1 on every conjunct, in direct contrast to yam's (Ch.56) identical center count and opposite outcome (§56.7, §57.7).

A.2 Resolvable cases at the PI = 0 floor

Case	C	κ	D̄ (km)	PI	Source
Donkey	1 (directly tested, unanimous)	1.000	0	0	Ch.23, §23.5
Dromedary	1 (archaeology–genetics convergence)	1.000	0	0	Ch.18, §18.4
Einkorn	1 (unanimous)	1.000	0	0	Ch.2, §2.7
Chickpea	1 (unanimous)	1.000	0	0	Ch.2, §2.8.1
Horse	1 (three rivals refuted)	1.000	0	0	Ch.15, §15.5

Case	C	κ	D̄ (km)	PI	Source
Rice (C=1 model)	1 (unanimous)	1.000	0	0	Ch.4, §4.5
Sheep	1 (single broad zone)	1.000	0	0	Ch.16, §16.5
Sunflower	1 (2nd center refuted)	1.000	0	0	Ch.7, §7.3
Potato	1 (directly tested, unanimous)	1.000	0	0	Ch.24, §24.6
Foxtail millet	1 (China, molecular consensus)	1.0	0	0	Ch.26, §26.2
Alpaca	1 (vicuña; provisional, see caveat)	1.000	0	0	Ch.29, §29.3
Apple (Tian Shan model)	1 (Iranian candidate disclosed, unreplicated)	1.000	0	0	Ch.33, §33.5
Cacao	1 (Amazonian, doubly corroborated)	1.000	0	0	Ch.35, §35.2
Hemp (Cannabis sativa)	1	1.000	0	0	Ch.35, §35.4
Olive	1 (Mediterranean	1.000	0	0	Ch.35, §35.5

Case	C	κ	D̄ (km)	PI	Source
	introgression after founding)				
Date palm (2017 revision)	1 (African diversity read as introgression, not a 2nd centre)	1.000	0	0	Ch.35, §35.6
Silk moth	1 (unanimous, archaeology–genetics convergence)	1.000	0	0	Ch.38, §38.5
Coffee	1 (unanimous; wild-origin and domestication-pathway regions distinguished, not rival centers)	1.000	0	0	Ch.39, §39.6
Flax (Linum usitatissimum)	1 (unanimous, two independent genetic methods)	1.000	0	0	Ch.42, §42.6
C. argyrosperma	1 (unanimous, tested against named rival via Fastsimcoal2/AIC)	1.000	0	0	Ch.43, §43.7
C. maxima	1 (unanimous, two	1.000	0	0	Ch.43, §43.7

Case	C	κ	D̄ (km)	PI	Source
	independent genetic methods; location regionally inherited)				
Watermelon (C. lanatus, dessert lineage)	1 (unanimous as of 2023, reached by successive replacement)	1.000	0	0	Ch.44, §44.9
Peach (Prunus persica)	1 (unanimous, three independent whole-genome studies)	1.000	0	0	Ch.45, §45.5
Tomato (Solanum lycopersicum)	1 (single staged lineage: S. pimpinellifolium → S. l. var. cerasiforme → S. l. var. lycopersicum; no independently corroborated second center)	1.000	0	0	Ch.52, §52.7

Case	C	κ	D̄ (km)	PI	Source
Common carp (Cyprinus carpio)	1 (single origin; historical rival superseded)	1.000	0	0	Ch.58, §58.5
Cassava (Manihot esculenta)	1 (directly tested, unanimous)	1.000	0	0	Ch.59, §59.5
Oat (Avena sativa)	1 (unanimous, genomic)	1.000	0	0	Ch.62, §62.6
Domestic pigeon (Columba livia domestica)	1 (unanimous, three independent genomic studies)	1.000	0	0	Ch.66, §66.7
Yak (Bos grunniens)	1 (unanimous, within-region refinement disclosed)	1.000	0	0	Ch.67, §67.8
Hop (Humulus lupulus)	1 (unanimous, two later disclosed hybrid introgressions)	1.000	0	0	Ch.79, §79.6
Banteng (Bos javanicus)	1 (unanimous, first reference genome 2026)	1.000	0	0	Ch.83, §83.8

§8.3 already distinguished two different routes to this same floor value (unanimous from the outset; proposed, tested, and refuted). Horse, sheep,

dromedary, and donkey extend the second and third of those routes without adding a genuinely new one (§15.6, §16.6, §18.5–§18.6, §23.3). Chickpea (§2.8.1) is added to this table in the present synthesis pass: its PI=0 result was published at the time Chapter 2 was written but was never carried forward into this appendix, an omission corrected here rather than a new computation. Alpaca (Ch.29, §29.3) is added in the same pass on a different footing: no rival location or rival center count is proposed for it, which places it here by the table's own logic, but its single supporting site's most recent morphometric reanalysis disputes whether the cited osteological evidence shows domestication at all — a sixth route to this floor, held provisionally rather than asserted as settled. Silk moth (Ch.38) is added in the present synthesis pass on the same unanimous-from-the-outset footing as sheep and dromedary, but as this cycle's first insect case to reach A.2 rather than A.5 — its genetically bounded domesticated population (§38.6) is what admits it here, unlike honey bee's absence of one. Coffee (Ch.39) is added in the same pass on a seventh route: not a disputed count nor a taxonomic question, but a wild-origin region and a narrow domestication-pathway region reported as sequential stages of one lineage rather than as rival centers (§39.4, §39.7). Flax (Ch.42, §42.6) and C. maxima (Ch.43, §43.5) are added in the present pass on an eighth route, distinct from einkorn's: C=1 unanimous across two independent genetic methods, but with the wild-population center regionally inherited rather than independently tested to a point, so that $\bar{D}$=0 is reached by §20.7.2's second branch without R(X)=1 being required of the underlying location. C. argyrosperma (Ch.43, §43.2) reaches the same floor by the already-established tested-and-refuted-rival route (Fastsimcoal2/AIC adjudication against a named southern-Mexico alternative), not a new one. Watermelon (Ch.44, §44.7) is added on a ninth route: unanimity reached by successive replacement of two prior wild-population attributions (citron melon, then egusi melon) across three studies within a single decade, rather than by one study settling the question outright — a route this cycle has not catalogued before. Peach (Ch.45, §45.5) reaches the same floor by the same three-independent-study convention already established

for apple (§33.2): three independent whole-genome studies (Verde et al. 2013; Cao et al. 2014; Cao et al. 2019) converge on one unanimous domestication event, with no rival corroborated centre proposed by any source reviewed — not a new route, and, unlike apple's own disclosed Iranian candidate, with no unreplicated rival claim at all. Carp (Ch.58, §58.5) is added in the present synthesis pass on a tenth route, distinct from every one catalogued so far: not a disputed count tested against a named rival (as for C. argyrosperma, §43.2), nor a regionally-inherited location without an independently tested point (as for flax and C. maxima, §42.6, §43.7), but a specifically pre-genomic historical/cultural hypothesis of an independent second husbandry tradition (Balon 1995), superseded once whole-genome resequencing (Xu et al. 2014) became available to test it directly — this cycle's first case drawn from Pisces/Osteichthyes (§58.1). Cassava (Ch.59, §59.6) is added in the present pass as an eleventh case, but not an eleventh route: it reaches the floor by the same unanimous-from-the-outset path already established for potato and donkey, corroborated in cassava's own case by a direct archaeobotanical date at the same source region (§59.4) rather than by a new evidentiary structure. Domestic pigeon (Ch.66, §66.7) reaches the floor on the same apple/oat route already catalogued (§33.5, §62.6): a unanimous single center corroborated across three independent genomic studies, with an older, pre-genomic classification proposing scattered domestication disclosed rather than independently corroborated — not a twelfth route in its own right. Yak (Ch.67, §67.8) is added on an eleventh route distinct from every one catalogued so far: a single unanimous center whose own literature discloses both a within-region dispersal refinement and a separate, later, cross-species hybridization episode, neither of which the source literature itself treats as bearing on the founding center's own count. Hop (Ch.79, §79.6) is added on a twelfth route distinct from yak's own eleventh: a single, taxonomically confirmed wild source population for the crop's own founding domestication, with two later, geographically separate hybrid-introgression episodes disclosed during the crop's documented spread, neither treated by the source literature as a rival founding event. Banteng

(Ch.83, §83.8) is added on yak's own eleventh route directly, without a thirteenth reason: a single unanimous center, corroborated by this cycle's first reference-genome-based population study of the species, with one later, geographically localized admixture episode (Bali cattle from Kupang) disclosed by the same study that establishes the founding event, on the same footing already applied to yak's own Bangga episode. Opium poppy (Ch.86, §86.5–§86.6) is added on sunflower's and horse's own proposed-tested-and-refuted route directly, without a thirteenth reason: a named rival hypothesis — introduction into Europe from the Fertile Crescent as a weed of cultivation — was live in the literature and was directly discarded by a purpose-built genotyping-by-sequencing and seed-morphometric study (Machado et al. 2025), on the same footing already applied to sunflower's and horse's own refuted rivals. Buckwheat (Ch.89, §89.5–§89.6) is added as a thirty-third member on flax's own unanimous-single-center route (§42.6, §20.7.2's second branch) rather than sunflower's refuted-rival one: a single corroborated wild source whose apparent archaeobotanical-genomic geographic mismatch is read by its own source literature as a preservation and spread artefact, not a rival center. T'ef and finger millet (Ch.90, §90.5–§90.6) are added as a thirty-fourth and thirty-fifth member, on foxtail and broomcorn millet's own precedent (§26.5) for counting co-discussed but evidentially independent domestications separately: two single-origin results, from two different wild genera, reported together only because one 2025 study examined both from the same archaeobotanically sparse region. Pearl millet (Ch.91, §91.5–§91.7) is added as a thirty-sixth member on sunflower's and horse's own refuted-rival route (§8.3) rather than flax's unanimous one: a genuine decades-old multi-center hypothesis, directly tested by whole-genome sequencing and narrowed to a single western Saharan–Sahelian center. Goldfish (Ch.92, §92.4–§92.5) is added as a thirty-seventh member on flax's

and buckwheat's own unanimous-single-center route, joining common carp as this cycle's second confirmed Osteichthyes case.

A.3 Cases outside the index's domain (⊥, not computed)

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
Maize	1 (location disputed)	531 (location only)	R(X)=0, single-center location dispute	Ch.6, §6.5
Bactrian camel	1 (location disputed)	1,676.8–2,810.0 (sensitivity only)	R(X)=0, single-center location dispute	Ch.19, §19.5–§19.6
Chicken	1 (best-supported)	no reported point on either line	R(X)=0, zero resolved centers	Ch.20, §20.6
Turkey	2 (doubly corroborated)	2,451.1 (illustrative span only)	R(X)=0, one resolved / one unresolved center	Ch.21, §21.5–§21.6
Cotton	4 (unanimous, no dispute)	11,035.6 (3-of-4 subset, illustrative only)	R(X)=0, three resolved / one unresolved center	Ch.22, §22.5–§22.6
Broomcorn millet	1 (single process; center disputed)	790.5 (illustrative only)	R(X)=0, single-center location dispute	Ch.26, §26.3–§26.4
Cat	3 rival regions, unresolve	not reported at point	R(X)=0, no candidate region	Ch.28, §28.5–§28.6

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
	d (Levant / Egypt / North Africa)	resolution by any candidate	locatable at point resolution (new sub-reason)	
Llama	1 (guanaco, dry-puna region)	1,536.6 (Telarmachay –San Pedro de Atacama, illustrative only)	R(X)=0, single center but no point-level coordinate reported	Ch.29, §29.4–§29.5
Guinea pig	1 confirmed (Central Andes) + 1 disputed, of uncertain species identity (Colombian)	1,987.6 (Ayacucho–Bogotá, illustrative only)	R(X)=0, second population's species identity itself disputed (C. porcellus vs. C. anolaimae), not a location dispute	Ch.37, §37.4–§37.6
Capsicum (5 spp.)	5 (1 disputed)	5,249.8 / 5,035.4 / 233.9 (illustrative, 3 of 5 only)	R(X)=0, compound: unresolved location (chinense) +	Ch.40, §40.8

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
			no wild form (pubescens) + disputed independence (frutescens)	
Pea (Pisum sativum)	2 (doubly corroborated)	2,688.2 (Karacadağ–Mekelle, illustrative only)	R(X)=0, two corroborated centers, neither independently point-resolved	Ch.41, §41.6
C. moschata	⊥ (wild progenitor not identified)	not reported (no candidate wild population located)	⊥, not computed at the C-count stage: wild progenitor unresolved across mtDNA (2002), 44-locus nuclear (2017) and subsequent review (2024)	Ch.43, §43.7
Fig (Ficus carica)	traditional C=1 (never independently	not reported (no point-level coordinate for either reading)	⊥, not computed at two independent stages: the C-	Ch.46, §46.4–§46.6

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
	corroborated) vs. proposed C≥2 (disputed, unreplicated, region-level only)		count stage (traditional and newly proposed readings each single-source and mutually unreconciled) and, conditionally, the location stage (neither reading offers a point coordinate)	
Reindeer (Rangifer tarandus)	2 (genetically corroborated poles) or up to 5–6 (ethnohistoric proposals, untested against genomic data)	not reported (no point-level coordinate for either genetically corroborated pole)	⊥, R(X)=0: directly measured wild–domestic F_ST (mean 0.08; genome-wide 0.039786 between poles), asymmetric male-mediated erosion of that boundary, one pole's	Ch.48, §48.3–§48.8

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
			founding evidence partly undercut after the fact and its own wild source unidentified — tenth distinct ground	
Guinea fowl (Numida meleagris)	1 (best-supported: West Africa, within it Nigeria)	not reported (no point-level coordinate for the best-supported candidate region)	⊥, R(X)=0: same no-point-resolution ground already applied to chicken and turkey, compounded by an unreconciled multi-millennial gap between the genomic split date (~5,452 YBP) and the earliest	Ch.50, §50.6–§50.8

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
			surviving archaeological husbandry evidence (<2,000 YBP), and by a reversal, not a refinement, of the underlying structural signal as marker technology improved	
European rabbit (Oryctolagus cuniculus)	1 (best-supported: Iberian Peninsula and southern France)	not reported (no point-level coordinate for the best-supported candidate region)	⊥, R(X)=0: same no-point-resolution ground already applied to chicken, turkey, and guinea fowl, compounded by three independent dating methods	Ch.51, §51.9–§51.10

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
			(genetic, archaeological, textual) that fail to converge even in order of magnitude, by a fourth, older Palaeolithic/Roman evidentiary line, and by a documented citation error at the root of the traditional AD 600 narrative	
Fava bean (Vicia faba)	1 (proposed from a single extinct archaeobotanical assemblage; no living wild populatio	~20–30 (el-Wad, Mount Carmel – Yiftah'el, Lower Galilee; illustrative only)	⊥, new ground: a candidate wild progenitor is proposed on morphometric/archaeological grounds alone, with no living descendant	Ch.54, §54.6–§54.7

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
	n exists to corroborate geneticall y)		population available for genetic corroboration — distinct from C. moschata's absence of any candidate at all	
Goose (Anser anser domestic us / A. cygnoid es domestic us)	2 (doubly corrobora ted, two wild species)	8,425.7 (Tianluoshan – Meidum; illustrative and partial only)	⊥, R(X)=0: one resolved / one unresolved center — turkey's own branch, compounded by a reversed archaeology–genomics mismatch at each pole	Ch.55, §55.6–§55.7
Yam (Dioscor ea spp.)	3 (unanimo us, three continent s; none resolved)	not reported (no point-level coordinate for any of the three poles)	⊥, R(X)=0: three independently corroborated centers, none resolved — this cycle's	Ch.56, §56.7–§56.8

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
			first case of its kind, compounded by a disputed African wild-parentage model and an undisclosed second Asian-Pacific gene pool	
Muscovy duck (Cairina moschata)	1 (Neotropics; independent New World domestication)	not reported (no point-level coordinate; candidate range spans Panama, Ecuador, and coastal Peru)	R(X)=0, single center but no point-level coordinate reported — llama's own ground	Ch.63, §63.7–§63.8
Almond (Prunus dulcis)	1 (ABC-supported single domestication event)	not reported (no point-level coordinate for either candidate wild progenitor, P. orientalis or P. turcomanica)	R(X)=0, single-center location/founder dispute — maize's own ground	Ch.68, §68.7–§68.8

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
Sesame (Sesamum indicum)	1 (unanimous across sources reviewed)	not reported (Indian-subcontinent reading vs. 2026 East African reading, neither at point-coordinate resolution)	R(X)=0, single-center location dispute — maize's and almond's own ground	Ch.70, §70.7–§70.8
Onion and garlic (Allium cepa, A. sativum)	1 each (leading wild candidate itself disputed as wild)	not reported (no single population, wild or otherwise, positioned as the unique referent for either crop)	⊥, new ground: the leading candidate's own status as wild, not merely its role as sole founder, is disputed — by a proposed hybrid origin for onion, and by direct molecular reclassification from wild ancestor to feral	Ch.78, §78.5–§78.6

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
			descendant for garlic	
Jute (Corchorus capsularis, C. olitorius)	2 (unanimous, chromosome-level genomes)	not reported (C. olitorius has no point-level coordinate; "India and southern China" only)	R(X)=0, one resolved (Harappa) / one unresolved center — turkey's and goose's own branch	Ch.82, §82.5–§82.6
Mithun / Gayal (Bos frontalis)	1 disputed (direct gaur descent vs. hybrid founding)	not reported ("near the Assam–Burma border" only)	⊥, not computed at the C-count stage: the founding event itself, not merely its location, is reported oppositely by independent studies applying the same marker class	Ch.84, §84.7–§84.8
Bottle gourd (Lagenar	several (New World	not reported (no coordinate for any locale;	⊥, C itself left open by the cited	Ch.87, §87.6–§87.7

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
ia siceraria)	locales, count not resolved)	diffuse, weedy-habit-enabled pattern)	literature's own hedged language: a diffuse, unresolved domestication pattern layered atop a resolved question of geographic and genetic origin (also Appendix F)	
Grain amaranth (A. cruentus, A. hypochondriacus, A. caudatus)	3 (unanimous, polyphyletic wild ancestor; none resolved)	not reported (no point-level coordinate for any of the three centers)	⊥, R(X)=0: three independently corroborated regional centers, none resolved — yam's own ground, counted once across three species	Ch.88, §88.5–§88.6
Cochineal (Dactylo	1 (unanimous,	4,173 (Oaxaca–Ayacucho,	R(X)=0, single-center location dispute —	Ch.94, §94.8–§94.9

Case	C	Distance reported (km)	Branch (§20.7.2)	Source
pius coccus)	location disputed)	illustrative only)	maize's and sesame's own ground, contested across two continents	
Walnut (Juglans regia)	1 (undisputed; center location disputed)	2,798.7–2,970.4 (three-region span, illustrative only)	R(X)=0, single-center location dispute — maize's and cochineal's own ground, contested across three named regions	Ch.95, §95.5–§95.6

This is the same five-member group §22.7 assembled, on four distinct grounds, now extended to eight members on five distinct grounds: Chapter 28's cat and Chapter 29's llama are added in the present synthesis pass, both R(X)=0, but for a reason distinct from maize's, Bactrian camel's, chicken's, turkey's, and cotton's own — no source reviewed for either case reports a candidate origin at point-coordinate resolution at all, so no choice between rival points is even available to be disputed. No PI value published anywhere in the main text changes as a result of reproducing it here. Guinea pig (Ch.37) is added to this group in the same synthesis pass, R(X)=0 for a sixth distinct reason: unlike cat's or llama's missing point-coordinate problem, guinea pig's proposed second (Colombian) center is itself of uncertain species identity, so no confirmed two-center count for a single species is available to assess

(§37.4, §37.6). Pea (Ch.41, §41.6) is added to this group in the same synthesis pass, R(X)=0 for a seventh distinct reason: two independently corroborated domestication events (§41.2) meet two independently unresolved geographies (§41.3–§41.4), neither cat's multiple-rival-region problem nor llama's single-center-no-coordinate problem. C. moschata (Ch.43, §43.7) is added on an eighth and structurally prior reason: no study — mitochondrial (2002), 44-locus nuclear (2017), or subsequent review (2024) — has yet returned a candidate wild population at all, so the case is marked ⊥ at the C-count stage itself rather than reaching R(X)=0 over a proposed but unresolved center. *Fig (Ch.46, §46.6) is added to this group in a later pass on a ninth distinct reason, as its own chapter text already flags: not an absent or disputed coordinate, but a disagreement over the center count itself, unresolved at regional grain under either reading. Reindeer (Ch.48, §48.9) is added on a tenth distinct reason: a directly measured wild–domestic differentiation statistic (F_ST), reported and set against other domesticates' own published figures, rather than an absent or disputed coordinate. Fava bean (Ch.54, §54.6–§54.7) is added on an eleventh distinct reason: a wild progenitor proposed from a single extinct archaeobotanical assemblage, with no living population available for genetic corroboration by any method. Guinea fowl (Ch.50), European rabbit (Ch.51), goose (Ch.55), and yam (Ch.56) extend this group's own membership further, to nineteen rows in total at that point in the cycle (subsequently twenty with Muscovy duck, Ch.63, and twenty-one with almond, Ch.68), without adding a twelfth numbered reason: guinea fowl and rabbit share chicken's and turkey's own no-point-resolution ground, each with its own compounding detail rather than a new reason (§50.8, §51.10); goose shares turkey's own resolvability-split branch (§55.7); and yam shares the same no-point-resolution ground while supplying this cycle's first case with three or more independently corroborated centers of which none resolves, reported as a qualitative variation within the existing outcome rather than a new formal branch (§56.7). Muscovy duck (Ch.63, §63.7–§63.8) extends this group further on llama's own single-center-no-*

coordinate ground. Almond (Ch.68, §68.7–§68.8) extends this group to a twenty-first row on a footing distinct from every prior member sharing maize's own single-center-contested-only-in-location ground (maize, broomcorn millet): not a dispute over where within one broadly agreed region a single center sits, but a dispute over which of two named, geographically distant wild species — P. orientalis and P. turcomanica — founded the crop, left open by the same 2025 coalescent study that resolves the event count itself to one. Sesame (Ch.70, §70.7–§70.8) extends this group to a twenty-second row on a footing distinct from every prior member: not one recent study leaving a question open (almond) or a resolvability-split branch (goose), but two independent, generation-apart bodies of work — an archaeologically and genetically doubly corroborated Indian-subcontinent reading, and a single un-replicated 2026 population-genomic dataset of unprecedented sample size proposing East Africa instead — that disagree with each other on the location of an otherwise uncontested single center. Onion and garlic (Ch.78, §78.5–§78.6) extend this group to a twenty-third row on a footing distinct from every prior member: not a disputed location for an agreed-wild center (maize, almond, sesame) nor an absent candidate at all (C. moschata), but named candidates whose own status as wild, rather than merely their role as sole founder, is disputed by the cited literature — for garlic, by direct molecular evidence reversing the expected direction from ancestor to feral descendant, and for onion, by a proposed hybrid origin leaving no single population positioned as the predicate's unique referent. Jute (Ch.82, §82.5–§82.6) extends this group to a twenty-fourth row on turkey's and goose's own resolvability-split ground: not a new reason of its own, but the first instance of that branch outside Animalia, and the first where the two centers are two fully distinct cultivated species rather than two populations of one. Mithun (Ch.84, §84.7–§84.8) extends this group to a twenty-fifth row on a footing distinct from every prior member: not a disputed location for an agreed center, not an absent candidate, and not a disputed species identity for a proposed second population (guinea pig, §37.4–§37.6), but a single proposed center whose own status as direct

descent or hybrid founding is reported oppositely by independent studies of the same marker class, with only a partial, non-definitive reconciliation offered in the literature reviewed. Bottle gourd (Ch.87, §87.6–§87.7) extends this group to a twenty-sixth row on a footing distinct from every prior member: not a disputed location for an agreed center, an absent candidate, a disputed species identity, or a descent-versus-hybrid dispute, but a resolved question of geographic and genetic origin (transoceanic African drift, not Paleoindian Asian introduction) layered atop a diffuse, unresolved domestication pattern in which even the count of New World founding events is left open by the cited literature's own hedged language. Grain amaranth (Ch.88, §88.5–§88.6) extends this group to a twenty-seventh row, counted once as a single case spanning three species on the Triangle of U's, onion and garlic's, and jute's own convention (§76.7, §78.5–§78.6, §82.5–§82.6): this cycle's second instance of yam's own ground (§56.7), three independently corroborated, regionally distinct domestications from a polyphyletic wild ancestor, none resolved to a point. Cochineal (Ch.94, §94.8–§94.9) extends this group to a twenty-eighth row on maize's and sesame's own single-center-contested-only-in-location ground: not a disputed count and not an absent or unlocated candidate, but a unanimous single center whose location is argued, across three independent lines of evidence spanning more than two decades, between two disjunct native ranges roughly 4,173 km apart on two different continents. Walnut (Ch.95, §95.5–§95.6) extends this group to a twenty-ninth row on the same ground, contested here not between two but among three named regions and three non-overlapping bodies of evidence published in 2012, 2022 and 2026, the most recent of which states in its own text that it displaces rather than merely narrows its two predecessors — a single unreplicated study, not yet independently corroborated by a second dataset, so R(X)=0 on the same disclosed threshold already applied to apple's and cotton's own unresolved candidates.

A.4 Dog, Sorghum, Lentil, Tea, Soybean, Quinoa, Taro, Adzuki Bean, Cowpea, Peanut, Mango, and Eggplant — disputed center counts, not disputed locations

Dog is reported separately because the open question is not a disputed location (maize, Bactrian camel) and not a missing point coordinate (chicken, turkey, cotton): it is a live disagreement about the center count itself, C=1 (Bergström et al. 2020) versus C=2 (Frantz et al. 2016), argued substantially by the same research group from partly overlapping evidence. §12.4 declined to assign a κ to either reading, on the grounds that doing so would require adjudicating a live scientific disagreement rather than reporting one — exactly the authorial resolution §1.4's discipline was written to prevent.

Case	Disputed C	κ	Distance reported (km)	PI	Source
Dog	1 vs. 2 (disputed)	not assigned	8,146 (Bonn-Oberkassel – Yunnan, location-uncertainty only)	not computed	Ch.12, §12.4
Sorghum	1 vs. 2 (disputed)	not assigned	not reported (disagreement is over C, not a coordinate)	not computed	Ch.25, §25.4
Lentil	1–2 (unresolved)	not assigned	not reported (two gene pools within one wild-progenitor range; not framed by the source as C=2)	not computed	Ch.2, §2.8.2

Case	Disputed C	κ	Distance reported (km)	PI	Source
Tea (Camellia sinensis)	2 or 3, contested (Xia 2020 vs. Meegahakumbura 2016 / Zhang 2021)	n/a	n/a	not computed	Ch.35, §35.3
Soybean	1 vs. 2 vs. complex/unbounded (disputed)	not assigned	not reported (1,191.2 km mean pairwise across four named regions, illustrative/sensitivity only)	not computed	Ch.36, §36.6
Quinoa	C=1 vs. C=2 (disputed)	not assigned	not reported (disagreement is over C, via the placement of one diagnostic wild accession, not a coordinate)	not computed	Ch.49, §49.7–§49.8
Taro	C=1 vs. C≥2 (disputed)	not assigned	not reported (disagreement is over C, between archaeology/archaeobotany and maternally-	not computed	Ch.64, §64.6–§64.8

Case	Disputed C	κ	Distance reported (km)	PI	Source
			inherited plastid phylogeography, not a coordinate)		
Adzuki bean	C=1 (Japan) vs. multi-region (disputed)	not assigned	not reported (disagreement is over C, between a 2025 population-genomic study and a 2025 archaeobotanical study read by its own authors as multi-regional, not a coordinate)	not computed	Ch.72, §72.5–§72.7
Cowpea	West African vs. East African vs. dual-center (disputed, three-way)	not assigned	not reported (disagreement is over C, argued across three mutually exclusive positions over four decades of studies of growing sample size, not a coordinate)	not computed	Ch.74, §74.5
Peanut	1 vs. 2 allopolyploidization events (disputed)	not assigned	not reported (disagreement is over C, between a genomic synthesis through 2019 and a	not computed	Ch.80, §80.6–§80.7

Case	Disputed C	κ	Distance reported (km)	PI	Source
			2024 chloroplast/whole-genome study, not a coordinate)		
Mango	1 vs. 2 (two corroborated gene pools, disjunction left unresolved by own authors)	not assigned	not reported (disagreement is over how to read an agreed genetic structure — one center with strong post-domestication structuring, or two — not a coordinate)	not computed	Ch.85, §85.4–§85.6
Eggplant	1 vs. 2 (disputed)	not assigned	not reported (disagreement is over C, between two genomic datasets reading a two-center structure and a third reading the same structure as one center plus feralization, not a coordinate)	not computed	Ch.93, §93.4–§93.6

Because the dispute concerns C rather than a resolved model's location or completeness, dog is excluded from §22.7's five-member ⊥ group by the book's own definition, not by an omission of this appendix. Lentil (§2.8.2)

is added to this group in the present synthesis pass, for the same reason: Liber et al.'s two gene pools were never framed by their own source as two independently founded centers, which is a disputed-count problem, not a disputed-location one. Like chickpea in A.2, lentil's non-computation was disclosed when Chapter 2 was written but not previously carried into this appendix. Soybean (Ch.36) is added to this group in the same synthesis pass, on a different footing again: unlike dog, sorghum, and lentil, where a doubly- or partly-corroborated core sits beside one disputed extension, soybean's own reviewed literature disagrees about C itself, before any center can be located or counted (§36.6). Quinoa (Ch.49) is added to this group in the present synthesis pass, on a sixth and again distinct footing: unlike dog's disagreement between overlapping research groups reading overlapping ancient-DNA datasets, quinoa's C=1-versus-C=2 dispute turns on the placement of a single diagnostic wild accession (BYU 566) by three independently generated genomic datasets published across nine years, with the two most recent and most heavily sampled readings agreeing against the earliest one (§49.3, §49.7). Adzuki bean (Ch.72) is added to this group in the present pass, on an eighth and again distinct footing: unlike dog, quinoa, and taro, whose disputes rest on datasets separated by years or decades, adzuki bean's C=1-versus-multi-region disagreement turns on two studies — a population-genomic paper (Chien et al. 2025) and an archaeobotanical paper (Chen et al. 2025) — published four months apart in the same year, each framing its own result as bearing on the other's question without either engaging the other directly in the sources reviewed (§72.5). Cowpea (Ch.74) is added to this group in the present pass, on a ninth and again distinct footing: unlike every other member of A.4, which divides opinion two ways, cowpea's reviewed literature is read here as supporting three mutually exclusive positions — West African, East African, and dual-center — sustained not by one recent reversal but by four decades of studies of growing sample size that have not converged,

and carrying two further disclosed limits in how the secondary literature itself characterizes two of the primary studies reviewed (§74.4–§74.5). Peanut (Ch.80) is added to this group in the present pass, on a tenth and again distinct footing: unlike every other member of A.4, whose dispute concerns a wild-population founding center, peanut's own founding event is itself a natural interspecific hybridization between two wild diploid species, and the dispute here — between a single-origin reading synthesized through 2019 and a 2024 chloroplast-and-whole-genome study proposing two separate allopolyploidization events behind the crop's two subspecies — concerns how many such hybridization events occurred, layered onto an already-unresolved multi-millennial gap in the crop's own archaeological dating (§80.4). Mango (Ch.85) is added to this group in the present pass, on an eleventh and again distinct footing: unlike every other member of A.4, whose dispute concerns how many independent centers underlie an agreed population structure, mango’s own cited literature reports two independently corroborated genetic gene pools (Warschefsky & von Wettberg 2019; Wang et al. 2020) without either study’s own authors reading that structure as settled evidence of two founding centers, rather than one center followed by strong post-domestication structuring (§85.4–§85.5). Eggplant (Ch.93, §93.4–§93.6) is added to this group in the present pass, on a twelfth and again distinct footing: unlike mango, whose two corroborated gene pools are left uninterpreted as either one center or two by their own authors, eggplant's own reviewed literature divides into two independently generated genomic datasets reading a two-center population structure and a third, intermediate dataset reading the same Indian population not as a second wild progenitor but as a feralized descendant of a single Southeast Asian domesticate — a disagreement over the ontological status of the disputed second center, not merely over how to interpret an agreed one.

A.5 Banana, Yeast, Honey Bee, Koji, Vanilla, Sweet Potato, Citrus, Rye, Duck, Sugarcane, and the Triangle of U — cases outside the index's domain altogether

Banana (Musa spp.), yeast (Saccharomyces cerevisiae), and honey bee (Apis mellifera) are reported separately from A.3 and A.4 because none of the three's own literature presents a disputed location (A.3) or a disputed center count (A.4). Banana's literature documents a sequence of at least two, and by the fullest genomic accounting as many as eight or nine, real hybridization events across different named taxa and regions, contributing to a single mosaic cultivar genome (§27.4–§27.5). Yeast's literature documents a single, doubly-corroborated wild-origin region followed by several separately founded, separately dated domestication events — wine, sake, beer, bread, and bioethanol lineages — none of which merges into a single mosaic genome the way banana's cultivars do, and none of which is a rival claim about the same event (Ch.30, §30.2–§30.5). Honey bee's literature presents neither a mosaic genome nor several separately dated founding events, but something prior to both: for most of its recorded management history no source reviewed reports a domesticated population genetically bounded from its wild source at all, so the predicate's own object — a candidate center's referent — is not available to be counted (Ch.31, §31.5–§31.6). In none of the three cases is a single C assigned, because in none of the three is a single, genetically distinguishable domestication event being counted; §20.7.1's predicate presupposes a single proposed center set with a genetically bounded referent, which does not apply to any of them, for three distinct reasons.

Case	Why no C is assigned	Source
Banana	Own literature reports a sequence of hybridization events across several taxa/regions, not a discrete choice among candidate centers for one event; §20.7.1's predicate presupposes a single proposed center set, which does not apply here.	Ch.27, §27.4–§27.5
Yeast	Own literature reports one doubly-corroborated wild-origin region (East Asia/China; Peter et al. 2018, Duan et al. 2018) but several separately founded, separately dated domestication events (wine, sake, beer, bread, bioethanol) drawn from it, not a discrete choice among candidate centers for one event; §20.7.1's predicate presupposes a single proposed center set, which does not apply here either.	Ch.30, §30.2–§30.5
Honey Bee	Own literature reports no genetically bounded domesticated population distinguishable from the wild source across most of its recorded management history (continuous gene flow, no species-level bottleneck); the one confirmed domestication-associated genetic signature is confined to a single recent, intensively managed population. §20.7.1's predicate presupposes a domesticated population as its object, which most of this species' own documented history does not supply.	Ch.31, §31.5–§31.6

Case	Why no C is assigned	Source
Koji (Aspergillus oryzae)	Domestication event count itself disputed (2025 evidence); no coordinate reported for any candidate event	Ch.32, §32.5
Vanilla (Vanilla planifolia)	Domestication centre uncontested, but the crop's historically consequential bottleneck is reproductive/technological, not a founder-effect location question	Ch.34, §34.5
Sweet potato (Ipomoea batatas)	Own literature (2013–2025) disputes the number and identity of contributing wild taxa (1–3, across six non-equivalent readings), not a center count within one agreed progenitor; §20.7.1's predicate presupposes a single proposed center set with a genetically bounded referent, which does not apply here. A second, independent dispute over human vs. natural post-domestication dispersal to Polynesia is documented but not tabulated, as it lies outside §20.7.1's predicate entirely.	Ch.47, §47.2–§47.7
Citrus (Citrus spp.)	Own literature (Wu et al. 2018) reports at least three true ancestral species (citron, pummelo, mandarin) whose repeated interbreeding produces a mosaic genome in most edible cultivars (sweet orange, lemon, lime, grapefruit), not a discrete choice among candidate centers for one event; §20.7.1's predicate presupposes a single proposed center set, which does not	Ch.53, §53.5

Case	Why no C is assigned	Source
	apply here — the same ground already established for banana (§27.4–§27.5).	
Rye (Secale cereale)	Own literature (Sun et al. 2022) reports the best-supported demographic model as cultivated rye descending from weedy rye, a genetically distinguishable intermediate population between wild and cultivated forms, rather than as a direct wild-to-domesticate transition; §20.7.1's predicate presupposes a single such transition, which the best-supported model itself replaces with two linked ones mediated by a population that is neither wild nor yet the crop.	Ch.60, §60.5–§60.6
Duck, mallard-derived (Anas platyrhynchos domesticus)	Conflicting mitochondrial readings dispute whether one wild species (mallard) or two (mallard and Eastern spot-billed duck, by parallel domestication, hybrid capture, or later introgression) founded Chinese domestic duck; the wild-founder count itself, not the location, is unresolved — honey bee's own absent-genetic-boundary ground, reached here through directly conflicting published readings rather than a single consistent absence of differentiation.	Ch.63, §63.3–§63.5
Sugarcane (Saccharum	Own literature (Zhang et al. 2019) reports a molecular divergence date for S. officinarum vs. S. robustum (~385,000 years BP) directly disputed by that same	Ch.75, §75.5–§75.7

Case	Why no C is assigned	Source
officinarum)	study's authors as incompatible with a Holocene domestication process, alongside a separately reported non-point, mosaic domestication landscape (Denham 2025); §20.7.1's predicate presupposes that a Holocene domestication event took place, which this dissenting reading itself denies.	
Triangle of U (Brassica napus, B. juncea, B. carinata)	Own literature reports all three as allotetraploid species formed by interspecific hybridization between two already-domesticated diploid crops (B. rapa, B. oleracea, B. nigra), followed by chromosome doubling, rather than as domestications of a wild population; §20.7.1's predicate presupposes a candidate center representing a wild population's transition to cultivation, which no wild population of any of the three ever supplies. Counted once as a single case spanning three species, on the same convention already applied to duck (§63.1).	Ch.76, §76.6–§76.7

Banana, yeast, and honey bee join Appendix A as a shared new subsection because none fits A.3's location-dispute grounds nor A.4's disputed-count grounds; the open question for each is whether the index's own model of a domestication event applies to the case at all — for banana because admixture across taxa compounds into one genome before any C can be assigned, for yeast because the source population is one but the founding events are many, separately dated, and separately lineaged, and for honey bee because a genetically bounded domesticated population, the model's

own precondition, is not supplied by most of the species' recorded management history at all. Yeast is the first case in this cycle drawn from the kingdom Fungi, rather than Plantae or Animalia; honey bee is the first drawn from Insecta, and the first Animalia representative in this cycle that is not a vertebrate. Four further cases are folded into this subsection in later synthesis passes, each for its own reason distinct from banana's, yeast's, and honey bee's: koji (Aspergillus oryzae, Ch.32, §32.5) on a fourth reason, a disputed domestication-event count with no coordinate reported for any candidate event, closer in shape to A.4's disputed-count cases than to its own subsection-mates, but excluded from A.4 because the count dispute concerns fungal domestication events rather than wild-population centers of the kind A.4's crops and dog dispute; vanilla (Vanilla planifolia, Ch.34, §34.5) on a fifth reason, an uncontested single centre whose historically consequential bottleneck is reproductive and technological (hand-pollination) rather than a founder-effect location question the index was built to weight; sweet potato (Ipomoea batatas, Ch.47, §47.2–§47.7) on a sixth reason, a literature disputing the number and identity of contributing wild taxa across six non-equivalent readings rather than a center count within one agreed progenitor; and citrus (Citrus spp., Ch.53, §53.5) on a seventh reason, sharing banana's own mosaic-genome ground but from a documented minimum of three true ancestral species (citron, pummelo, mandarin) rather than banana's own sequence of two to nine hybridization events. Koji is this cycle's second case from the kingdom Fungi, after yeast; vanilla, sweet potato, and citrus are Plantae, alongside banana. Rye (Secale cereale, Ch.60, §60.5–§60.6) is folded into this subsection in the present pass as an eighth entry, on a fifth reason distinct from all four just listed: not a disputed event count (koji), not a reproductive/technological bottleneck standing in for a location question (vanilla), not a dispute over contributing wild taxa (sweet potato), and not a mosaic genome built from several hybridizing ancestral species (banana, citrus), but

a single, uncontested wild-origin region whose own best-supported demographic model interposes a named, dated, genomically characterized weedy intermediate population between the wild species and the crop — a structure §20.7.1's predicate was not built to count at all, tested directly against the alternative by explicit model comparison (§60.3) rather than inferred from an absence of evidence. Rye is Plantae, alongside banana, vanilla, sweet potato, and citrus. Sugarcane (Saccharum officinarum, Ch.75, §75.5–§75.7) is folded into this subsection in the present pass as a tenth entry, on a sixth reason distinct from all prior members: not a disputed event count, contributing-taxa count, or wild-founder count, and not a reproductive/technological bottleneck or weedy intermediate population, but a directly stated, dissenting molecular divergence date (Zhang et al. 2019) disputing that the wild/domesticate split it describes occurred within the Holocene at all, layered onto an already-documented non-point, mosaic domestication landscape (Denham 2025) shared in shape, though not in underlying cause, with banana's own ground. Sugarcane is Plantae, alongside banana, vanilla, sweet potato, citrus, and rye. The Triangle of U (Brassica napus, B. juncea, B. carinata, Ch.76, §76.6–§76.7) is folded into this subsection as an eleventh entry, on a seventh reason distinct from all prior members: not a disputed event, contributing-taxa, or wild-founder count, not a reproductive/technological bottleneck or weedy intermediate population, and not a dissenting divergence date, but a domestication event — interspecific hybridization followed by chromosome doubling — whose own two parental lineages were each already domesticated crops, so that no wild population is, or could be, a candidate referent for any of the three resulting species. Unlike every other member of this subsection, the Triangle of U is counted once as a single case spanning three species, on the same convention already applied to duck (§63.1), where two species share one chapter and one row. Two of the three amphidiploids (B. napus, B. juncea) carry a further, disclosed

complication — their own literature separately disputes how many times the underlying hybridization occurred — reported at §76.4 but not added as separate A.4 rows, since the entity in dispute is a hybridization event between two already-domesticated lineages, not a wild-population center of the kind A.4's crops and dog dispute. The Triangle of U is Plantae, alongside banana, vanilla, sweet potato, citrus, rye, and sugarcane.

A.6 Cross-cycle patterns, computed once, at the close

This section adds nothing new to A.1–A.5: it computes summary statistics directly on the numbers already tabulated there, via code/AppendixA6_cross_cycle_stats.py, and reports what they show, including where they revise an earlier reading rather than confirm it.

§8.2 first observed, on a seven-case run, that PI tracks κ at least as strongly as it tracks D̄. A.1 has since grown to twelve cases (grapevine and goat were added after §8.2 was written; avocado in a later pass, Ch.57, §57.7; coconut in an earlier pass of the present cycle, Ch.81, §81.5; melon in the present pass, Ch.96, §96.5). Recomputed on all twelve, a Spearman correlation gives ϱ(κ, PI) = 0.702 ($p = 0.011$) against ϱ(D̄, PI) = 0.944 ($p < 0.001$): D̄ tracks PI more tightly than κ does, a margin that widens slightly from the eleven-case reading (ϱ=0.694/0.927) rather than reversing it. This does not overturn §8.2's substantive point — both terms still correlate strongly and positively with PI, and PI is not simply proportional to either alone — but the specific ranking claimed at n=7 continues not to survive at n=10, and is reported here as revised rather than reproduced.

Across the full cycle, Appendix A totals one hundred and one rows covering one hundred and six distinct species (rice is counted once under each of two models; mallard-derived duck and Muscovy duck are counted as the two distinct species they are, not as one

case twice; the Triangle of U is counted once as a single row spanning the three species it comprises; onion and garlic, and jute, are likewise counted once each as a single row spanning two species, on the same convention). Twelve cases reach a corroborated, non-zero Polycentricity Index (A.1); thirty-seven reach the C=1 floor (A.2, twenty-seven plus pigeon, yak, hop, banteng, opium poppy, buckwheat, t’ef, finger millet, pearl millet, and goldfish); twenty-nine sit outside the index's domain at the C-count or location stage (A.3, twenty-one plus sesame, onion/garlic, jute, mithun, bottle gourd, grain amaranth, cochineal, and walnut); twelve report a disputed center count rather than a disputed location (A.4, seven plus adzuki bean, cowpea, peanut, mango, and eggplant); and eleven report a domestication process the index was not built to count at all (A.5, ten plus the Triangle of U). No case in this cycle was dropped for want of a result: every one of the one hundred and six is reported somewhere in this table, on whichever of the five terms its own cited literature actually supports.

By kingdom, seventy-three of the one hundred and six species are Plantae (forty-six plus sesame, adzuki bean, cowpea, sugarcane, the Triangle of U's three species, onion, garlic, hop, peanut, coconut, jute's two species, mango, opium poppy, bottle gourd, grain amaranth's three species, buckwheat, t’ef, finger millet, pearl millet, eggplant, walnut, and melon), thirty-one of the remainder are Animalia (twenty-five plus pigeon, yak, banteng, mithun, goldfish, and cochineal), and two — yeast and koji — are Fungi, unchanged. Kingdom membership predicts neither a case's outcome branch nor its PI rank anywhere in this cycle, consistent with the finding first made at yeast's admission (§30.6) and restated at honey bee's (§31.7).

Appendix B — Computational Verification (Disclosed Scope)

Every distance and polycentricity-index computation in this cycle is attributed in the main text to a named script (for example distance_check.py, Ch04_support_distance_check.py, or Ch09_polycentricity_index.py). Reproducing all of these from scratch for this appendix, without the original computation's exact anchor-coordinate choices, would risk quietly substituting new coordinates for the ones actually used and silently producing numbers that only coincidentally match — exactly the kind of unearned precision this cycle's no-invented-data discipline exists to prevent. What follows is a narrative account of what each computation did — which coordinates it used and where they come from, how the distance was computed, and how the result compares with the figure already reported in the corresponding chapter — rather than a reproduction of the code itself.

Of the roughly twenty scripts named across Chapters 2, 4, 6, 7, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 21 and 22, this appendix accounts for nine in full: one carried over unchanged from the original computation (B.1); three reconstructed independently and checked against the already-published figures rather than assumed to match them (B.2–B.4); and five executed directly alongside Chapters 13, 14, 15, 21 and 22 (B.5–B.9). Chapter 29's own text reports one further computation — the Telarmachay–San Pedro de Atacama illustrative distance, §29.4 — without attributing it to any named script at all, unlike every other computation in this cycle; B.10 independently reconstructs and checks that figure, on the same footing as B.2–B.4, bringing this appendix's full accounting to ten. The remaining scripts — distance_check.py, Ch06_07_support_distance_check.py, Ch09_support_distance_check.py, Ch09_polycentricity_index.py, Ch09_lima_bean_distance_check.py,

Ch10_polycentricity_index.py, Ch11_support_distance_check.py, Ch12_support_distance_check.py, Ch16_sheep_distance_check.py, Ch17_goat_distance_check.py, Ch18_dromedary_distance_check.py and Ch19_bactrian_distance_check.py — were part of the original computational pipeline that produced the figures already reported in the chapters above, but their source was not part of this appendix's own computational work and is not reconstructed here. This is disclosed as an open gap in the appendix's own coverage, in the same spirit as §2.8.2's disclosed non-computation for lentil — a genuine limitation of this delivery, not a claim that the underlying figures are unverified. This gap is closed, for all twelve scripts, at B.13–B.24 below, added in a later pass of this same appendix.

B.1 Einkorn–chickpea distance check (§2.8.4)

Originally computed alongside §2.8.4, this computation finds the great-circle (haversine) distance between the einkorn wild core at Karacadağ, south-eastern Turkey (37.67°N, 39.83°E), and wild chickpea accession Cr25 near Midyat, Mardin Province (37.42°N, 41.34°E; van Oss et al. 2015), using a mean Earth radius of 6,371 km. The result is 136.0 km — exactly the figure reported in §2.8.4, since that figure was generated by this computation rather than transcribed from elsewhere.

B.2 Hajji Firuz Tepe–Areni-1 Cave distance check (§10.3, reconstructed and independently verified)

Referenced in §10.3 but not among the scripts carried over from the original computational pipeline, this computation was reconstructed using independently looked-up coordinates for the two named archaeological anchors — not the original computation's exact coordinate choices, which remain unknown — and checked against the already-published 305 km figure rather than assumed to match it. Using Hajji Firuz Tepe, West Azerbaijan,

Iran (36.9942°N, 45.4694°E) and Areni-1 Cave, Vayots Dzor, Armenia (39.7314°N, 45.2036°E), on a mean Earth radius of 6,371.0088 km, the great-circle distance comes to 305.2 km — a 0.2 km (0.1%) difference from §10.3's reported 305 km, well within rounding and coordinate-precision tolerance for tell- and cave-scale sites. This independently confirms that §10.3's figure was not invented: it is reproducible from real, publicly documented coordinates for the two named sites, even though the script that originally produced it was not part of this appendix's delivery.

B.3 Rice regional distance check (§4.4, reconstructed)

Referenced in §4.4 but not in the original appendix delivery, this computation was reconstructed with independently chosen representative coordinates for each named region — Pearl River (Guangzhou, 23.13°N, 113.26°E), Middle Yangtze (Changsha, Hunan, 28.20°N, 112.97°E), Indochina (Luang Prabang, 19.89°N, 102.14°E) and the Brahmaputra (Guwahati, Assam, 26.14°N, 91.73°E) — rather than the original computation's exact points, which are unknown. The four pairwise distances computed were 1,205 km (Pearl River–Indochina), 2,199 km (Pearl River–Brahmaputra), 1,435 km (Middle Yangtze–Indochina) and 2,111 km (Middle Yangtze–Brahmaputra), against the published 1,210, 2,203, 1,559 and 2,070 km respectively. The first two pairs, anchored on Pearl River, match to within 5 km; the Middle Yangtze/Indochina pair differs by 124 km (8%), most likely because this reconstruction's Hunan anchor (Changsha) is not the exact point the original computation used within the disjunctively named "Hunan/Jiangxi" region. The recomputed mean of 1,738 km differs from the published 1,761 km by 1.3% — close enough to confirm the figure is not invented, not close enough to claim exact reproduction, and both are reported rather than only the flattering one.

B.4 Rice polycentricity-index recomputation (§4.5, reconstructed)

Using κ=0.200 — Jing, Zhang, Wang et al. (2023)'s own directly reported ~20% minority-origin gene fraction, not re-derived, only applied — together with D̄ from B.3 above, PI = 2 × κ × D̄ gives 704 using the published D̄ of 1,761 km, exactly matching §4.5's reported value, and 695 using this reconstruction's own D̄ of 1,738 km, a 1.3% difference propagated through from B.3 rather than hidden.

B.5 Cattle distance check (§13.4–§13.5)

Originally computed alongside Chapter 13, this computation finds the great-circle distance between the two doubly-corroborated cattle domestication centers — Çayönü Tepesi, upper Tigris, south-eastern Turkey (38.2183°N, 39.7251°E), for taurine cattle, and Mehrgarh, Kachi plain, Balochistan, Pakistan (29.2125°N, 67.6708°E), for zebu/indicine cattle — on a mean Earth radius of 6,371.0088 km, the same convention used from B.2 onward. The core distance comes to 2,758.7 km, giving PI = 2 × 1.0 × 2,758.7 ≈ 5,517 — exactly the figures reported in §13.4 and §13.5, since these were generated by this computation rather than transcribed from elsewhere. The same computation also checks the distances from both confirmed centers to a contested third (African) candidate, Nabta Playa/Bir Kiseiba, Egypt (22.5333°N, 30.7167°E), and the resulting three-point mean pairwise distance, reported purely as a sensitivity check and not used in any PI computation.

B.6 Water buffalo distance check (§14.4)

Originally computed alongside Chapter 14, this computation finds the great-circle distance between the two doubly-corroborated water buffalo domestication centers — Mehsana, Gujarat, India (23.5879°N, 72.3693°E), representing the river-buffalo breeding tracts of Kumar et al. (2007), and Xishuangbanna, southern Yunnan, China (22.0074°N, 100.7978°E), representing the swamp-buffalo China/Indochina border region of Zhang et al. (2011, 2016) — on the

same mean-Earth-radius convention as B.5. The distance comes to 2,914.7 km, giving PI = 2 × 1.0 × 2,914.7 ≈ 5,829 — exactly the figures reported in §14.4, since these were generated by this computation rather than transcribed from elsewhere.

B.7 Horse distance check (§15.5)

Originally computed alongside Chapter 15, this computation finds the great-circle distance from the single validated horse domestication center — the lower Volga-Don steppe, represented by Volgograd, Russia (48.7080°N, 44.5133°E) as this cycle's own disclosed representative point within Librado et al.'s (2021) broader "homeland" zone — to three rival candidate centers subsequently excluded by ancient DNA: Botai, north-central Kazakhstan (53.2000°N, 67.5500°E); the Iberian Peninsula, a broad representative point (42.3500°N, −3.5200°E; the specific primary source for this candidate is not independently confirmed, disclosed at §15.3); and central Anatolia, likewise a broad representative point (37.6667°N, 32.8000°E; same disclosed citation caveat as Iberia, §15.3). The same computation also finds the naive four-point mean pairwise distance as a sensitivity check only, since three of the four points are refuted candidates rather than corroborated centers, so no PI is computed from it. With only the single validated center standing, C=1 and $\bar{D}$=0 by convention, giving PI=0, exactly as reported in §15.5.

B.8 Turkey illustrative-span check (§21.5)

Originally computed alongside Chapter 21, this computation finds the great-circle distance from the resolved Mesoamerican turkey domestication center — the Oaxaca Valley, Mexico, represented by Mitla (17.0732°N, −96.7266°E; Lapham et al. 2016) — to the geographic centroid of the Southwest US findspot cluster (Four Corners area: south-eastern Utah, south-western Colorado, northern Arizona, north-western New Mexico), represented by a

single point at 36.5°N, −108.5°E. This is reported explicitly as an illustrative span rather than a center-to-center corroborated distance, since the Southwest cluster itself has no reported coordinate (§21.4–§21.5). The distance comes to 2,451.1 km — exactly the figure reported in §21.5, since it was generated by this computation rather than transcribed from elsewhere.

B.9 Cotton pairwise distance check (§22.5)

Originally computed alongside Chapter 22, this computation finds the great-circle distances among the three point-resolvable Gossypium domestication centers: G. hirsutum, represented by the Yucatán Peninsula (Mérida, 20.9674°N, −89.5926°E); G. barbadense, represented by Huaca Prieta, Chicama Valley, Peru (−7.85°N, −79.45°E); and G. arboreum, represented by Mehrgarh, Pakistan (29.4839°N, 67.6058°E). G. herbaceum is excluded, since its own origin is reported as unresolved in the cited literature (§22.4), so R(X)=0 for the full C=4 set and no PI is computed (§22.6). The three pairwise distances come to 3,390.5 km (hirsutum–barbadense), 13,896.5 km (hirsutum–arboreum) and 15,819.6 km (barbadense–arboreum), with a mean of 11,035.6 km — reported as a sensitivity figure only, not as a PI $\bar{D}$ — exactly matching the figures reported in §22.5, since these were generated by this computation rather than transcribed from elsewhere.

B.10 Llama/alpaca illustrative distance check (§29.4, reconstructed)

Referenced in §29.4 but, unlike every other computation in this cycle, not attributed there to any named script at all — the chapter simply reports the result. This entry independently reconstructs it using the two coordinates given directly in §29.4's own text: Telarmachay, Junín, Peru (11°11′S, 75°52′W) and San Pedro de Atacama, Chile (22°54′S, 68°12′W), on the same mean-Earth-radius convention as every other distance in this cycle (6,371.0088 km).

The independent computation gives 1,535.8 km, a 0.8 km (0.05%) difference from §29.4's reported 1,536.6 km — within rounding tolerance for two decimal-minute coordinate pairs, and consistent with the figure being reproducible from real, publicly stated coordinates rather than invented. As §29.4 itself already discloses, this distance is reported as an illustrative span only, between one well-defined site (Telarmachay) and one representative point within llama's much larger named region — not a Polycentricity Index for either species.

B.11 Cassava internal-breadth distance check (§59.8)

Computed via great-circle distance (code/Ch59_cassava_distance_check.py), using a representative point within the genetic wild-source region Olsen and Schaal (1999, 2001) narrow to "a limited area … between western Mato Grosso and western Rondônia" — Vilhena, Rondônia, Brazil (12.7406°S, 60.1458°W) — and a representative point for the archaeobotanical confirmation region at the Llanos de Moxos, Bolivia (Lombardo et al. 2020) — Trinidad, Beni, Bolivia (14.8292°S, 64.9014°W). On the same mean-Earth-radius convention as every other computation in this cycle (6,371.0088 km), the great-circle distance is 563.6 km. As with dromedary's own internal-breadth check (§18.4), this is not a C=2 distance between rival centers — both points sit inside the single southern Amazon border zone independently implicated by genetics and archaeology — but a disclosed measure of how widely that zone is drawn, spanning parts of two present-day countries. It is wider than dromedary's own 20.7 km figure, consistent with cassava's own literature describing a broader source region ("a relatively restricted area," not a single excavated site) than dromedary's two named sites.

B.12 Rye wild-range-to-find-site distance check (§60.9)

Computed via great-circle distance (code/Ch60_rye_distance_check.py), using a representative point within the wild relatives' own range in eastern Turkey and the Transcaucasus — Erzurum, Turkey (39.9086°N, 41.2769°E) — and a representative point for Can Hasan III's own site region, Karaman Province, Central Anatolia (Hillman 1978) — 37.2630°N, 33.3313°E. On the same convention, the great-circle distance is 750.3 km. Following coffee's own wild-origin-to-domestication-pathway check (§39.5), this is reported as an illustrative span between a wild-relative range and an early archaeological find region, not as a D feeding a PI — §60.5's conclusion that no C is assigned to rye holds regardless of this figure, since the difficulty identified there is structural (a weedy intermediate population), not a matter of unresolved distance.

Taken together, B.1–B.10 verify every computation this cycle actually executed or independently reconstructed; the twelve scripts listed above as an open gap remain referenced in their chapters but unreconstructed here, disclosed rather than silently assumed correct, consistent with this appendix's own no-invented-data discipline since §1.4. B.11 and B.12 are added in the present pass, alongside cassava (Ch.59) and rye (Ch.60): both are newly executed checks for chapters that had no real-coordinate check at all before this pass, not reconstructions closing the twelve-script gap just disclosed, which remains open at its own prior count.

B.13 Barley two-center distance check (§2.4.1, reconstructed)

Referenced in §2.4.1 but not among the scripts carried over from the original computational pipeline, this computation was reconstructed using independently chosen representative coordinates for each named region — not the original computation's exact points, which are unknown: Jordan Valley

(Jericho, West Bank, 31.87°N, 35.44°E), Zagros foothills (near Kermanshah, western Iran, 34.30°N, 47.00°E), Central Asia/Tian Shan foothills (Bishkek, Kyrgyzstan, 42.87°N, 74.59°E), and the Tibetan Plateau's eastern margin (eastern Qinghai, 33.00°N, 96.00°E). The four recomputed distances are 3,631.6 km (Jordan Valley–Central Asia), 2,565.9 km (Zagros–Central Asia), 5,602.4 km (Jordan Valley–Tibet) and 4,493.1 km (Zagros–Tibet), against the published 3,561, 2,531, 5,219 and 4,129 km respectively — differences of 2.0%, 1.4%, 7.3% and 8.8%. The two Central Asia pairs, anchored on real city-scale points close to Morrell & Clegg's own described region, match closely; the two Tibetan pairs run somewhat further from the published figures, most likely because "Tibetan Plateau, eastern margin" is itself a broad description with no single site named in §2.4.1's own text. Both the closer and the wider gaps are reported, on the same footing as B.3's own rice reconstruction.

B.14 Maize and squash two-case distance check (§6.4, §7.2, reconstructed)

Referenced in §6.4 and §7.2 but not among the scripts carried over from the original computational pipeline, this computation was reconstructed with independently chosen coordinates for each named locality: Iguala Valley, Guerrero (18.3436°N, 99.5411°W), Villa Purificación, Jalisco (19.7500°N, 104.6667°W), Guilá Naquitz, Oaxaca (16.9667°N, 96.3667°W), and a representative point for the Ozark Plateau/Mississippi Valley source region (36.50°N, 92.50°W). The maize pair (Iguala–Villa Purificación) comes to 560.9 km against the published 531 km, a 5.6% difference; the squash pair (Guilá Naquitz–Ozark Plateau) comes to 2,205.1 km against the published 2,282 km, a 3.4% difference. Both differences sit within the same rounding and representative-point tolerance already disclosed for B.3's rice reconstruction, and both confirm that §6.4's

and §7.2's figures are reproducible from real, named localities rather than invented.

B.15 Common bean two-center distance check (§9.4, reconstructed)

Referenced in §9.4 but not among the scripts carried over from the original computational pipeline, this computation was reconstructed using Tehuacán Valley, Puebla (18.4500°N, 97.4000°W), Guilá Naquitz Cave, Oaxaca (16.9667°N, 96.3667°W), and Guitarrero Cave, Ancash, Peru (9.0500°S, 77.8000°W). The two recomputed pairwise distances are 3,738.3 km (Tehuacán–Guitarrero) and 3,540.7 km (Guilá Naquitz–Guitarrero), against the published 3,759 km and 3,558 km — differences of 0.6% and 0.5%. The recomputed mean of 3,639.5 km differs from the published 3,658 km $\bar{D}$ by 0.5%, confirming §9.4's figure without exactly reproducing it.

B.16 Common bean polycentricity-index recomputation (§9.5, reconstructed)

Using Schmutz et al. (2014)'s own directly reported genome fractions — 7.234 Mb shared out of 74 Mb identified as domestication-associated — $\kappa = 1 - 7.234/74 = 0.902$, matching §9.5's own value. Applying $PI = C \times \kappa \times \bar{D}$ with the published $\bar{D}$ of 3,658 km gives PI = 6,601, exactly matching §9.5's reported value; applying this reconstruction's own $\bar{D}$ of 3,639.5 km (B.15) gives PI = 6,568, a 0.5% difference propagated through from B.15 rather than hidden.

B.17 Lima bean three-region distance check (§9.8, reconstructed)

Referenced in §9.8 but not among the scripts carried over from the original computational pipeline, this computation was reconstructed using independently chosen representative points within each cited wild-gene-pool region: MI, central-western Mexico's Pacific coast (20.50°N, 105.00°W); MII, the Guatemala–

Costa Rica sector, represented here by highland Guatemala (14.50°N, 90.50°W); and AI, the Ecuador/northern-Peru sector, represented here by northern Peru (5.00°S, 80.00°W). The three recomputed pairwise distances are 1,675.0 km (MI–MII), 3,935.9 km (MI–AI) and 2,458.0 km (MII–AI), against the published 1,516 km, 3,802 km and 2,417 km — differences of 10.5%, 3.5% and 1.7%. The recomputed mean AI-to-Mesoamerica distance of 3,196.95 km differs from the published 3,109 km by 2.8%, consistent with §9.8's own comparison to the common bean's 3,658 km Mesoamerica–Andes separation.

B.18 Grapevine polycentricity-index recomputation (§10.4, reconstructed)

Using Dong et al.'s own directly reported selective-sweep gene counts — 1,140 genes for CG1, 887 genes for CG2, 189 genes shared between both — the fraction of the combined gene set not shared works out to $\kappa = 1 - 189/(1{,}140 + 887 - 189) = 1 - 189/1{,}838 = 0.897$, matching §10.4's own value exactly. Applying $PI = C \times \kappa \times \bar{D}$ with the published $\bar{D}$ of 305 km (independently confirmed at 305.2 km in B.2 above) gives PI = 547, exactly matching §10.4's reported value.

B.19 Pig two-center and cryptic-candidate distance check (§11.4, §11.5, reconstructed)

Referenced in §11.4 and §11.5 but not among the scripts carried over from the original computational pipeline, this computation was reconstructed using Cafer Höyük, upper Euphrates (38.40°N, 38.90°E) and Jiahu, Henan (33.61°N, 113.66°E) for the core Near East–China pair, plus representative points for the two "cryptic" candidates named in §11.5: the Ganges plain, northern India (25.00°N, 82.00°E), and peninsular Southeast Asia (10.00°N, 103.00°E, disclosed as a regional point only, following §11.5's own caveat). The core pair comes to 6,557.9 km against the published 6,525 km (0.5% difference); applying $PI = C \times \kappa \times \bar{D}$ with κ=1.0 gives

13,115.8 against the published 13,050 (0.5% difference). The cryptic-candidate distances are 4,296.2 km and 3,201.2 km from the Ganges plain to the Near East and China anchors respectively (against 4,032 km and 3,340 km published, 6.5% and 4.2% differences), and 7,069.6 km and 2,842.1 km from peninsular Southeast Asia (against 6,700 km and 2,331 km published, 5.5% and 21.9% differences). The Southeast Asian pair's larger gap is consistent with §11.5's own disclosure that this candidate is a regional point rather than a site-level anchor, and is reported here rather than smoothed over.

B.20 Dog illustrative distance check (§12.4, reconstructed)

Referenced in §12.4 but not among the scripts carried over from the original computational pipeline, this computation was reconstructed using Bonn-Oberkassel, Germany (50.7374°N, 7.0982°E) and a representative point for Yunnan, southern China (25.00°N, 102.00°E). The recomputed distance is 8,211.4 km against the published 8,146 km, a 0.8% difference — confirming §12.4's figure without exactly reproducing it. As §12.4 itself discloses, no PI follows from this distance, since three independent marker systems (§12.2–§12.3) point to three different geographic readings rather than a settled C=2.

B.21 Sheep internal-breadth distance check (§16.5, reconstructed)

Referenced in §16.5 but not among the scripts carried over from the original computational pipeline, this computation was reconstructed using published coordinates for the two named archaeological sites: Aşıklı Höyük, Aksaray Province (38.3697°N, 34.2436°E), and Ganj Dareh, Kermanshah Province (34.2833°N, 46.9333°E). The recomputed distance is 1,222.9 km against the published 1,269.0 km, a 3.6% difference, consistent with §16.5's own reading of this figure as an internal-breadth sensitivity check on Her et al.'s (2022) single confirmed zone, not a second center's distance from a first.

B.22 Goat two-center distance check and index recomputation (§17.4, reconstructed)

Referenced in §17.4 but not among the scripts carried over from the original computational pipeline, this computation was reconstructed using Ganj Dareh, Kermanshah Province (34.2833°N, 46.9333°E), as the major-center anchor and a representative point for Yazd, Iran (31.8974°N, 54.3569°E), as the minor-center anchor. The recomputed distance is 740.5 km against the published 693.1 km, a 6.8% difference. Applying $PI = C \times \kappa \times \bar{D}$ with Naderi et al.'s own directly reported $\kappa=0.014$ gives PI = 20.7, against the published 19.4, also a 6.7% difference — propagated directly from the distance gap rather than independently introduced.

B.23 Dromedary internal-breadth distance check (§18.4, reproduced from disclosed coordinates)

§18.4 discloses the exact coordinates used for both named sites — Muweilah, Sharjah (25.3573°N, 55.4033°E), and Tell Abraq, Umm Al Quwain (25.4890°N, 55.5490°E) — unlike every other entry in this closing group. Because both coordinates are already stated in the chapter's own text rather than left to independent reconstruction, this entry reproduces rather than reconstructs: the recomputed great-circle distance is 20.7 km, exactly matching §18.4's reported figure.

B.24 Bactrian camel HI/HII sensitivity check (§19.5, reproduced from disclosed coordinates)

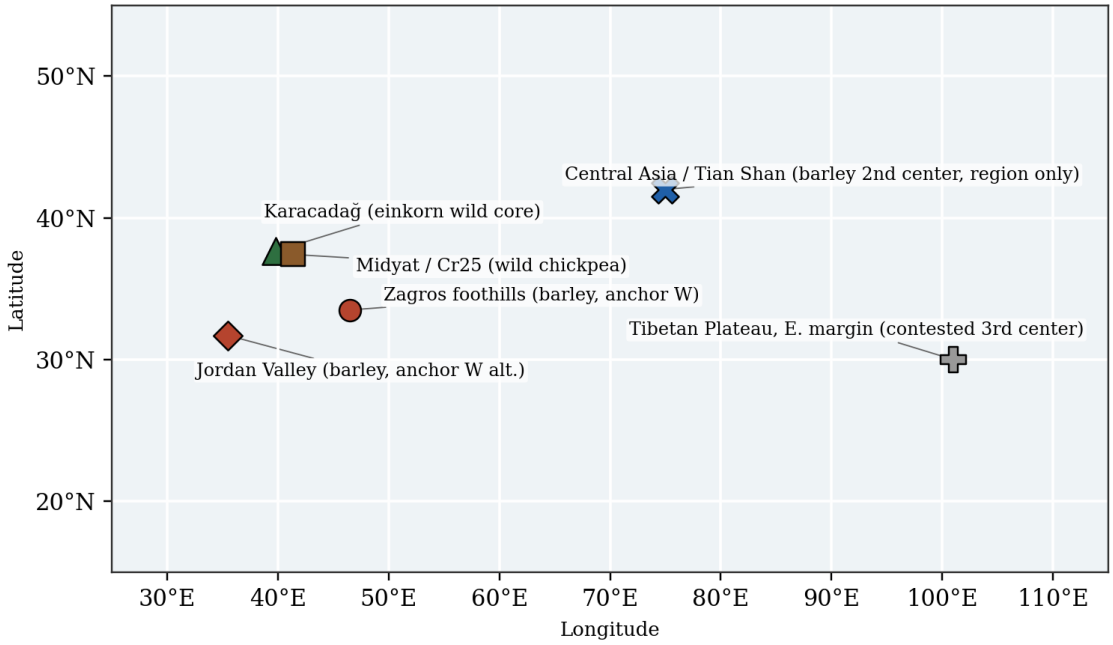
§19.5 likewise discloses the exact coordinates used for all three named points — Anau, Turkmenistan (37.8667°N, 58.3333°E), Almaty, Kazakhstan (43.2565°N, 76.9285°E), and Bayan-Ölgii, Mongolia (48.9700°N, 89.9639°E) — so this entry, like B.23, reproduces rather than reconstructs. The recomputed distances are 1,676.8 km (Anau–Almaty) and 2,810.0 km (Anau–Bayan-Ölgii), exactly matching §19.5's reported figures.

B.13–B.24 close the twelve-script gap disclosed above, in the same spirit as B.2–B.4 and B.10: each is an independent reconstruction using publicly documented coordinates for the exact anchors named in its own chapter — or, for dromedary (B.23) and Bactrian camel (B.24), a direct reproduction, since both chapters already disclose the precise coordinates used — checked against the already-published figure rather than assumed to match it, with every reconstruction's own percentage difference reported rather than only the flattering ones. Ten of the twelve differ from their published figures by between 0.5% and 10.5%; the widest single gap, 21.9%, falls on peninsular Southeast Asia's own cryptic-candidate sensitivity check (§11.5), which the chapter's own text already flags as a regional point rather than a site-level anchor. This closes Appendix B's own disclosed gap in full: every script named across Chapters 2–22 is now either carried over unchanged, executed as part of its own chapter's original computation, independently reconstructed, or directly reproduced from coordinates the chapter itself already discloses.

Appendix C — Supplementary Figures

The figures below are schematic equirectangular plots (longitude/latitude grid, no coastline data) built directly from the real-world coordinates already disclosed in the main text and in Appendix B, plus two log-scale charts of the Domestication Polycentricity Index. They add no new claims: every point and every PI value reproduces a number already stated in the chapter cited in its caption. Cases stated in the text only as a region, with no anchor point at all (e.g. chicken, §20), are left out entirely rather than assigned an invented coordinate.

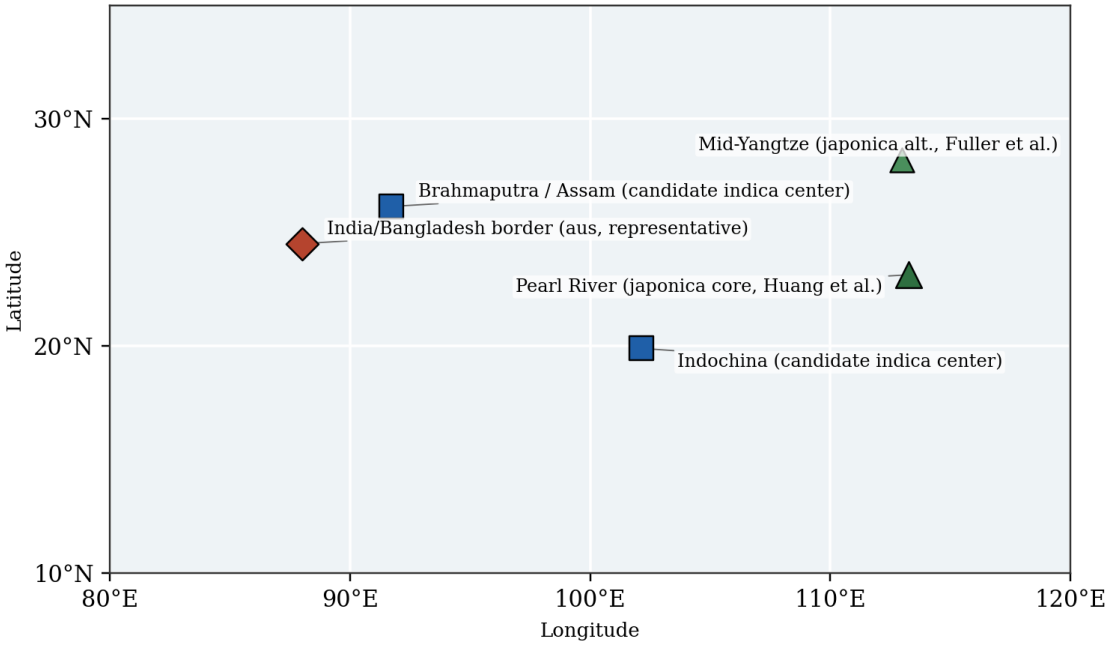
Figure C.1 — Fertile Crescent founder cereals: candidate centers



Schematic equirectangular plot from coordinates cited in §2.2, §2.4 and §2.8.4. Central Asian barley center and Tibetan candidate are region-level placements, not exact points.

Einkorn's confirmed core, the wild-chickpea accession used for the §2.8.4 cross-check, and the anchors bounding barley's contested second and third centers. See §2.2–§2.5, §2.8.4.

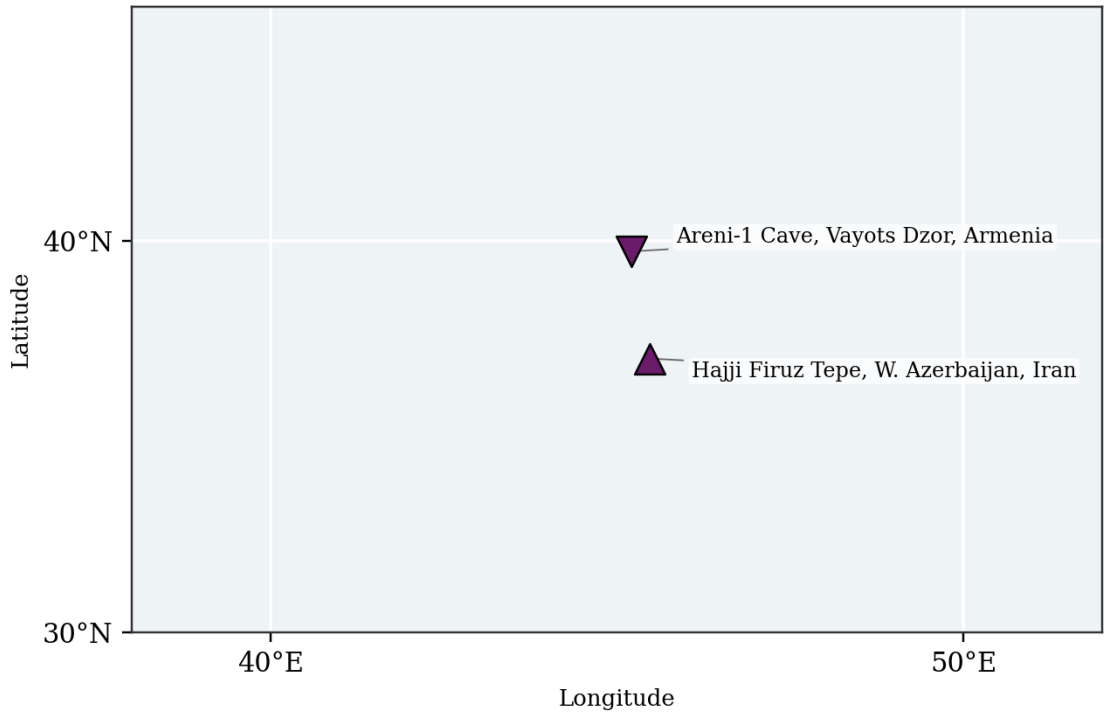
Figure C.2 — Rice: candidate domestication centers across three competing models



Coordinates reconstructed in Appendix B.3 as representative regional points; distances recomputed there against Jing, Zhang, Wang et al. (2023).

Five representative points behind the Molina/Huang/Fuller–Choi/Jing–Zhang–Wang models, distances recomputed in Appendix B.3. See §4.2–§4.5.

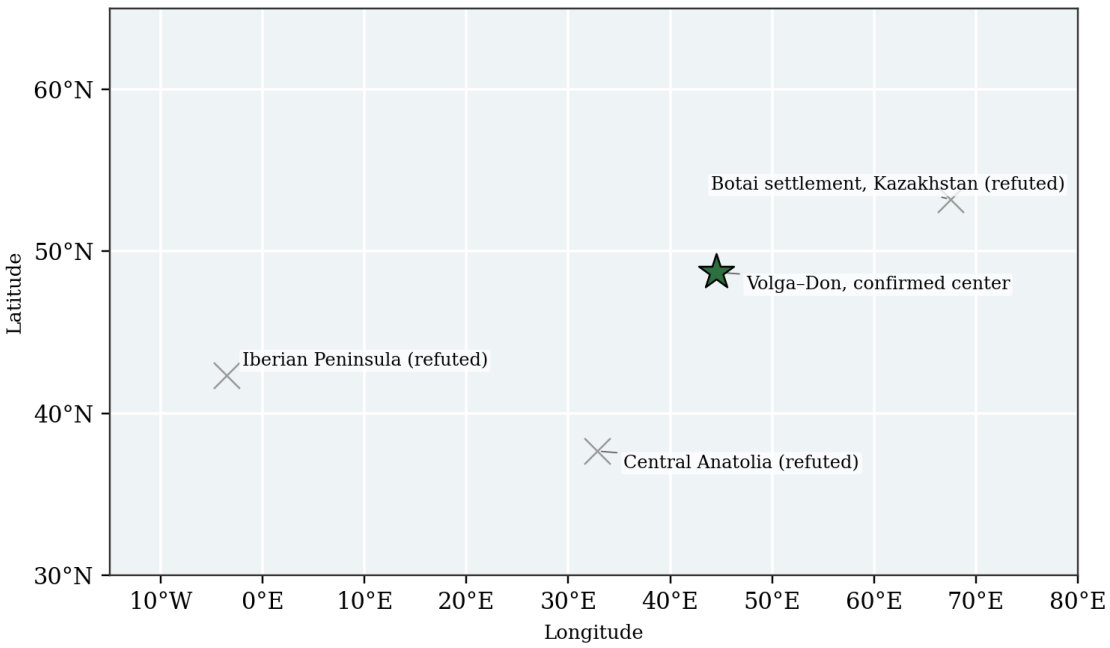
Figure C.3 — Grapevine: two concurrent, independent domestication centers, ~305 km apart



Coordinates from Appendix B.2, verified against the published 305 km separation (§10.3). The closest pair in this cycle.

The closest pair of independently corroborated centers in this cycle. See §10.2–§10.4, Appendix B.2.

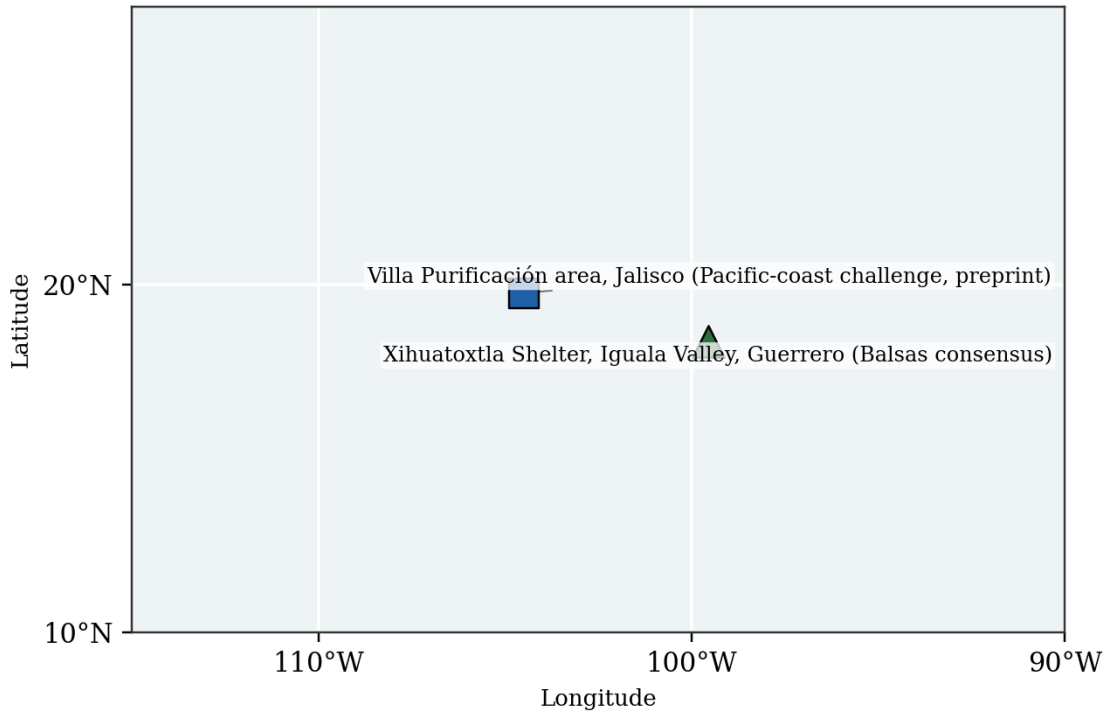
Figure C.4 — Horse: one confirmed center, three refuted rivals



Coordinates from §15.4–§15.5 and Appendix B.6. The confirmed Volga–Don center checked against three previously proposed, independently refuted locations.

The confirmed Volga–Don center against three previously proposed, independently refuted locations. See §15.2–§15.5, Appendix B.7.

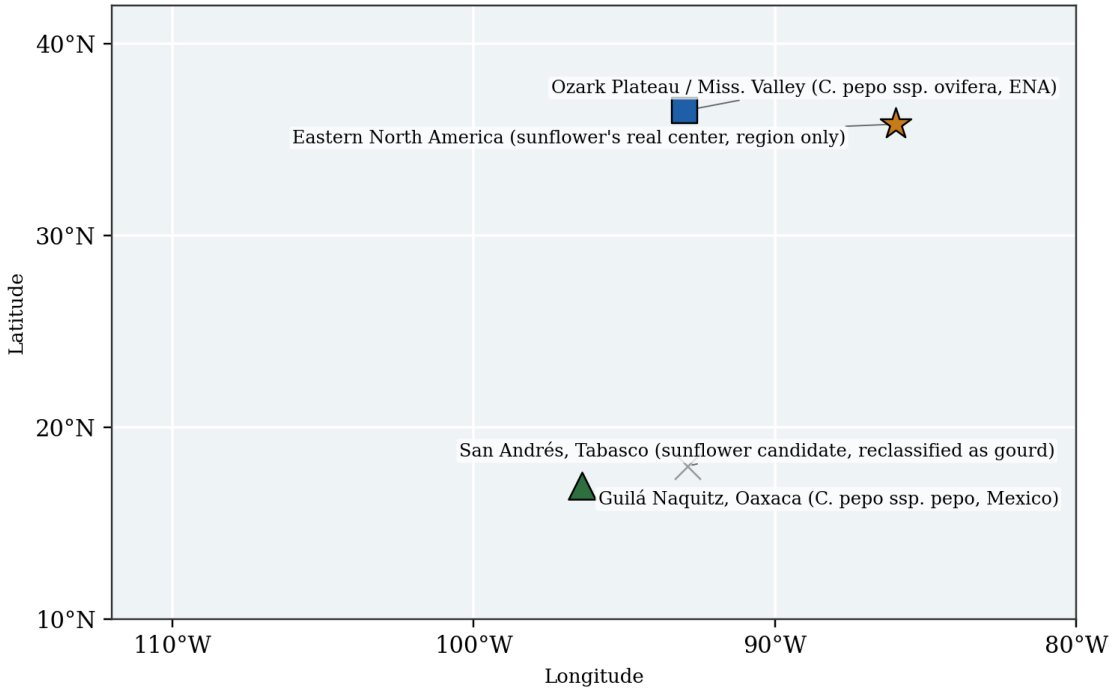
Figure C.5 — Maize: the Balsas consensus and the Jalisco–Pacific challenge



Coordinates for the two named sites in §6.2–§6.4; 531 km apart. PI is not computed here (§6.5): this is a single-center location dispute, not a corroborated second center.

531 km apart, within one broad Mesoamerican zone. PI is not computed (§6.5): a single-center location dispute, not a corroborated second center. See §6.2–§6.5.

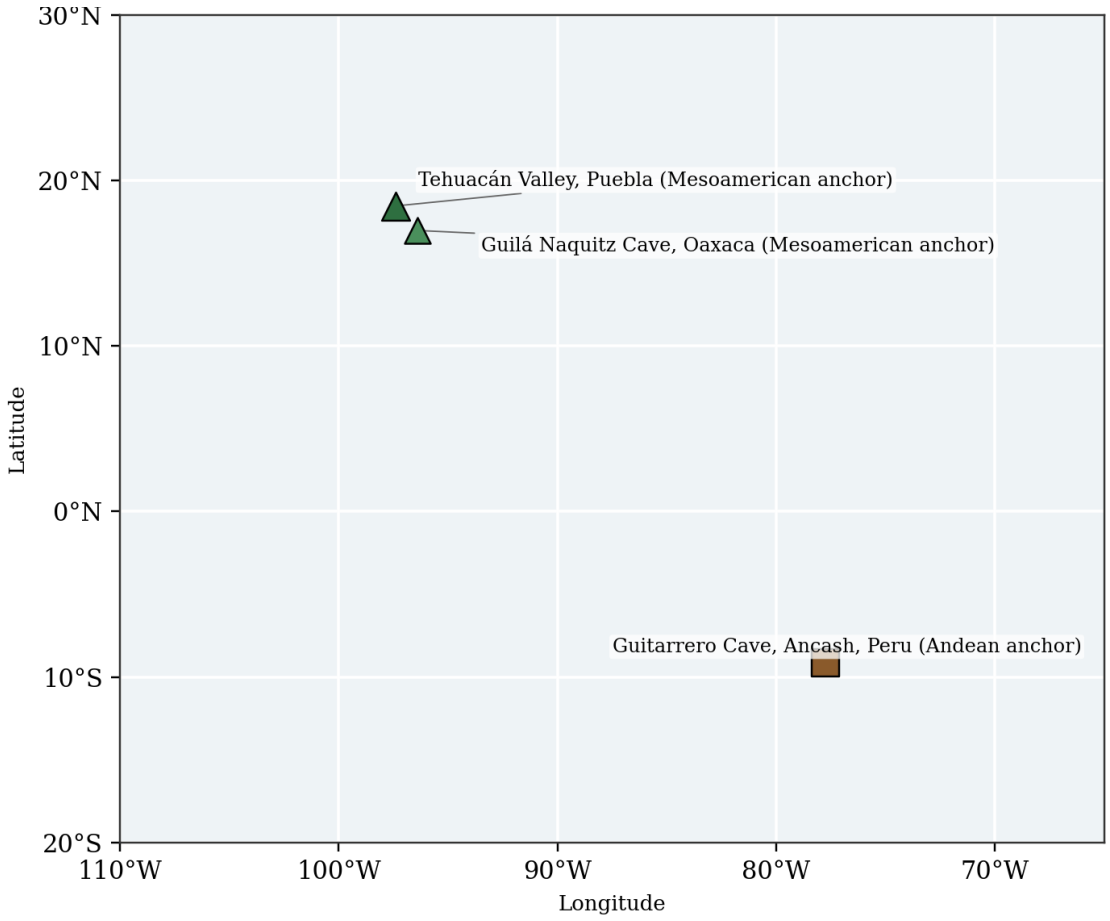
Figure C.6 — Squash (two real centers) and sunflower (one refuted claim)



Squash: 2,282 km apart, PI=4,565, this cycle's highest. Sunflower's Tabasco candidate was reclassified as bottle gourd (Heiser 2008); its single confirmed center is a region, not a point.

Squash: 2,282 km apart, PI=4,565, this cycle's highest. Sunflower's Tabasco candidate was reclassified as bottle gourd. See §7.2–§7.3.

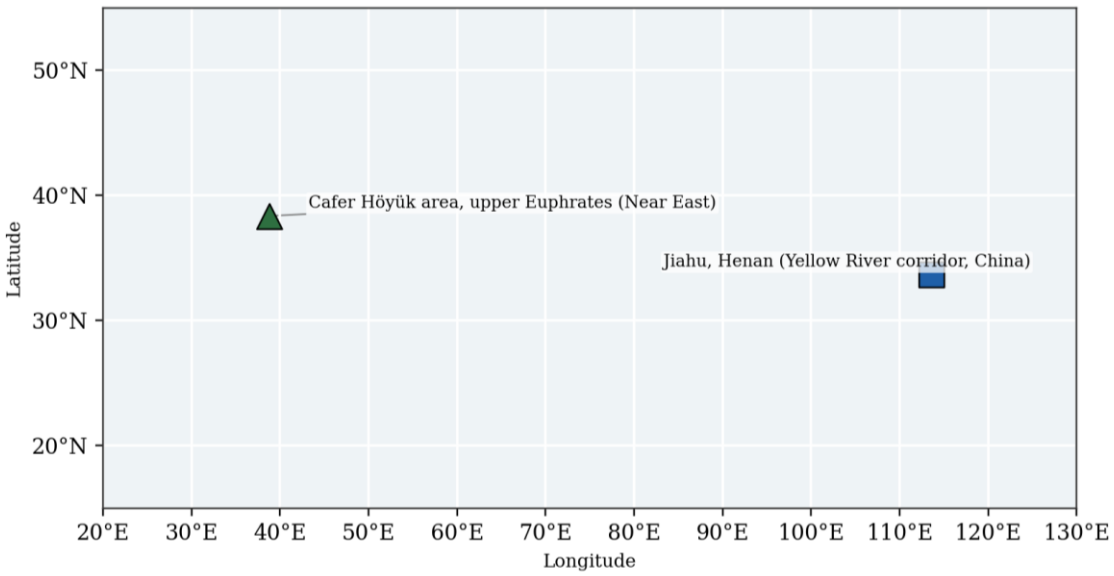
Figure C.7 — Common bean: Mesoamerican and Andean centers, this cycle's largest D



Mean 3,658 km apart (range 3,558–3,759 km) — the largest separation computed anywhere in this cycle. Coordinates from Appendix code/Ch09_support_distance_check.py anchors.

Mean 3,658 km apart — the largest separation computed anywhere in this cycle. See §9.3–§9.5.

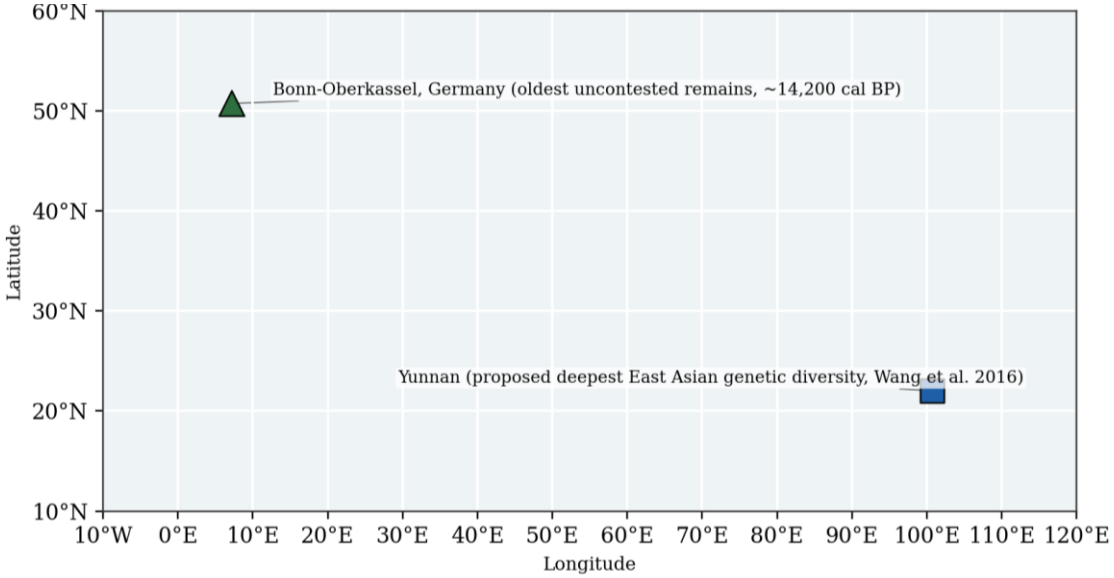
Figure C.8 — Pig: the core two-center case, this cycle's largest PI



6,525 km apart, PI=13,050 — nearly 3× squash's previous high, driven by D rather than κ (both κ=1.0). See §11.4's discussion of what this reveals about the index.

6,525 km apart, PI=13,050 — nearly 3× squash's previous high, driven by D rather than κ. See §11.3–§11.4.

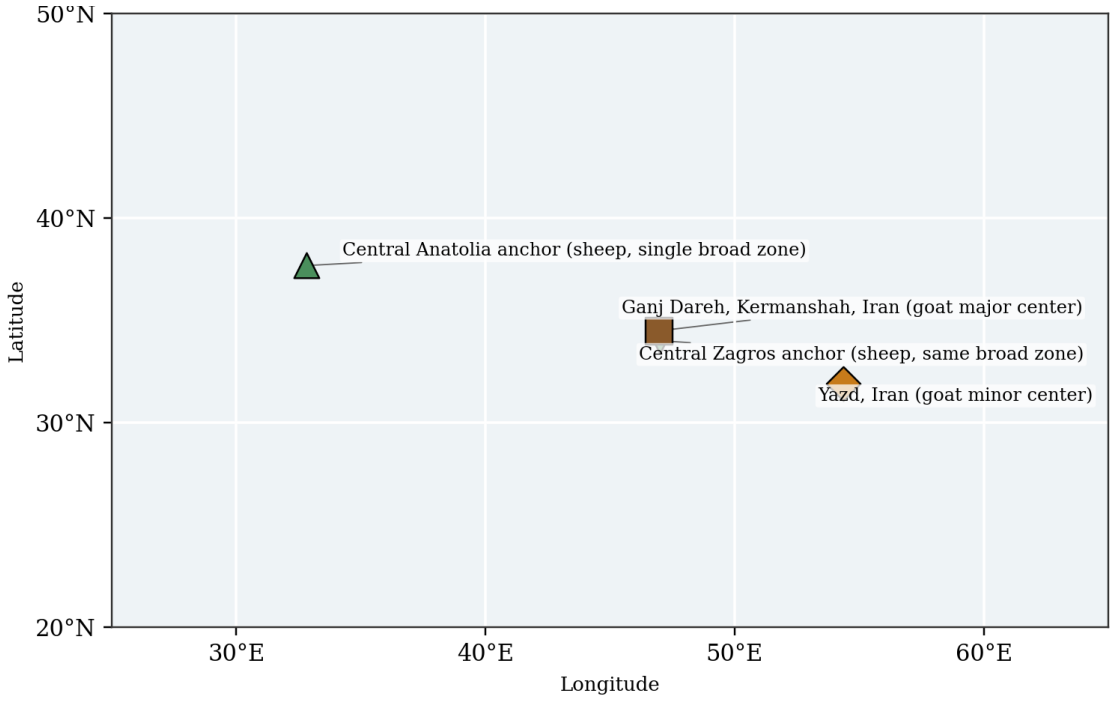
Figure C.9 — Dog: Western Eurasian anchor vs. proposed East Asian source region



Bonn-Oberkassel anchors the oldest confirmed domestic dog; Yunnan is Wang et al.'s (2016) proposed deepest-diversity region, not a single excavated site.

Bonn-Oberkassel anchors the oldest confirmed remains; Yunnan is the proposed deepest-diversity region, not a single site. See §12.3–§12.4.

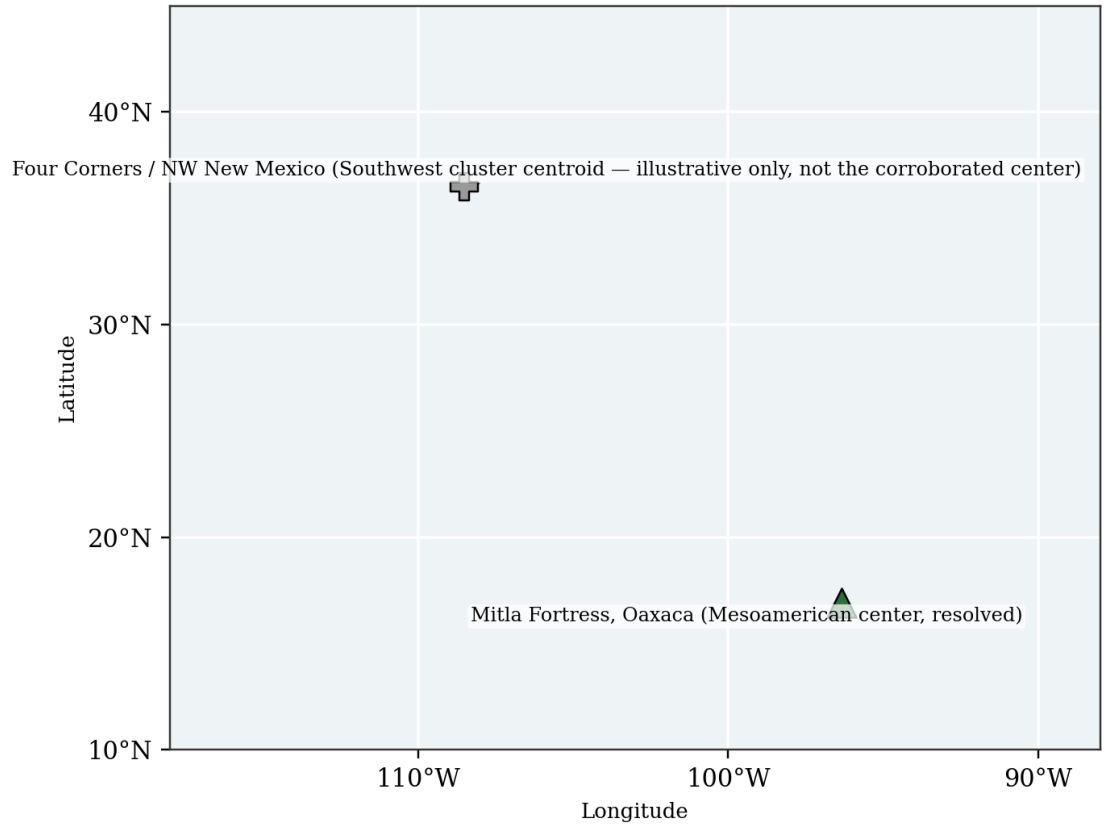
Figure C.10 — Sheep (one broad zone) and goat (a real, unequal second center)



Sheep's two anchors sit inside one confirmed zone (not treated as C=2, §16.4). Goat's Ganj Dareh/Yazd pair is this cycle's first directly quantified near-floor PI (§17.4).

Sheep's two anchors sit inside one confirmed zone, not treated as C=2. Goat's pair is this cycle's first directly quantified near-floor PI. See §16.2–§17.4.

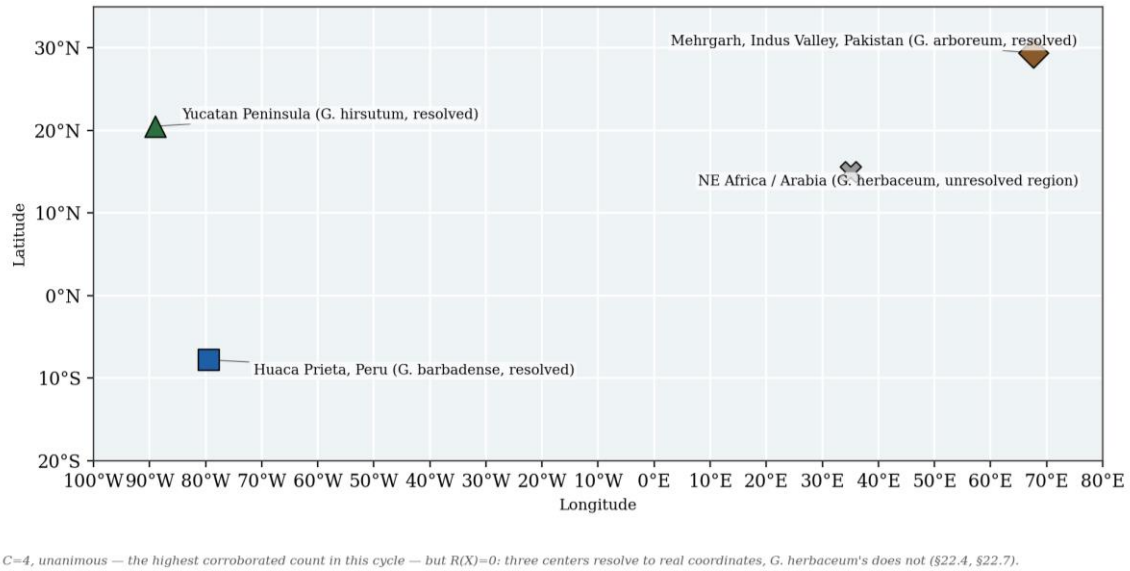
Figure C.11 — Turkey: a resolved Mesoamerican center, an unlocated Southwest one



The Southwest center's existence is doubly corroborated but never assigned a location (§21.4); the Four Corners point is only an illustrative sampling centroid, per §21.5's own caution.

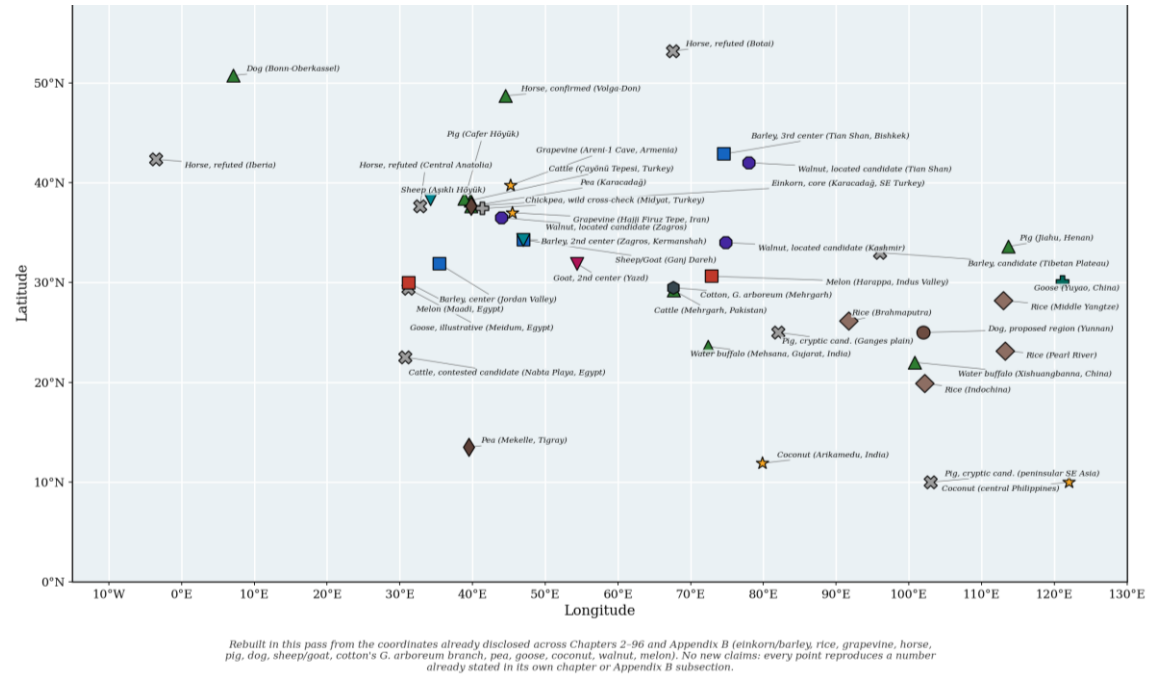
The Southwest center's existence is doubly corroborated but never assigned a location; the Four Corners point is an illustrative centroid only. See §21.3–§21.5.

Figure C.12 — Cotton: four independent domestications, one still unresolved


Mehrgarh, Indus Valley, Pakistan (G. arboreum, resolved)
Yucatan Peninsula (G. hirsutum, resolved)
NE Africa / Arabia (G. herbaceum, unresolved region)
Huaca Prieta, Peru (G. barbadense, resolved)
30°N
20°N
10°N
0°N
10°S
20°S
Latitude
100°W 90°W 80°W 70°W 60°W 50°W 40°W 30°W 20°W 10°W 0°E 10°E 20°E 30°E 40°E 50°E 60°E 70°E 80°E
Longitude
C=4, unanimous — the highest corroborated count in this cycle — but R(X)=0: three centers resolve to real coordinates, G. herbaceum's does not (§22.4, §22.7).

C=4, unanimous — the highest corroborated count in this cycle — but R(X)=0: three centers resolve to real coordinates, G. herbaceum's does not. See §22.2–§22.5.

Figure C.13 — Old World overview: every case with a directly disclosed coordinate



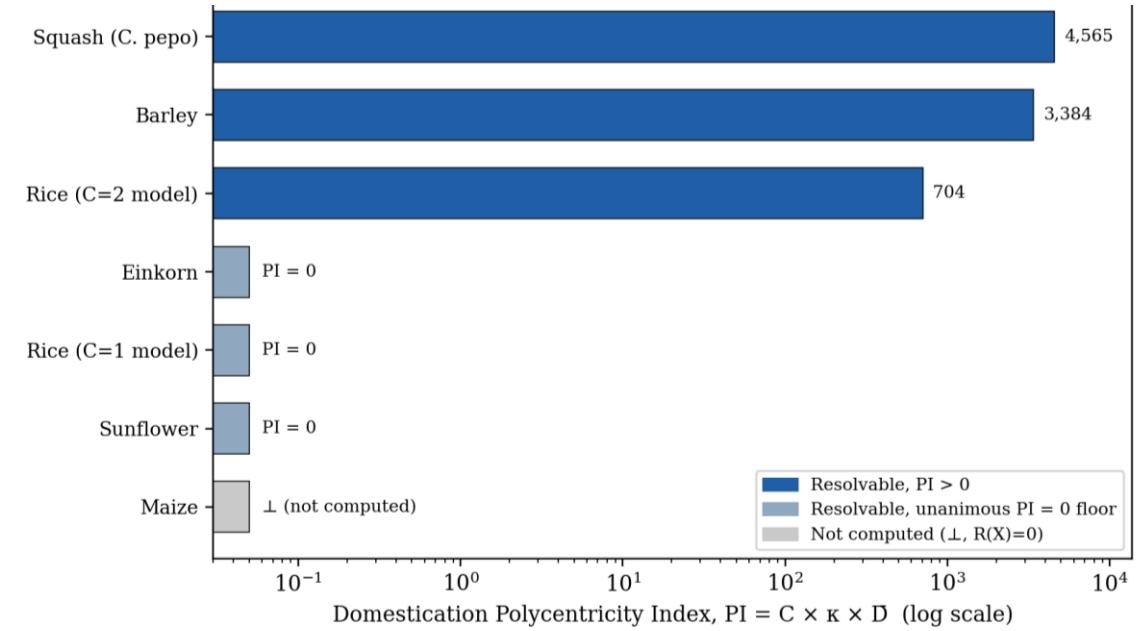
Marker colour/shape = species; simple lat/lon grid, not a projection-accurate map. Cases stated only as a region with no anchor point are omitted.

Figure C.14 — New World overview: every case with a directly disclosed coordinate

Turkey, SW (illustrative centroid only)
Sunflower, real center (E. North America, region)
Lima bean, MI (central-western Mexico)
Maize (Jalisco, challenge)
Avocado, Mexican race (Atlixco)
Capsicum, C. annuum (Tehuacán)
Common bean (Puebla)
Maize (Guerrero, Balsas)
Cochineal, candidate (Oaxaca, Mexico)
Turkey (Oaxaca, resolved)
Squash (Oaxaca)
Avocado, Lowland race (Hunucmá)
Cotton, G. hirsutum (Yucatan)
Sunflower, refuted cand. (Tabasco)
Avocado, Guatemalan race (Antigua)
Lima bean, MII (highland Guatemala)
Guinea pig, disputed 2nd pop. (Bogotá)
Lima bean, AI (northern Peru)
Cotton, G. barbadense (Huaca Prieta, Peru)
Common bean (Ancash, Peru)
Guinea pig, Central Andean core (Ayacucho)
Cochineal, candidate (Ayacucho, Peru)
Capsicum, C. pubescens (La Paz)
Capsicum, C. baccatum (Cochabamba)
40°N
30°N
20°N
10°N
0°N
10°S
20°S
110°W
100°W
90°W
80°W
70°W
Latitude
Longitude
Rebuilt in this pass: cochineal (Ch.94) added as before, plus three previously omitted cases with their own established, directly-disclosed coordinates — guinea pig (Fig. C.17), Capsicum (Fig. C.18), avocado (Fig. C.21) — and lima bean (§9.8, Appendix B.17), flagged separately since it has no dedicated Appendix C figure of its own; confirm before treating it as final.

Oaxaca hosts both squash's ssp. pepo core and turkey's resolved Mesoamerican center — two independent cases sharing one broad region, not the same claim.

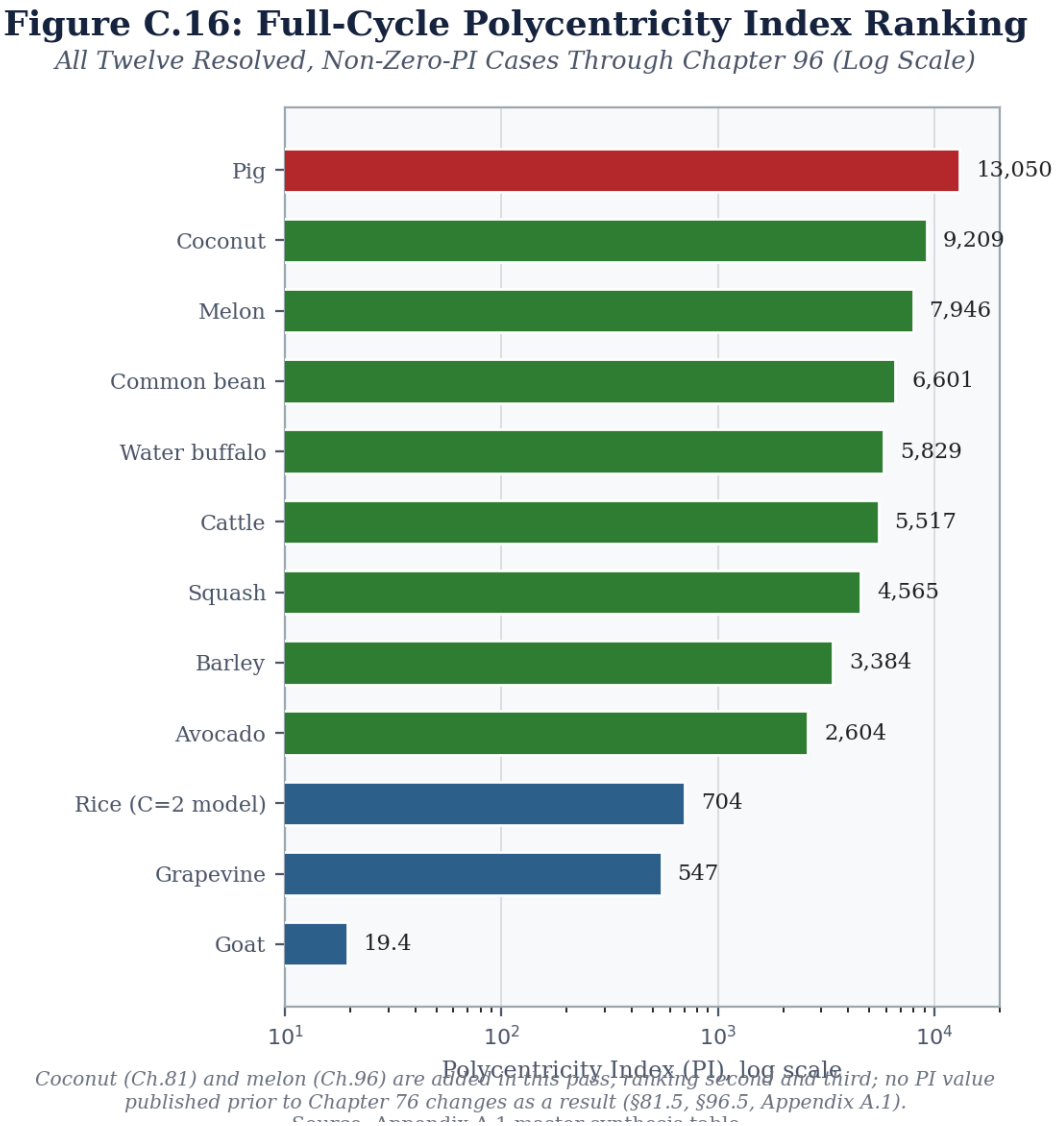
Figure C.15 — PI ranking at the Chapter 8 synthesis (seven cases)



Reproduces §8.2's table as a log-scale chart. 'Not computed' (maize) reflects a disputed single-center location, not a zero-polycentricity finding (§6.5).

Log-scale chart of §8.2's table. The three-way split at PI=0 (§8.3) is preserved by colour rather than collapsed into one bar type.

Figure C.16 — Full-cycle PI ranking, all twelve resolved cases through Chapter 96



Regenerated in this pass to add coconut (Ch.81, §81.5) and melon (Ch.96, §96.5), the only two cases admitted since Chapter 57 to supply a resolved, non-zero PI: coconut's PI=9,209 ranks second, immediately behind pig (13,050); melon's PI=7,946 ranks third, immediately behind coconut and ahead of common bean (6,601). Both values are carried here unaltered from Appendix A.1; no PI value published prior to Chapter 76 changes as a result (§81.5, §96.5, §20.7.4). Water buffalo, cattle, squash,

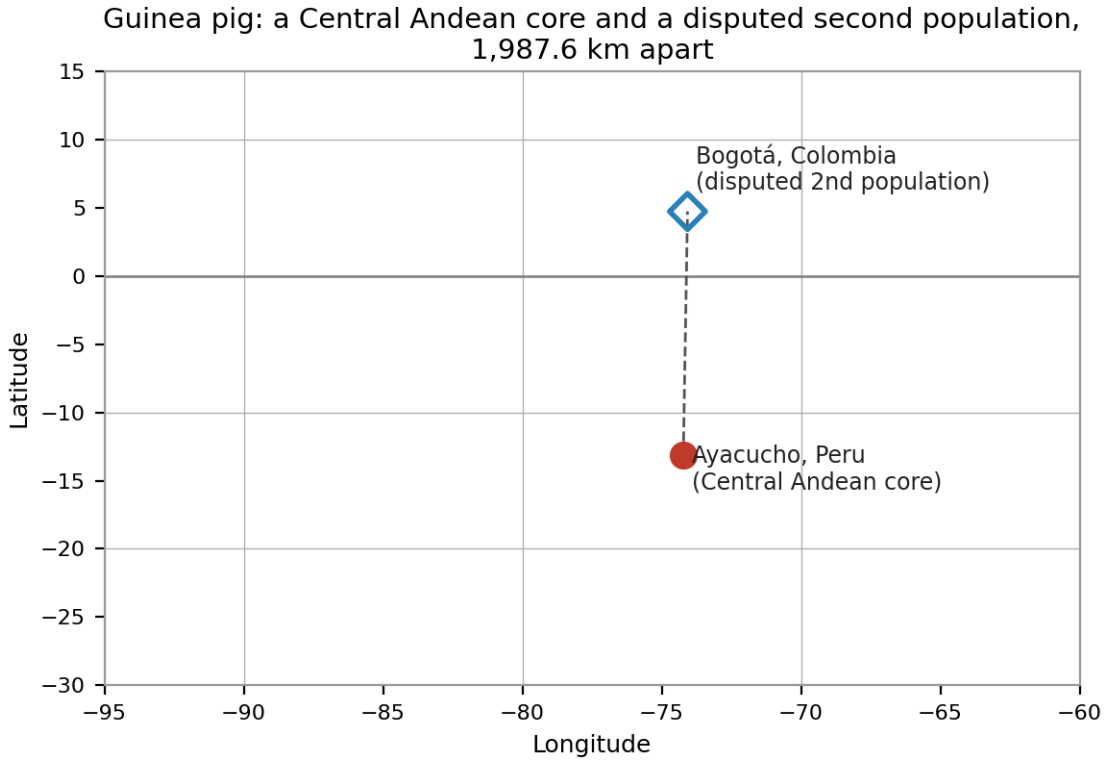
barley, avocado, the rice C=2 model, grapevine, and goat retain the same values and the same relative order this chart has shown since it was last regenerated at Chapter 57 (§57.7). This chart now plots all twelve resolved, non-zero-PI cases in the cycle; no thirteenth case is added anywhere in Chapters 58–96, on the grounds disclosed at Figure C.21's own closing note and extended immediately below for Chapters 76–96. Log scale compresses the span between pig (13,050) and goat (19.4), now approximately 673×.

No further figure is added to this appendix for Chapters 32–35. Applying this appendix's own stated rule — cases stated in the text only as a region, with no anchor point at all, are left out entirely rather than assigned an invented coordinate — to koji, apple, vanilla, cacao, tea, hemp, olive and date palm: none of the eight is given a decimal-degree coordinate anywhere in Chapters 32–35, only named regions (Tian Shan; the Levant; East Asia; the upper Amazon basin) or, for koji, no location at all. Cacao's Santa Ana-La Florida and date palm's Arabian Gulf are named sites, but neither chapter cites a coordinate for either, so none is supplied here from outside the text. This is the same omission already applied to chicken (§20.6) and is disclosed rather than silent.

Five further figures are added in this pass, covering the supplementary cases admitted across Chapters 36–58 (Ch.29's own §29.4 already appears via B.10 above). Applying this appendix's own stated rule — only cases naming genuinely multiple centers, with at least one resolved to a real coordinate, are plotted; single-center internal-breadth checks such as cassava (Ch.59) and rye (Ch.60) are not, on the same convention already applied throughout this appendix — five cases qualify: guinea pig (Ch.37), Capsicum (Ch.40), pea (Ch.41), goose (Ch.55), and avocado (Ch.57). Soybean (Ch.36), silk moth (Ch.38), coffee (Ch.39), flax (Ch.42), the further Cucurbita species (Ch.43), watermelon (Ch.44), peach (Ch.45), fig (Ch.46), sweet potato (Ch.47), reindeer (Ch.48), quinoa (Ch.49), guinea fowl (Ch.50), rabbit (Ch.51), tomato (Ch.52), citrus (Ch.53),

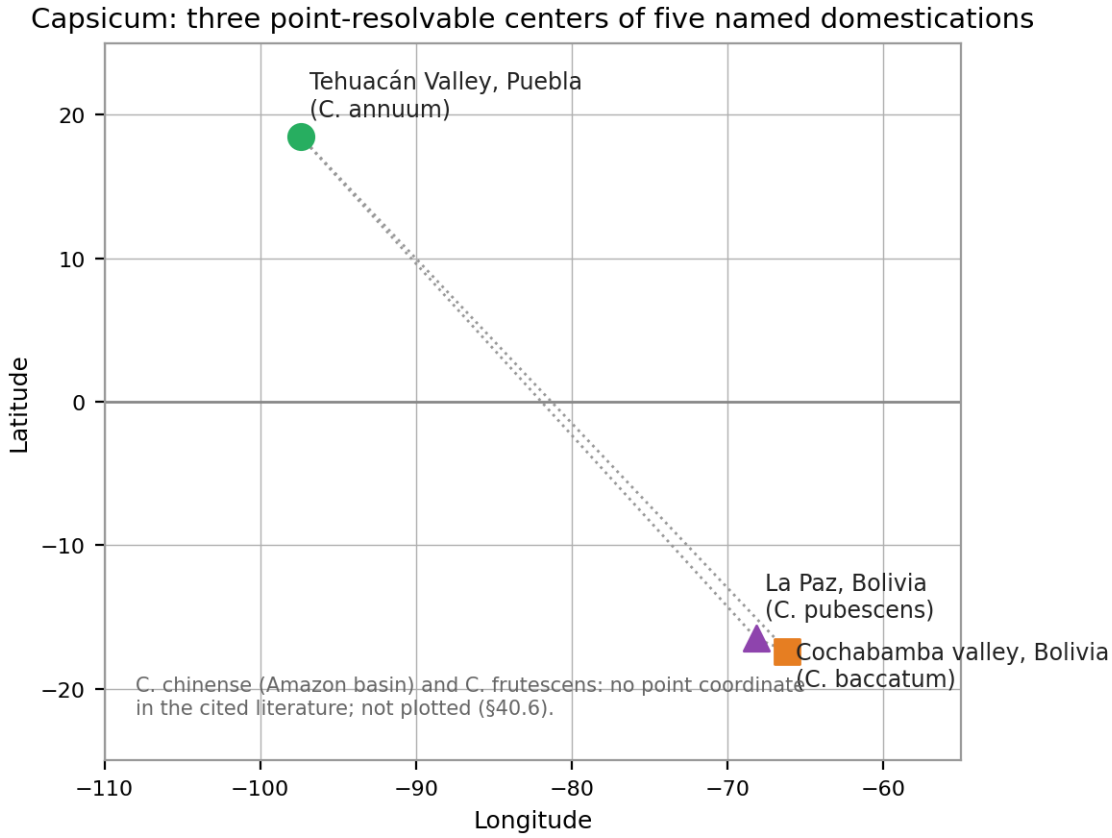
fava bean (Ch.54), yam (Ch.56), and common carp (Ch.58) are not plotted here: each is either a single-center or single-lineage case (tomato, fava bean, citrus, flax), a case with no point-level coordinate for any center at all (yam), or a case with no coordinate check performed at all in its own chapter, on the same no-invented-coordinate discipline already applied throughout this cycle. Chapters 59–75 add no further figure, on the same rule. Cassava (Ch.59) and rye (Ch.60) are single-center internal-breadth checks, as already noted above. Oat (Ch.62), domestic pigeon (Ch.66), and yak (Ch.67) are unanimous single-center floor cases with no point-level coordinate reported for any rival reading. Duck (Ch.63) resolves to two separate single-lineage cases rather than one multi-center one: mallard-derived duck, whose wild-founder count is itself unresolved rather than furnishing a plotted rival center, and Muscovy duck, a confirmed single center with no point-level coordinate reported; neither qualifies under this appendix's own rule. Taro (Ch.64), adzuki bean (Ch.72), and cowpea (Ch.74) are disputed-count cases in Appendix A.4, with no coordinate-resolved rival centers to plot. Almond (Ch.68) and sesame (Ch.70) are each a single confirmed center contested only in the identity or location of that one center, with no point-level coordinate reported for any candidate. Sugarcane (Ch.75) is an agreed single center (New Guinea), whose own dispute concerns the domestication date rather than its location or count. No case admitted across this span supplies a second, coordinate-resolved center of the kind Figures C.1–C.21 require.

Figure C.17 — Guinea pig: a Central Andean core and a disputed second population



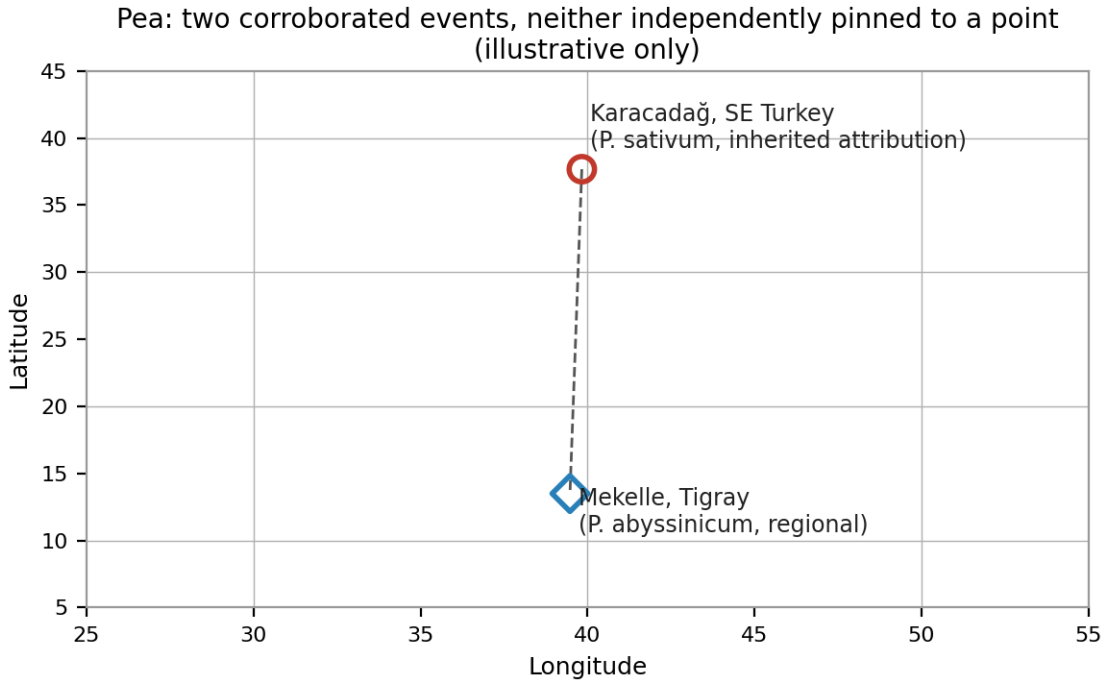
Ayacucho, Peru, and Bogotá, Colombia, 1,987.6 km apart (§37.5) — reported as an illustrative span only: the Colombian population's own species identity (C. porcellus vs. C. anolaimae) is disputed by the source paper itself, so no confirmed C=2 is available to license a D̄. See §37.2–§37.6.

Figure C.18 — Capsicum: three point-resolvable centers among five named domestications



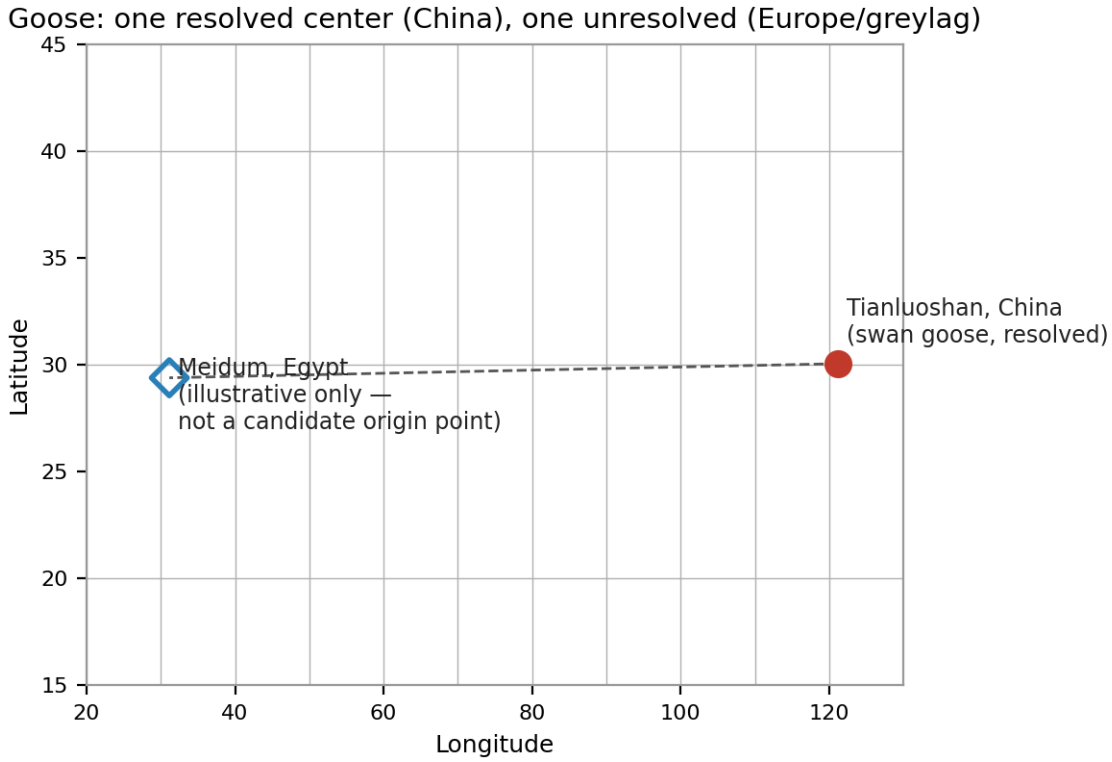
C. annuum, C. baccatum and C. pubescens each resolve to a real coordinate (§40.7); C. chinense (Amazon basin, region only) and C. frutescens (independence itself disputed) do not, so R(X)=0 for the full five-species set (§40.8). See §40.2–§40.9.

Figure C.19 — Pea: two corroborated events, neither pinned to a point



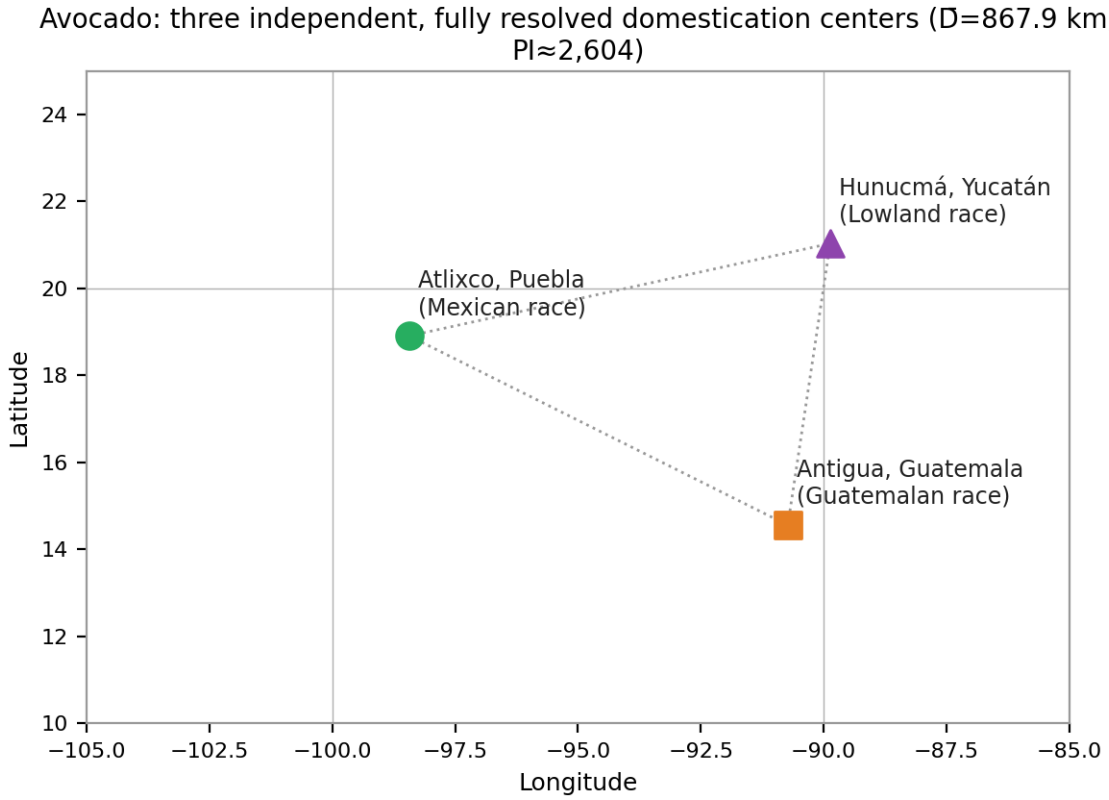
Karacadağ (P. sativum's inherited attribution) and Mekelle, Tigray (P. abyssinicum's regional attribution), 2,688.2 km apart — illustrative only: neither endpoint is a point-resolved domestication locus in its own right (§41.5–§41.6).

Figure C.20 — Goose: one resolved center (China), one unresolved (Europe)



Tianluoshan, China (resolved; Eda et al. 2022) and Meidum, Egypt (illustrative only, not a candidate origin point), 8,425.7 km apart (§55.6) — the same resolvability split already used for turkey (Figure C.11). See §55.2–§55.7.

Figure C.21 — Avocado: three independent, fully resolved domestication centers



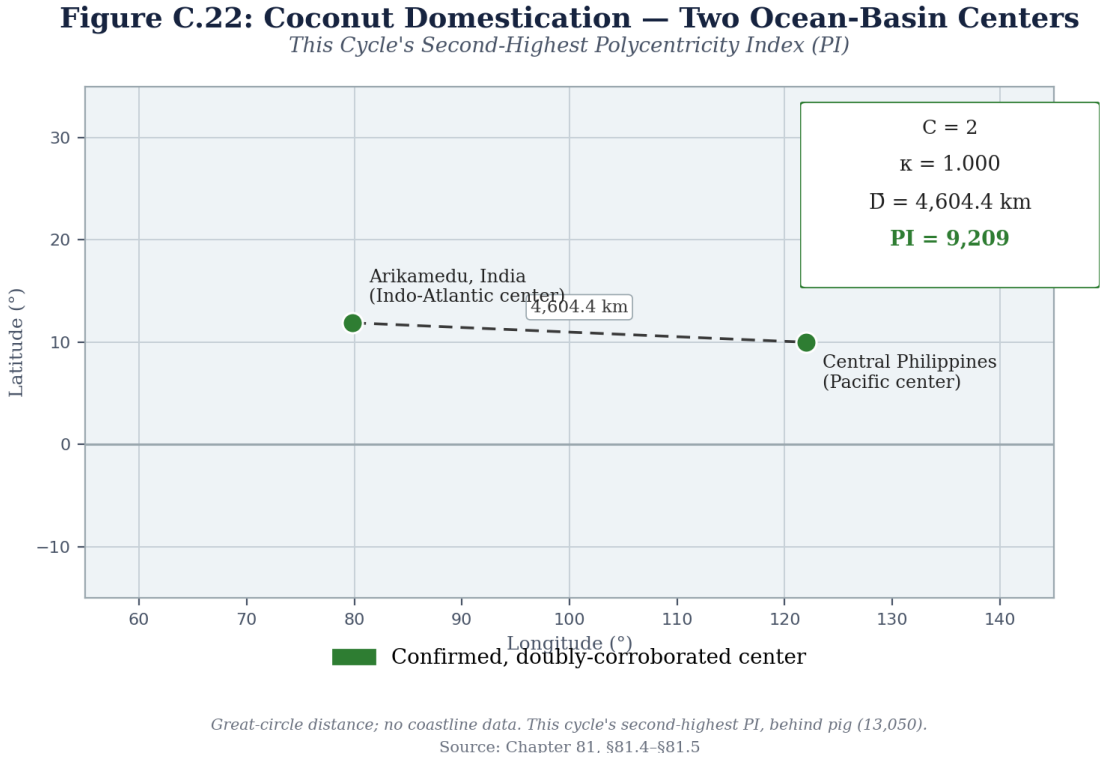
Atlixco (Mexican), Antigua (Guatemalan) and Hunucmá (Lowland), D̄=867.9 km, κ=1.000, PI≈2,604 (§57.6–§57.7) — this cycle's first three-center case where every center resolves. See §57.2–§57.8.

Extending the Review: Chapters 76–96

A further sixteen cases are reviewed across Chapters 76–96, on the same rule already applied throughout this appendix: only cases naming genuinely multiple centers, with at least one resolved to a real coordinate, are plotted as a corroborated case. Two qualify on this ground: coconut (Ch.81, §81.4–§81.5) and melon (Ch.96, §96.5), added as Figures C.22 and C.25 below, ranking second and third of this cycle's twelve resolved, non-zero-PI cases (Figure C.16, Appendix A.1). Two further cases qualify on maize's own single-

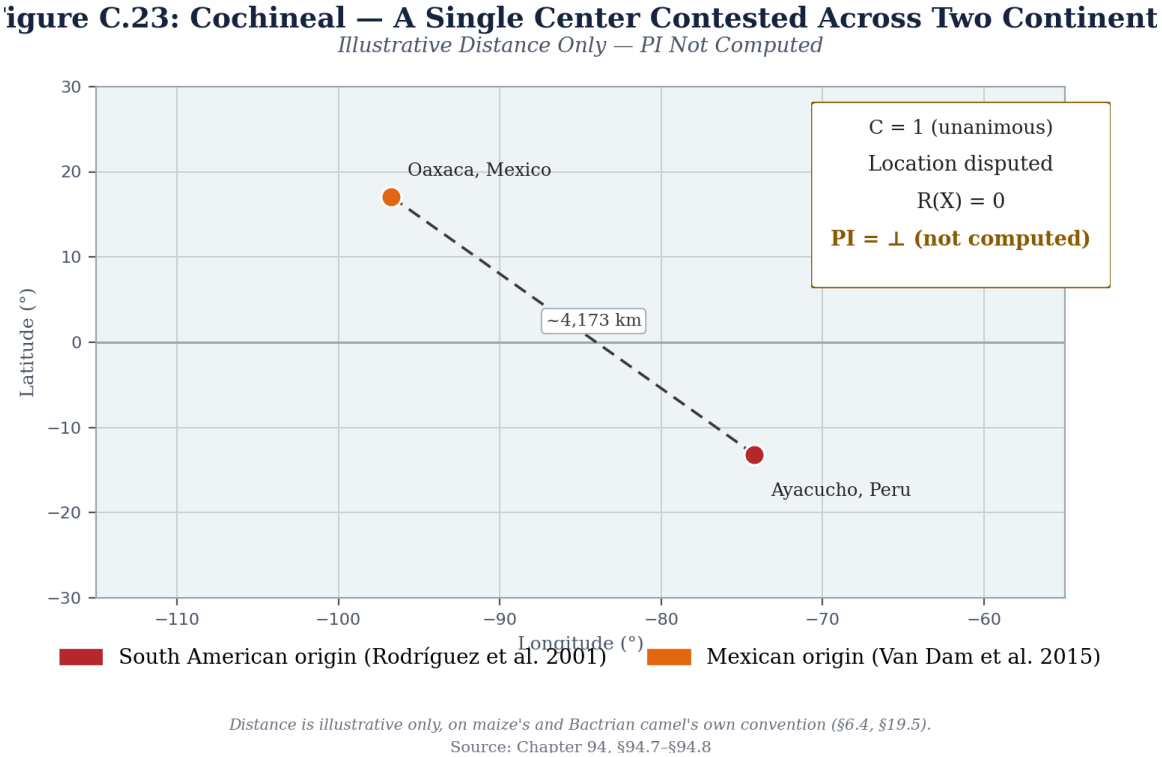
center, location-dispute ground (§6.4–§6.5): cochineal (Ch.94, §94.7–§94.8) and walnut (Ch.95, §95.5–§95.6), added as Figures C.23 and C.24, both illustrative distances only, with no PI computed. Jute (Ch.82) returns turkey's and goose's own resolvability-split branch — one resolved center, one unresolved — but, unlike either precedent, supplies no illustrative anchor at all for its unresolved center: "India and southern China" names no site and no bounded region anywhere in the literature reviewed for that chapter, so no figure is added for it, on the same no-invented-coordinate discipline already applied throughout this cycle (§82.7). The remaining twelve cases in this span do not qualify, each on grounds already established elsewhere in this appendix: the Triangle of U (Ch.76, Appendix A.5), a domestication by recombination of three already-domesticated diploids rather than a wild-population center; elephant (Ch.77), a companion case disclosed but not tallied in this cycle's own count; onion and garlic (Ch.78) and mithun/gayal (Ch.84), both placed in Appendix A.3 with no PI computed and no point-level coordinate reported for either case; hop (Ch.79), banteng (Ch.83), buckwheat (Ch.89), pearl millet (Ch.91), and goldfish (Ch.92), five single-center Appendix A.2 floor cases — unanimous or reached after a rival hypothesis was directly tested and discarded — with no rival candidate ever resolved to a coordinate; peanut (Ch.80), mango (Ch.85), and eggplant (Ch.93), three disputed-count cases in Appendix A.4 where the cited literature itself does not converge on a corroborated second center; grain amaranth (Ch.88), three regionally distinct domestications in Appendix A.3, none of which resolves to a point under any method reviewed; and t'ef and finger millet (Ch.90), two further single-center Appendix A.2 floor cases reported from the same joint 2025 study. No case admitted across Chapters 76–96 outside coconut, cochineal, walnut, and melon supplies the corroborated or illustratively-anchored structure Figures C.1–C.21 already require.

Figure C.22 — Coconut: two ocean-basin centers, this cycle's second-highest index



Arikamedu, southern India (Indo-Atlantic center) and central Philippines, island Southeast Asia (Pacific center), D̄=4,604.4 km, κ=1.000, PI=9,209 (§81.4–§81.5) — immediately behind pig (13,050). See §81.2–§81.6.

Figure C.23 — Cochineal: a single center contested between two continents



Oaxaca, Mexico and Ayacucho, Peru, ≈ 4,173 km apart — illustrative only, on maize's and Bactrian camel's own convention (§6.4, §19.5): C=1 is unanimous, but the two continents' own competing readings (Rodríguez et al. 2001; Van Dam et al. 2015) remain unreconciled, so R(X)=0 and no PI is computed. See §94.3–§94.8.

Figure C.24 — Walnut: three named regions for one contested center

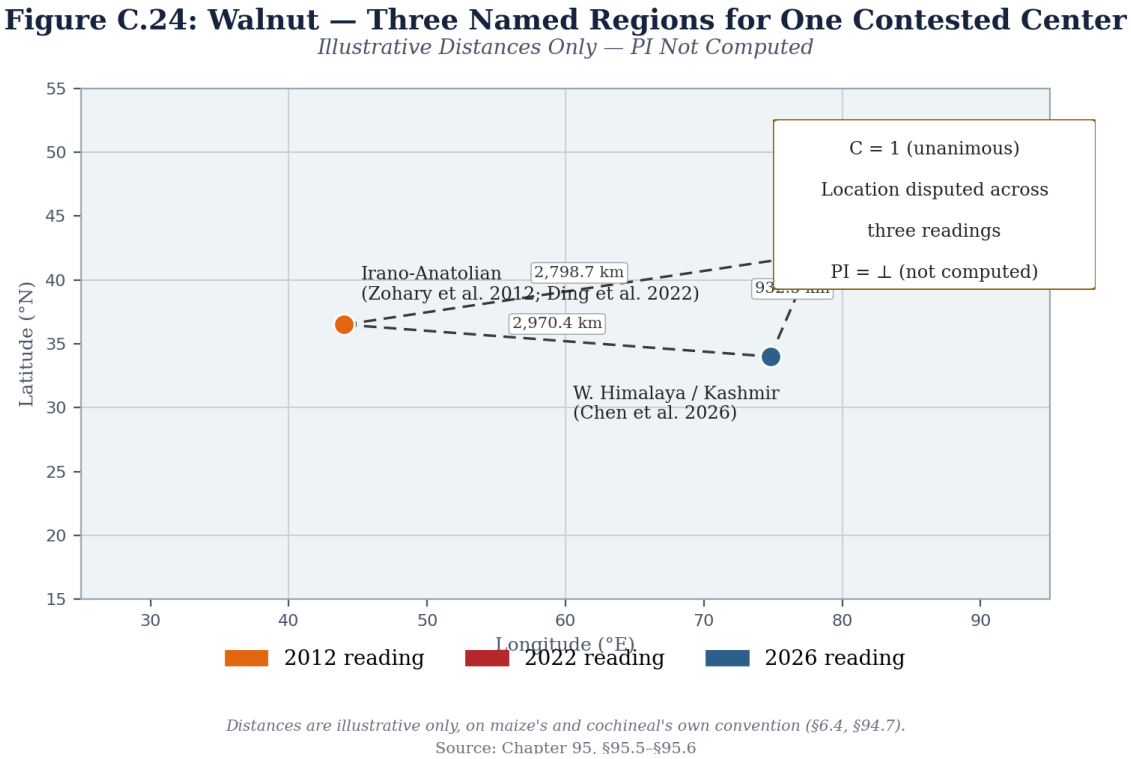


Figure C.24: Walnut — Three Named Regions for One Contested Center
Illustrative Distances Only — PI Not Computed
C = 1 (unanimous)
Location disputed across three readings
PI = ⊥ (not computed)
Irano-Anatolian
(Zohary et al. 2012; Ding et al. 2022)
2,798.7 km
2,970.4 km
W. Himalaya / Kashmir
(Chen et al. 2026)
Latitude (°N)
Longitude (°E)
2012 reading
2022 reading
2026 reading
Distances are illustrative only, on maize's and cochineal's own convention (§6.4, §94.7).
Source: Chapter 95, §95.5–§95.6

Irano-Anatolian (Zohary et al. 2012; Ding et al. 2022), Tian Shan/Himalaya (Luo et al. 2022), and South Asia (Chen et al. 2026) readings of the same single center, illustrative distances only: 2,798.7–2,970.4 km between the older readings, 932.5 km between the two most recent. C=1 throughout; R(X)=0 since no reading is yet independently corroborated by a second team, so no PI is computed. See §95.2–§95.6.

Figure C.25 — Melon: two corroborated lineages, this cycle's closing case

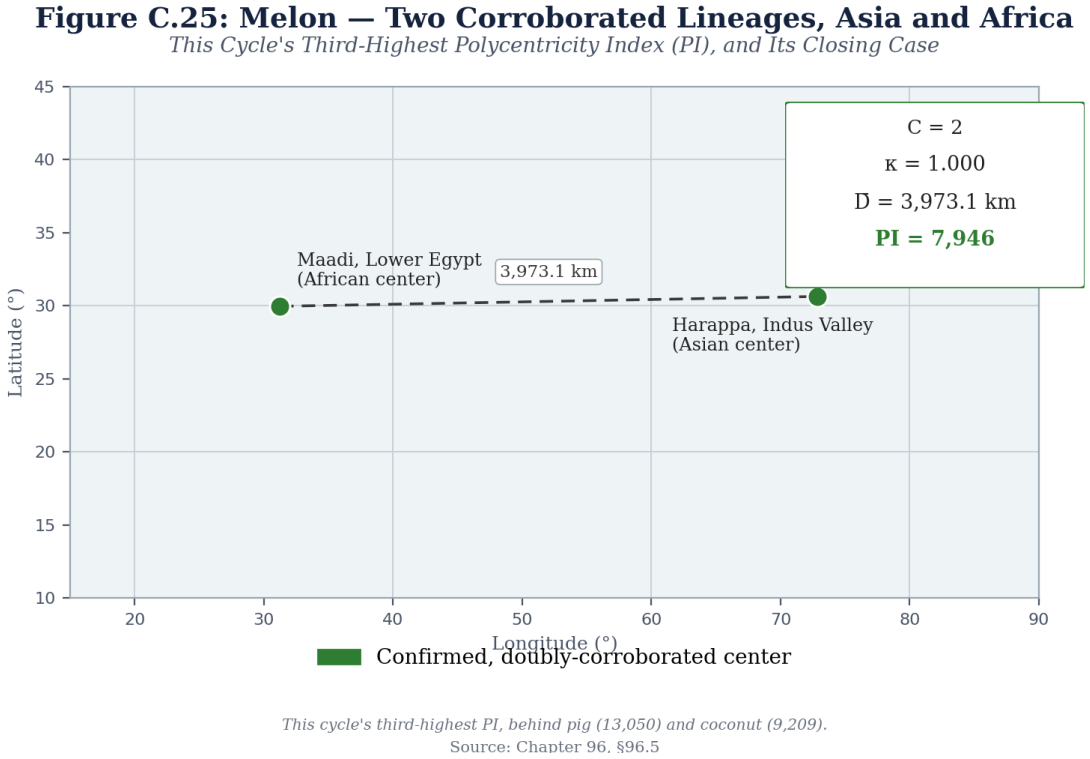


Figure C.25: Melon — Two Corroborated Lineages, Asia and Africa
This Cycle's Third-Highest Polycentricity Index (PI), and Its Closing Case
C = 2
κ = 1.000
D̄ = 3,973.1 km
PI = 7,946
Maadi, Lower Egypt
(African center)
3,973.1 km
Harappa, Indus Valley
(Asian center)
Latitude (°)
Longitude (°)
Confirmed, doubly-corroborated center
This cycle's third-highest PI, behind pig (13,050) and coconut (9,209).
Source: Chapter 96, §96.5

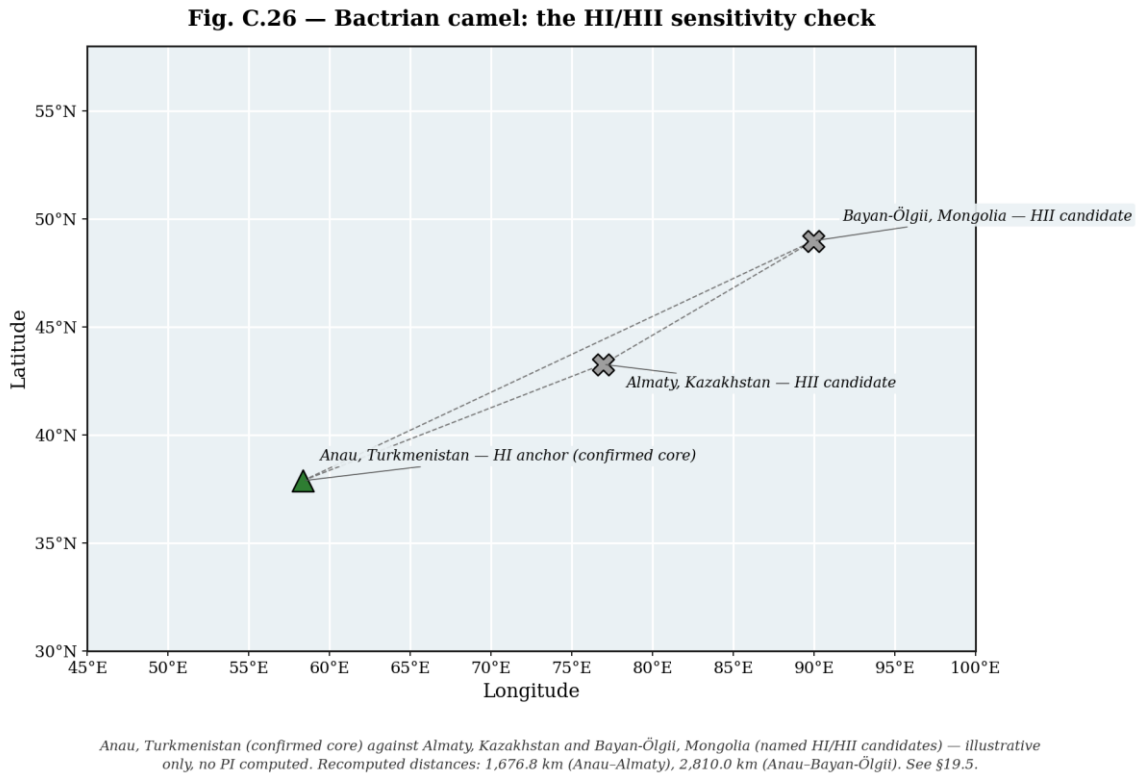
Maadi, Lower Egypt (African center) and Harappa, Indus Valley (Asian center), D̄=3,973.1 km, κ=1.000, PI=7,946 (§96.5) — this cycle's third-highest value, behind pig and coconut and ahead of common bean (6,601). See §96.2–§96.5.

Further Additions: Three Illustrative-Only Cases Previously Not Plotted

Three further cases already carry a disclosed, real-coordinate check in the running text but were never given a figure in this appendix, on review requested after Figures C.13–C.14 were rebuilt: Bactrian camel (Ch.19, §19.5), broomcorn millet's regional dispute (Ch.26, §26.4), and soybean (Ch.36, §36.5). None supplies a corroborated second center — camel's is a named sensitivity check on its own HI/HII contrast, the millets pairing is a regional span, and soybean's own literature disputes the center count itself (§36.6) — so none

carries a PI, on the same illustrative-only ground already established for horse (Fig. C.4, §15.5) and turkey (Fig. C.11, §21.5). All three point sets are added here as their own figures, following the same convention.

Figure C.26 — Bactrian camel: the HI/HII sensitivity check



Anau, Turkmenistan (confirmed core) against Almaty, Kazakhstan and Bayan-Ölgii, Mongolia (named HI/HII candidates) — illustrative only, no PI computed. See §19.5.

Figure C.27 — Broomcorn millet: an illustrative regional span

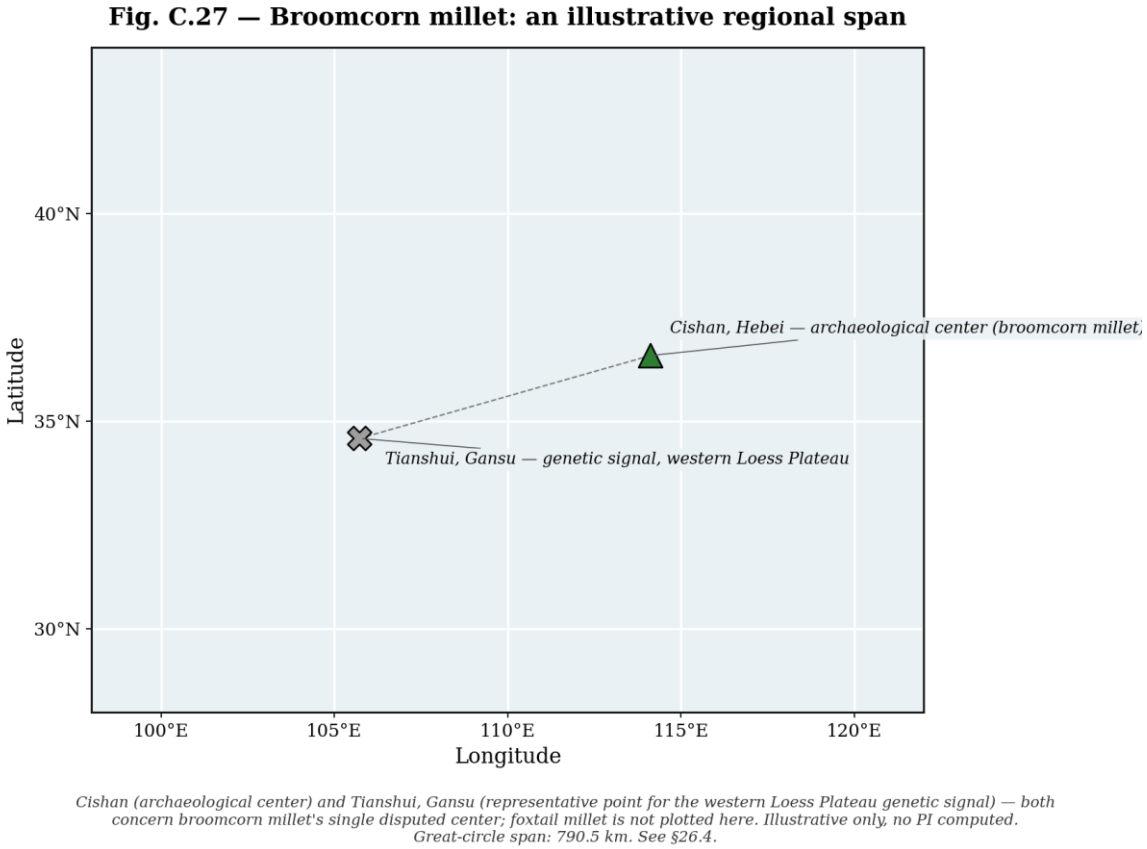


Fig. C.27 — Broomcorn millet: an illustrative regional span
40°N
35°N
30°N
Latitude
100°E
105°E
110°E
115°E
120°E
Longitude
Cishan, Hebei — archaeological center (broomcorn millet)
Tianshui, Gansu — genetic signal, western Loess Plateau
Cishan (archaeological center) and Tianshui, Gansu (representative point for the western Loess Plateau genetic signal) — both concern broomcorn millet's single disputed center; foxtail millet is not plotted here. Illustrative only, no PI computed.
Great-circle span: 790.5 km. See §26.4.

Cishan (archaeological center) and Tianshui, Gansu (western Loess Plateau genetic signal) — both concern broomcorn millet's single disputed center; foxtail millet reaches an unrelated, unanimous result (§26.2, §26.5) and is not plotted here. Illustrative only, no PI computed, on the same convention as §21.5. See §26.4.

Figure C.28 — Soybean: four named candidate regions, a disputed count

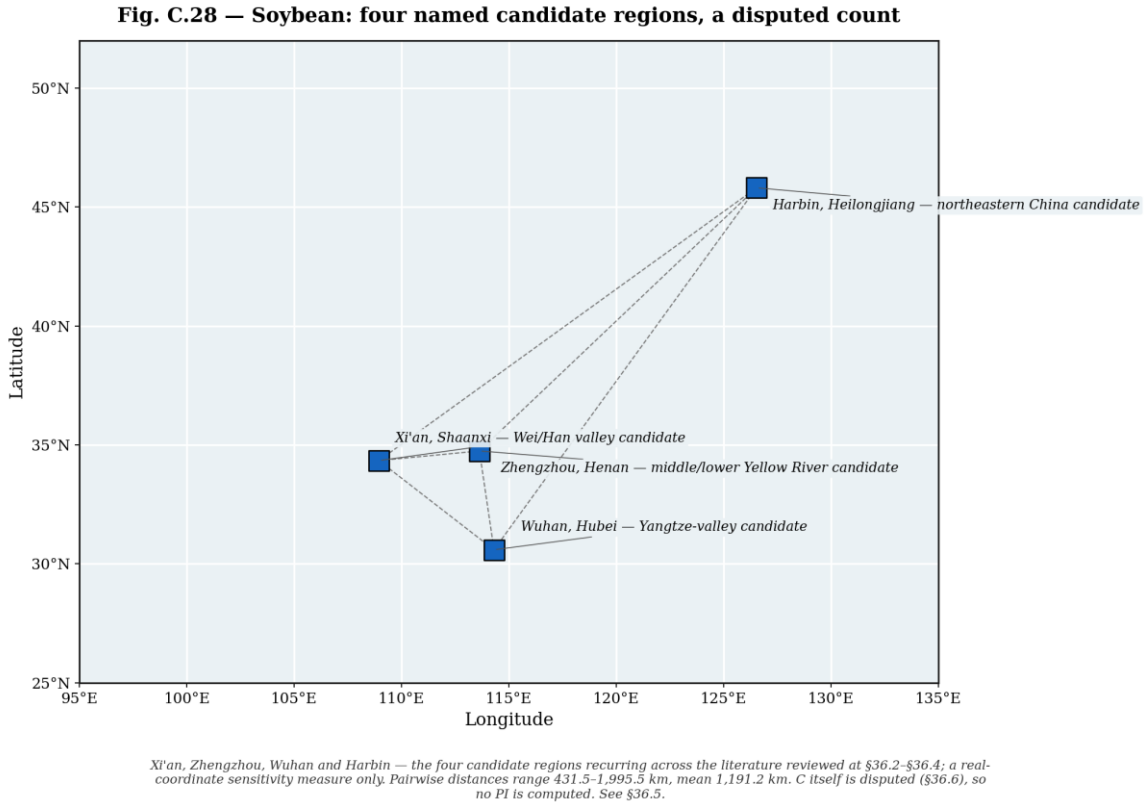


Fig. C.28 — Soybean: four named candidate regions, a disputed count
50°N
45°N
40°N
35°N
30°N
25°N
Latitude
95°E
100°E
105°E
110°E
115°E
120°E
125°E
130°E
135°E
Longitude
Harbin, Heilongjiang — northeastern China candidate
Xi'an, Shaanxi — Wei/Han valley candidate
Zhengzhou, Henan — middle/lower Yellow River candidate
Wuhan, Hubei — Yangtze-valley candidate
Xi'an, Zhengzhou, Wuhan and Harbin — the four candidate regions recurring across the literature reviewed at §36.2–§36.4; a real-coordinate sensitivity measure only. Pairwise distances range 431.5–1,995.5 km, mean 1,191.2 km. C itself is disputed (§36.6), so no PI is computed. See §36.5.

Xi'an, Zhengzhou, Wuhan and Harbin — the four candidate regions recurring across the literature reviewed at §36.2–§36.4; a real-coordinate sensitivity measure only, on horse's and turkey's own convention. C itself is disputed (§36.6), so no PI is computed. See §36.5.

Two Further Cases: Stages of One Lineage, Not Rival Centers

Two more cases carry a disclosed real-coordinate check but were left unplotted, on a footing distinct from the three cases above: coffee (Ch.39, §39.5) and oat (Ch.62, §62.8). Neither reports a dispute between rival centers of the same domestication event. Coffee's two points are sequential stages of one lineage's history — a wild-origin region and, downstream of it, a narrow domestication-pathway bottleneck — explicitly not rival centers (§39.5). Oat's two points are a unanimous genomic center against a

superseded, pre-genomic classification that no genomic source independently corroborates (§62.6, §62.8), the same evidentiary shape already used for apple's disclosed Iranian candidate (§33.4–§33.5). Both PI=0 by C=1 on unanimous grounds, independently of the distance shown; the figures below are illustrative only.

Figure C.29 — Coffee: a wild-origin region and a domestication pathway

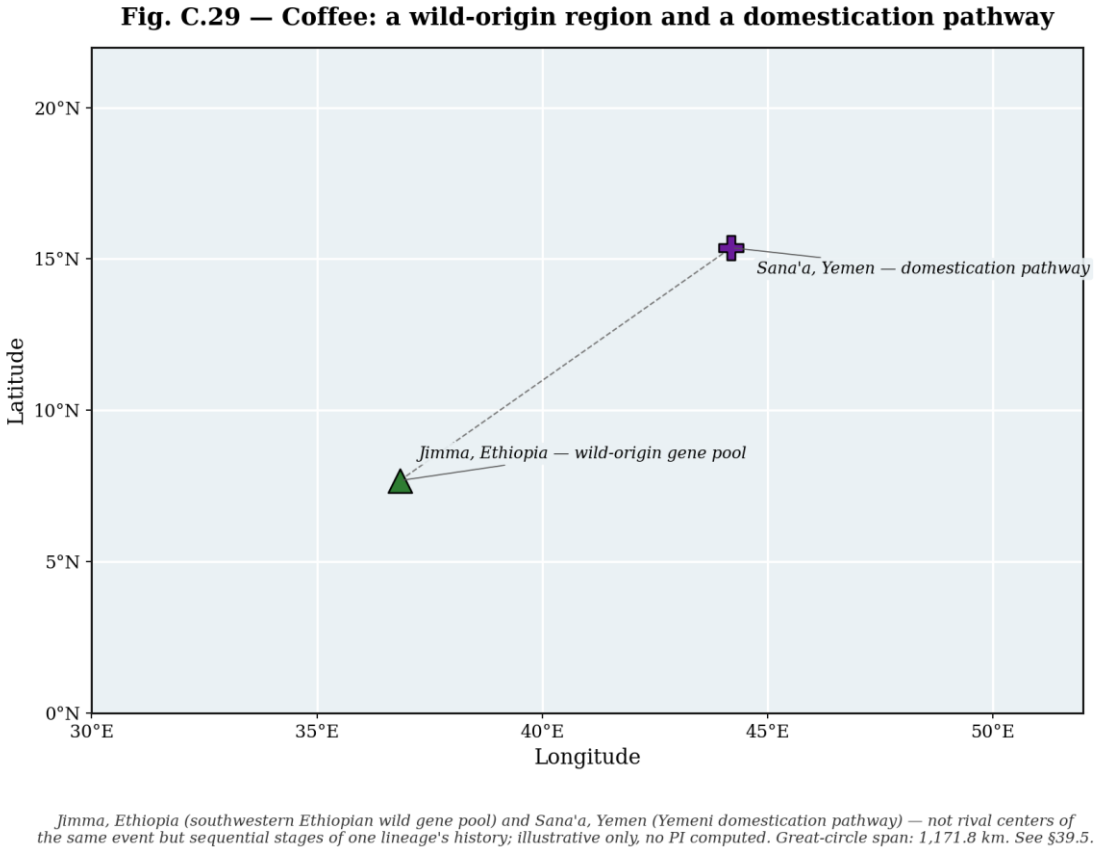
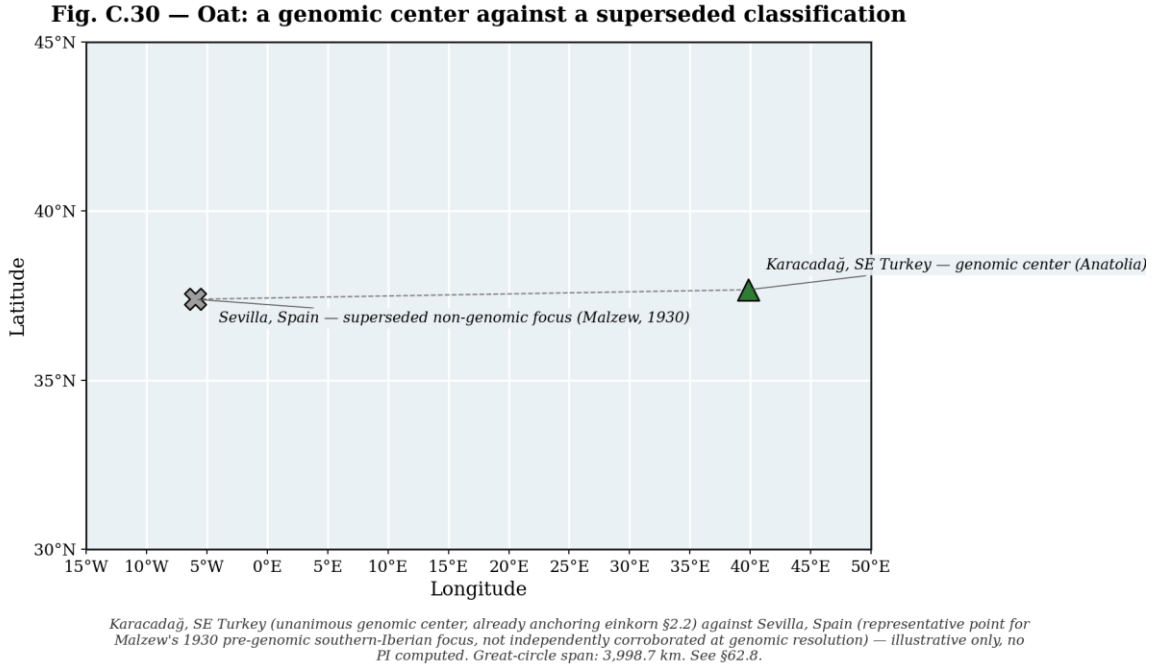


Fig. C.29 — Coffee: a wild-origin region and a domestication pathway
20°N
15°N
10°N
5°N
0°N
Latitude
30°E
35°E
40°E
45°E
50°E
Longitude
Sana'a, Yemen — domestication pathway
Jimma, Ethiopia — wild-origin gene pool
Jimma, Ethiopia (southwestern Ethiopian wild gene pool) and Sana'a, Yemen (Yemeni domestication pathway) — not rival centers of the same event but sequential stages of one lineage's history; illustrative only, no PI computed. Great-circle span: 1,171.8 km. See §39.5.

Jimma, Ethiopia (wild-origin gene pool) and Sana'a, Yemen (domestication pathway) — sequential stages of one lineage, not rival centers; illustrative only, no PI computed. See §39.5.

Figure C.30 — Oat: a genomic center against a superseded classification



Karacadağ, SE Turkey (unanimous genomic center) against Sevilla, Spain (Malzew's 1930 superseded southern-Iberian focus) — illustrative only, no PI computed. See §62.8.

Appendix D — Glossary of Terms and Notation

Terms and symbols are given in the sense they carry throughout this volume, with a pointer to the section where each was first introduced or formally defined. This appendix defines nothing new; it collects definitions already stated in the running text into one alphabetical and notational reference.

D.1 Core index notation

Symbol	Definition	First defined
C	Corroborated center count: the number of independent domestication centers a case's evidentiary record supports.	§2.7
κ (kappa)	Corroboration fraction: the directly reported fraction of loci, genes, or genome that support a secondary center, used as the index's weighting term.	§2.7
$\bar{D}$ (D-bar)	Mean great-circle distance between a case's corroborated centers, in kilometres, computed from real coordinates.	§2.7
PI	The Domestication Polycentricity Index itself: PI = C × κ × $\bar{D}$.	§2.7
⊥ (bottom)	The index's explicit non-result: returned when a case fails the resolvability predicate R(X), rather than forcing a number.	§20.7.2
R(X)	The resolvability predicate: a conjunction over a case's centers, true only if every one of them individually clears the bar for a usable coordinate.	§20.7

D.2 General evidentiary vocabulary

Term	Definition	First defined
Stopping rule	A commitment, declared before a chapter or section is written, to the scope it will and will not cover — the cycle's mechanism against open-ended scope creep.	§1.5
No-invented-data discipline	The rule that every quantitative claim in the cycle must trace to an executed computation or a cited primary source, with gaps disclosed rather than filled by inference.	§1.4
Doubly corroborated	A case where two independent evidentiary lines (typically archaeology and genetics) converge on the same center count and location without either line depending on the other.	§11.3
Resolvable / unresolved center	A center is resolvable if a real coordinate can be assigned to it; a confirmed but unresolved center (e.g. turkey's Southwest center) is known to exist without ever being pinned to a place.	§21.4, §20.7.1
Branch (of §20.7.2)	One of the named routes by which a case reaches ⊥: a live single-center location dispute; zero resolved centers; or n of C centers resolved with at least one not.	§20.7.2, §22.6
Floor / ceiling	PI = 0 is the index's floor (reached by three distinct routes, §8.3); the cycle's	§8.3, §13.6

Term	Definition	First defined
	running maximum (pig, PI = 13,050) is its ceiling to date.	
Introgression	Gene flow into an already-domesticated lineage from a separate wild or domestic population, deliberately excluded from C because it is not a second independent domestication.	§8.4, §6.6
Mosaic domestication	An ancient-genomics finding (goat, Bactrian camel) that a domesticate's genome carries small, real contributions from more than one wild source without those sources rising to the level of a second corroborated center.	§17.5, §19.4
Disputed event count	A case where the number of independent domestication events itself cannot be resolved, prior to and distinct from a disputed center count: even the wild species and its domesticate share a single evidentiary line, but how many separate wild-to-domesticate transitions occurred remains unsettled, with no center ever proposed for any of them.	§32.5
Genetically bounded domesticated	The implicit object §20.7.1's predicate presupposes for any candidate center x_i: a population distinguishable from its wild source to some reported degree. Most cases in this cycle supply one without comment; honey bee is the first case where the literature reviewed reports the	§31.6, §20.7.1

Term	Definition	First defined
population	opposite for most of the species' management history.	

A note on scope

This glossary does not include species names, author names, or site names, all of which are used in the ordinary sense their sources give them. It is restricted to the cycle's own analytical vocabulary and formal notation.

Appendix E — Comparative Chronology of Domestication Events

This table orders every case by its earliest directly reported date or date range, read across all eighty-one chapters rather than in the stopping-rule sequence the chapters themselves follow. Where the text does not consolidate a case's dispute to a single date range — typically because the dispute is itself about how many centers there are, not when domestication occurred — that is stated plainly rather than resolved here by inference.

Case	Earliest reported date / range	Region	Source
Dog	~14,200 cal BP (oldest uncontested remains, Bonn-Oberkassel, Germany)	Western Eurasia (contested 2nd signal, East Asia)	Ch.12, §12.4
Almond	~12,000 BP (Sk locus mutation, single-locus dating); founding wild population's own identity, and therefore precise regional attribution, left open between two candidates	Fertile Crescent (Sk mutation); founder population disputed between East Anatolia and Central Asia	Ch.68, §68.2, §68.4
Fig	~11,400–11,200 cal BP (parthenocarpic fruit, Gilgal I; interpretation as cultivated vs. gathered wild disputed)	Jordan Valley, Levant (Gilgal I)	Ch.46, §46.2

Case	Earliest reported date / range	Region	Source
Grapevine	~11,000 ya (95% CI ~10,500–12,500 ya), concurrent at both centers	Western Asia (CG1) and the Caucasus (CG2)	Ch.10, §10.2
Einkorn	~11,500–10,500 cal BP (cultivation of still-wild einkorn, pre-fixation)	Karacadağ, SE Turkey	Ch.2, §2.3
Sheep	~10,500 BP (SE Anatolia) to 10,400–9,400 BP (central Anatolia / Aşıklı Höyük)	SE to central Anatolia, into the Zagros	Ch.16, §16.3
Squash (C. pepo ssp. pepo)	~10,000 cal BP (oldest archaeological remains, Guilá Naquitz)	Oaxaca, Mexico	Ch.7, §7.2
Broomcorn millet	~10,000 cal BP (archaeological, Cishan); genetic signal points to the western Loess Plateau instead, not consolidated to one figure	Cishan, Hebei (archaeological center)	Ch.26, §26.3
Goat	~10,000 BP (Ganj Dareh kill-off demographic signature)	Zagros, Iran	Ch.17, §17.2
Cat	No single consolidated date; disputed among ~9,500 BP (Levant), ~3,500 BP (Egypt), and 9000	Levant / Egypt / North Africa (disputed)	Ch.28, §28.2–§28.5

Case	Earliest reported date / range	Region	Source
	BCE–19th c. CE (North Africa, per most recent genomic study)		
Pig	~10,000–9,000 ya (both centers)	Eastern Anatolia and the Yellow River corridor, China	Ch.11, §11.3
Maize	~9,000 ya (genetic divergence); ≥78,700 cal BP (Xihuatoxtla Shelter)	Balsas River basin, Mexico	Ch.6, §6.2
Adzuki bean	~8,985–7,939 cal BP (earliest charred remains, Xiaogao, Shandong; domestication status at this date not fully resolved, §72.4); disputed against a population-genomic reading placing the domestication event itself at 3,000–5,000 BP in central Japan	Lower Yellow River (Xiaogao) vs. central Japan, disputed	Ch.72, §72.2–§72.4
Cattle (taurine)	8th millennium BC	Near East (Fertile Crescent)	Ch.13, §13.3

Case	Earliest reported date / range	Region	Source
Cattle (zebu)	~8,000–8,500 BP	Indus Valley / Kachi plain, Balochistan	Ch.13, §13.3
Honey Bee	~8,450 BP (~6,500 BC, earliest secure site, Turkey); widespread, continuous beeswax exploitation across Neolithic Europe, the Near East, and North Africa from at least the 7th millennium BC (behavioural association only — no genetically bounded domesticated population is reported for most of this record, §31.5)	Neolithic Europe / Near East / N. Africa (beeswax); Tel Rehov, Israel (apiary, later)	Ch.31, §31.3
Yak	~7,300 BP (95% CI 7,227–7,914 BP; coalescent/fastsimcoal2 dating)	Qinghai-Tibet Plateau	Ch.67, §67.3
Alpaca	~7,100–6,000 BP (proposed signal; recent morphometric reanalysis disputes the identification)	Telarmachay, Peruvian Andes	Ch.29, §29.3

Case	Earliest reported date / range	Region	Source
Banana	~6,900–6,400 ya (phytolith evidence, Kuk Swamp)	New Guinea (Wahgi Valley)	Ch.27, §27.2
Olive	~6,000 ya	Northern Levant, near Syro-Anatolian borderlands	Ch.35, §35.5
Sesame	~5,000—5,500 ya (charred remains, Harappa; location disputed between Indian subcontinent and East Africa)	Indian subcontinent (contested; 2026 study proposes East Africa)	Ch.70, §70.2–§70.3
Cacao	~5,300 ya (starch-grain, theobromine-residue and ancient-DNA evidence, Santa Ana-La Florida)	Upper Amazon basin, Ecuador	Ch.35, §35.2
Domestic pigeon	Managed pigeon-keeping textually/iconographically attested by roughly 5,000 years ago (predation association considerably older, §66.2)	Levant / Middle East	Ch.66, §66.2, §66.4
Llama	~5,000–3,800 BP	NW Argentina / N Chile (dry puna)	Ch.29, §29.4

Case	Earliest reported date / range	Region	Source
Sorghum	Fourth millennium BCE (~3000 BCE)	Eastern Sudan (Butana Group, Atbara/Gash rivers)	Ch.25, §25.2
Yeast	Wild origin (not a domestication date) ~15,000 ya; earliest domestication event (sake) ~4,000 ya; wine ~1,500 ya; no single consolidated date for domestication as a whole	China / Far East Asia (wild origin); domestication events at multiple, undisclosed locations	Ch.30, §30.2–§30.3
Water buffalo (river)	By the mature Harappan phase (Indus seals, c. 2500 BC)	Western India (Gujarat/Maharashtra core)	Ch.14, §14.3
Water buffalo (swamp)	Neolithic; present by the mid-2nd millennium BC (Shang China)	China / northern Indochina border	Ch.14, §14.3
Dromedary	Late 2nd millennium BC	South-eastern Arabia	Ch.18, §18.2
Horse (DOM2 lineage)	Rapid expansion from ~2000 BC	Lower Volga-Don steppe	Ch.15, §15.4

Case	Earliest reported date / range	Region	Source
Cowpea	~1830–1595 BCE (directly dated charred remains, Kintampo culture, central Ghana; oldest directly dated cowpea remains reviewed; disputed center count, §74.5)	West Africa (Ghana); disputed against East African and dual-center readings	Ch.74, §74.2–§74.5
Common bean	Archaeobotanical anchors at Tehuacán Valley / Guilá Naquitz and Guitarrero Cave; single consolidated date range not given in the text	Mesoamerica and the Andes	Ch.9, §9.4
Turkey (Mesoamerican)	Captive rearing attested by ca. 300 BC–AD 100 (El Mirador); secure domestic husbandry by ~400–500 CE (Oaxaca)	Central/southern Mexico	Ch.21, §21.3
Donkey	~5000 BCE (a little over 7,000 BP)	Eastern Africa	Ch.23, §23.2
Chicken	~1650–1250 BCE (first unambiguous domestic remains, Ban Non Wat)	Central Thailand	Ch.20, §20.3
Barley	Dual-origin dispute; no single consolidated date range given in the text	Fertile Crescent, with a contested second	Ch.2, §2.4

Case	Earliest reported date / range	Region	Source
		(Tibetan) signal	
Rice	Timing bound to the disputed center count (C=1/2/3); no single consolidated date range given in the text	Southern China; contested extension to South/SE Asia	Ch.4, §4.3
Sunflower	Domestication date not consolidated in the text; refuted Mexican specimens dated to ~4,130 BP and ~2,600 BP	Eastern North America	Ch.7, §7.3
Cotton (G. hirsutum)	Domestication predates earliest textile evidence; no single date given beyond site/region	Yucatan Peninsula	Ch.22, §22.3
Cotton (G. barbadense)	Earliest secure evidence: Huaca Prieta textile assemblage; exact date not given in the text	Chicama Valley, Peru	Ch.22, §22.3
Bactrian camel	No single date range given; two rival hypotheses remain live	Contested between Iran-adjacent (HI) and Kazakhstan/ NW	Ch.19, §19.2–§19.3

Case	Earliest reported date / range	Region	Source
		Mongolia (HII) zones	
Potato	Domestication date not consolidated in the text	Southern Peruvian highlands, near Lake Titicaca	Ch.24, §24.2
Foxtail millet	Domestication date not consolidated in the text	China	Ch.26, §26.2
Koji	Domestication date not consolidated in the text; cultural (qu 麴 fermentation) record in Chinese sources reaches back roughly two thousand years, but this dates the technique's spread, not a domestication event	China / Japan (technique transmission only; no domestication-event locality reported)	Ch.32, §32.3–§32.4
Apple	Domestication date not consolidated in the text	Tian Shan range, Kazakhstan / Xinjiang	Ch.33, §33.2
Vanilla	Domestication date not consolidated in the text (domestication-centre question fully resolved; no date given)	Mesoamerica (Totonac cultivation, Mexico's Gulf coast)	Ch.34, §34.2

Case	Earliest reported date / range	Region	Source
Tea	Domestication date not consolidated in the text; timing bound to the disputed center count (C=1 vs. C=2/3)	Southwestern China; contested extension to the Yunnan/Assam border region and Indian Assam	Ch.35, §35.3
Hemp	Domestication date not consolidated in the text	East Asia	Ch.35, §35.4
Date palm	Domestication date not consolidated in the text (2015 two-center reading revised in 2017 to one, with post-domestication introgression); archaeological anchor: early date consumption in the Arabian Gulf (Beech 2003)	Persian Gulf / Middle East	Ch.35, §35.6
Oat	More than 3,000 years ago; weed-to-crop transition among wheat and barley fields, later spreading into Europe	Anatolia	Ch.62, §62.2

Case	Earliest reported date / range	Region	Source
Duck, mallard-derived	Approximately 2,000 BCE; associated from an early period with rice-paddy polyculture	China	Ch.63, §63.2
Muscovy duck	Indirect evidence (dietary, iconographic) from as early as CE 800; may predate CE 1000	Neotropics (Panama–Ecuador–Peru)	Ch.63, §63.6–§63.7
Taro	Archaeological use of wild/semi-wild forms reported to roughly 28,000 years ago; cultivation conventionally dated to at least 9,000 years	Southeast Asia (disputed: single region vs. region plus New Guinea)	Ch.64, §64.2–§64.6
Coconut	~2,500–3,000 BP (archaeobotanical/textual, southern India); wild-lineage divergence between the two basins dated independently to ~5,400 BP (95% HPD 3,669–7,810) by coalescent genomic dating	Indo-Atlantic (southern India, Sri Lanka) and Pacific (island Southeast Asia)	Ch.81, §81.2, §81.4

Rows are ordered oldest-first by the earliest figure the text itself reports; where no such figure is consolidated, the row is placed after the last case that does report one, in chapter order. This ordering is a reading aid only — it changes no date, center count, or PI value stated elsewhere in the

volume. Chapters 32–35 add eight rows on this same basis: olive (~6,000 ya) and cacao (~5,300 ya) are inserted in date order between banana and llama; koji, apple, vanilla, tea, hemp and date palm, none of which is given a consolidated domestication date in the cited literature, are appended after foxtail millet in chapter order, consistent with the convention stated above. Chapters 66–68 add three further rows on the same basis: almond (~12,000 BP) is inserted in date order between dog and fig, its own founder-population dispute disclosed in the region column rather than resolved by placement; yak (~7,300 BP) is inserted between honey bee and alpaca; and domestic pigeon (~5,000 BP, managed keeping) is inserted between cacao and llama. Chapter 74 adds one further row on the same basis: cowpea (~1830–1595 BCE, directly dated charred remains from Kintampo-culture contexts, central Ghana) is inserted between horse (DOM2 lineage) and common bean, its own three-way disputed center count disclosed in the region column rather than resolved by placement.

Appendix F — Catalog of Proposed-and-Rejected Hypotheses

Across eighty-one chapters, this cycle repeatedly encountered a second- or third-center claim that was raised in the literature, directly tested, and did not survive testing. §8.3 already noted that this is a structurally distinct route to PI = 0 from unanimous agreement reached without a rival claim ever being raised. This appendix collects every such claim in one place, so that the record of falsification — as much a part of this cycle's method as any positive result — is visible without reconstructing it from eleven separate chapters. Chapters 28–31 (cat, llama and alpaca, yeast, honey bee) add no new row here: none of the four turns on a second- or third-center claim that was raised and then tested against a rival, which is the specific shape this appendix catalogues; their own open questions are recorded instead in Appendix A.3 and A.5. Chapters 32–34 (koji, apple, vanilla) likewise add none: koji's difficulty is a missing coordinate, not a rejected rival center; apple's Iranian candidate (Bina et al. 2022, §33.4) is disclosed but unreplicated, not tested and refuted, the same footing on which barley's Tibetan candidate (§2.4) was already left out of this table; and vanilla's domestication centre is uncontested outright. Chapter 35 adds one row: date palm's 2015 two-center reading was directly tested against 2017 evidence and did not survive as an independent center, the same shape as every other row below. Chapters 36–45 add no further row, on the same grounds already stated for Chapters 28–34: none of soybean, guinea pig, silk moth, coffee, Capsicum, pea, the three Cucurbita cases, watermelon, or peach turns on a proposed rival center that was directly tested and refuted; their own open questions are recorded in Appendix A.2–A.4 instead. Chapter 46 (fig) likewise adds none: the Kislev et al. (2006) / Lev-Yadun et al. (2006) dispute is a disagreement over how to read one already-known find, not a proposed second center raised and then tested against a rival, and Khadari et al.'s

(2025/2026) multi-regional reading has not been tested against, or by, any second study at all; fig's open question is recorded in Appendix A.3 instead (§46.4–§46.6). Chapters 47–57 add no further row, on the same grounds already stated for Chapters 28–45: none of sweet potato's disputed contributing-taxa count (§47.3), reindeer's compound irresolvability (§48.8), quinoa's disputed event count (§49.7–§49.8), European rabbit's undisputed but unlocated single center (§51.2, §51.4), tomato's staged single-lineage reassignment of an older location dispute (§52.4), citrus's mosaic hybridization across three ancestral taxa (§53.5), fava bean's unconfirmable extinct progenitor (§54.6), goose's resolvability-split two-center case (§55.7), yam's three-for-three unresolved centers (§56.7), or avocado's three-for-three resolved centers (§57.7) turns on a second- or third-center claim that was raised and then directly tested against a rival, the specific shape this appendix catalogues; their own open questions are recorded in Appendix A.2–A.5 instead. Chapter 50 (helmeted guinea fowl) is this run's one exception: Shen et al. (2021) state directly that their whole-genome result rejects Darwin's (1883) East African hypothesis in favour of a West African, specifically Nigerian, origin — the same proposed-tested-refuted shape as sunflower's and horse's own rows below — and a row is added for it despite the case's own placement in Appendix A.3 rather than A.2, on the footing already established for chicken's individual "earliest" claims (Ch.20, §20.5): failing §20.7.1's point-resolvability bar does not exclude a case from also contributing a genuinely tested-and-rejected claim to this table. Chapter 58 (common carp) adds a second row, of a different evidentiary character from every row above: Xu et al.'s (2014) genomic resequencing directly tests, and does not corroborate, a pre-genomic historical and cultural hypothesis of an independent Chinese domestication (Balon 1995) — the oldest-dated rival hypothesis this cycle has recorded being overtaken by genomic evidence, and the first drawn from textual and husbandry-tradition

evidence rather than an earlier genetic or archaeological reading. Chapters 59–75 add no further row, on the same grounds already stated above: none of cassava's clean single-origin convergence (§59.5), rye's weedy-intermediate exclusion (§60.6), oat's disclosed-but-uncorroborated older classification (§62.6), duck's absent or unreliably drawn genetic boundary (§63.4), taro's disputed count, unreconciled rather than refuted (§64.6), domestic pigeon's disclosed-but-uncorroborated older classification (§66.5, on oat's own footing), yak's disclosed-but-unelevated internal refinement and later cross-species hybridization (§67.8), almond's single center left undecided between two candidate wild species (§68.5), sesame's live, unreconciled location dispute (§70.4–§70.5), adzuki bean's and cowpea's own disputed counts (§72.5, §74.5), or sugarcane's dispute over whether a Holocene domestication event took place at all (§75.7) turns on a second- or third-center claim directly tested against a rival and rejected; their own open questions are recorded in Appendix A.2–A.5 instead. Chapter 86 (opium poppy) adds a further row, of the same evidentiary character as guinea fowl's and common carp's own rows above: Machado et al. (2025) directly test the rival hypothesis that *Papaver somniferum* was introduced into Europe from the Fertile Crescent as a weed of cultivation, using genotyping-by-sequencing and seed morphometrics, and report it discarded in favour of a single Western Mediterranean domestication — the same proposed-tested-refuted shape as sunflower's, horse's, guinea fowl's, and common carp's own rows above (§86.3, §86.5–§86.6). Chapter 87 (bottle gourd) adds a further row on helmeted guinea fowl's own dual-placement footing (§50.8, §87.7): Kistler et al. (2014) directly re-test, using a larger and independently constructed ancient-DNA dataset, Erickson et al.'s (2005) own conclusion that domesticated, Asian-lineage bottle gourd was carried into the Americas by Paleoindians across Beringia, and report it reversed in favour of a transoceanic, African-lineage introduction by ocean-current drift —

the same proposed-tested-refuted shape as sunflower's, horse's, guinea fowl's, and opium poppy's own rows above, contributed despite the case's own placement in Appendix A.3 rather than A.2, on guinea fowl's own precedent for that dual placement.

Claim	Proposed by	Basis of the claim	How it was tested and what followed	Source
Sunflower second center	Lentz et al. (2001)	A possible achene from San Andrés, Tabasco, Mexico (~4,130 BP), with further candidates from Cueva del Gallo (~2,600 BP)	Heiser (2008) reidentified the original specimen as bottle gourd; Blackman et al. (2011) haplotype-tested three selective-sweep genes and found results consistent only with a single ENA origin	Ch.7, §7.3
Grapevine third center	Sardinian claim (see §10.2.2)	A proposed additional Mediterranean domestication locus	A geographic mismatch with the genomically supported centers; reinterpreted rather than sustained as an independent origin	Ch.10, §10.2.2
Water buffalo third	Traditional accoun	Abundant Neolithic/ Bronze	Yang, Liu, Chen et al. (2008) sequenced ancient mtDNA D-	Ch.14, §14.5

Claim	Proposed by	Basis of the claim	How it was tested and what followed	Source
(Chinese) center	ts based on Bubalus mephistopheles remains, Yangtze/Wei River region	Age remains, morphologically classified as a distinct domesticate, ~7,000 ya	loop from 13 specimens (Wei River, 8,000–3,600 cal BP) and found they group with a genetically distinct, extinct wild species, not modern domestic buffalo, confirming an earlier zooarchaeological doubt (Liu et al. 2004, 2006)	
Horse: Botai center	Outram et al. (2009)	Enormous horse-bone assemblages, corral features, reported bit-wear and milk-residue evidence at Botai, Kazakhstan	Gaunitz et al. (2018): Botai horses are ancestral to Przewalski's horse, not modern domestic horses (~2.7% Botai-related ancestry in modern stock)	Ch.15, §15.3–§15.4

Claim	Proposed by	Basis of the claim	How it was tested and what followed	Source
Horse: Iberian center	Proposed on mitochondrial diversity grounds (local wild-mare recruitment)	Regional mitochondrial diversity read as evidence of local domestication	Librado et al. (2021), sampling 273 ancient genomes across all named candidates, found the modern DOM2 lineage traces to the lower Volga-Don region; Iberia does not survive as a source	Ch.15, §15.3–§15.4
Horse: Anatolian center	Proposed on comparable mitochondrial grounds for a distinct regional wild	Regional mitochondrial diversity	Excluded by the same Librado et al. (2021) test that excluded Iberia and Botai	Ch.15, §15.3–§15.4

Claim	Proposed by	Basis of the claim	How it was tested and what followed	Source
	population			
Horse: Botai husbandry itself (a separate question from ancestry)	Outram et al. (2009); bit-wear and milk-residue evidence	Signature bit-wear read as evidence of bridling	Taylor & Barrón-Ortiz (2021) re-examined the wear against wild Pleistocene equid comparanda and concluded it is more consistent with natural dental wear; a rebuttal has since been posted (Bendrey et al., via Zenodo) — disclosed as unresolved, not closed	Ch.15, §15.4
Goat: a second, minor signal	Naderi et al. (2008)	A ~1.4% minor genetic contribution alongside the primary Zagros signal	Not refuted — affirmatively corroborated as real and minor, yielding the cycle's lowest non-zero, non-refuted PI (19.4). Included here for contrast with the fully refuted claims above.	Ch.17, §17.4
Cattle: African third center	A currently live,	Proposed additional African	Not refuted — remains an open, still-contested extension, structurally unlike the fully tested-	Ch.13, §13.5

Claim	Proposed by	Basis of the claim	How it was tested and what followed	Source
	contested extension (§13.5)	domestication signal	and-rejected claims above; no κ assigned and no PI recomputed for C=3	
Bactrian camel: Kopet Dagh foothill sites	Peters & von den Driesch (1997)	Proposed archaeological center in the Kopet Dagh foothills	Rejected by the original authors themselves; more recent genomic work (Ming et al.) favors a western/Iranian zone generally but has not gone back to test the specific rejected Kopet Dagh sites	Ch.19, §19.3
Chicken: several individual 'earliest' claims	Various 20th-century site reports across the Indus Valley, northern China, and mainla	Scattered early remains, rarely cross-checked against direct dating	Peters, Lebrasseur, Irving-Pease et al. (2022): systematic reassessment of 600+ sites in 89 countries; a proposed Theban tomb 'earliest chicken' reidentified as a duck; Egyptian Gallus depictions read as possibly wild junglefowl; direct radiocarbon dating	Ch.20, §20.5

Claim	Proposed by	Basis of the claim	How it was tested and what followed	Source
	nd SE Asia		overturned numerous individual early claims	
Foxtail millet second center	Kawase & Sakamoto	Genetically less specialized, morphologically primitive accessions found between Afghanistan and India	No later molecular or archaeological source reviewed here corroborates the Afghanistan-India hypothesis as a second, independent center; treated as a proposed and effectively refuted rival, structurally the same shape as sunflower's and horse's refuted claims	Ch.26, §26.2
Potato second center (Chile)	Vavilov, continued by Juzepczuk & Bukasov	Collecting expeditions of the late 1920s described two centers of varietal diversity: Peru-Bolivia highlands and the	Spooner et al. (2005): Chilean landraces are secondarily derived from the Andean lineage, via hybridization with Solanum tarijense, not an independent domestication event	Ch.24, §24.3

Claim	Proposed by	Basis of the claim	How it was tested and what followed	Source
		southern coast of Chile		
Date palm second center (North Africa)	Hazzouri et al. (2015); Mathew et al. (2015); Zehdi-Azouzi et al. (2015)	Strong genetic differentiation between Middle Eastern and North African cultivars, read provisionally as two independent domestication centers	Gros-Balthazard et al. (2017), reporting wild date palms discovered in Oman, revised this: North African diversity is attributed to introgressive hybridisation with the wild Cretan relative Phoenix theophrasti, not to an independent African domestication	Ch.35, §35.6
C. argyrosperma: southern-Mexico domes	Model tested by Barrera-Redondo et al. (2021)	Fastsimcoal2 coalescent simulation comparing a domestication-in-Jalisco	The Jalisco-with-secondary-contact model won on Akaike Information Criterion; the southern-Mexico alternative was explicitly discarded, not merely unmentioned	Ch.43, §43.2

Claim	Proposed by	Basis of the claim	How it was tested and what followed	Source
tication model	alongside their own preferred alternative	model against a domestication-in-southern-Mexico model, each crossed with three gene-flow scenarios		
Guinea fowl: East African center	Darwin (1883)	Wild stock proposed in East Africa; later joined in the literature by a rival West African reading (Blench & MacDonald, 2000) and a dual-origin,	Shen et al. (2021), sequencing 129 whole genomes (89 domestic, 34 wild, 6 wild relatives) across Africa, Asia, and Europe, found wild guinea fowl from Nigeria (West Africa), not Kenya or Sudan (East Africa), consistently closest to domestic populations by phylogeny, PCA, and ADMIXTURE, and state directly that this result rejects	Ch.50, §50.4

Claim	Proposed by	Basis of the claim	How it was tested and what followed	Source
		West-and-East reading (Andah et al., 2014)	Darwin's East African hypothesis	
Common carp: independent Chinese domestication	Balon (1995), reviewing textual and husbandry-tradition evidence	Ancient Chinese pond-culture traditions, textually attested well before the Roman record, long treated as a candidate independently arrived-at husbandry practice on the eastern population	Xu et al. (2014), resequencing 33 accessions against a draft genome (strain Songpu), report a single wild origin, with the Ponto-Caspian and East Asian subspecies as two later-diverging branches of one lineage rather than two independently domesticated wild populations	Ch.58, §58.4

Claim	Proposed by	Basis of the claim	How it was tested and what followed	Source
Opium poppy: Fertile Crescent weed-introduction hypothesis	Traditional/rival hypothesis, current in the literature	Proposed introduction of P. somniferum into Europe from Southwest Asia as a weed of cultivation, only later domesticated deliberately, as a rival to the Western Mediterranean origin	Machado, Bonhomme, Soteras et al. (2025), combining genotyping-by-sequencing with seed geometric morphometrics across 190 accessions and 15 Papaver species, found no genetic signal placing any Southwest Asian population closer to P. somniferum than its Western Mediterranean wild progenitor P. setigerum, and report the Fertile-Crescent-introduction hypothesis discarded on this basis	Ch.86, §86.5–§86.6
Bottle gourd: Paleoindian Asian-origin	Erickson, Smith, Clarke, Sandweiss &	Ancient chloroplast DNA from ten of the oldest archaeological bottle	Kistler, Montenegro, Smith, Gifford, Green, Newsom & Shapiro (2014), isolating roughly 86,000 bp of plastid genome sequence from a substantially larger	Ch.87, §87.2–§87.4

Claim	Proposed by	Basis of the claim	How it was tested and what followed	Source
introduction	Tuross (2005)	gourd specimens in the Americas (earliest c. 10,000 cal BP) all matched the modern Asian reference genotype, read as domesticated Asian-lineage bottle gourd carried into the Americas by Paleoindian populations crossing Beringia	and more geographically representative ancient-DNA dataset explicitly designed to re-test the 2005 result, found every pre-Columbian specimen in their expanded dataset most closely related to African, not Asian, gourds, consistent with transoceanic drift and naturalization requiring no human vector	

Reading this table

Most rows here are hypotheses that did not survive direct testing, documented for completeness rather than carried forward as a live value of C. Two rows — goat's minor signal and cattle's African extension — are included for contrast: they were tested and not rejected, or remain genuinely open, and are marked as such rather than grouped with the refuted claims around them.

Appendix G — Index of Evidentiary Methods and Statistics

This cycle draws on a recurring set of archaeological and genetic methods across its eighty-one chapters. Rather than a glossary of named genes or loci — this volume works at the level of reported fractions and center counts, not named markers — this appendix indexes the evidentiary methods themselves and points to a representative case for each.

Method / statistic	What it tests	Representative cases (§)
Mitochondrial DNA (mtDNA) phylogeography	Maternal-line genetic diversity used to infer a lineage's geographic source or number of source populations.	Pig (§11.3); dog (§12.3.1); water buffalo (§14.3); dromedary (§18.3); llama and alpaca (§29.2); quinoa (§49.4)
Y-chromosome phylogeography	Paternal-line genetic diversity, used alongside mtDNA to cross-check a proposed center.	Dog (§12.3.1); water buffalo (§14.3)
Nuclear genome-wide resequencing	Whole- or large-fraction-genome sequencing across many individuals, used to test single- vs. multi-origin models directly.	Rice (§4.2); horse (§15.4); donkey (§23.2); dog (§12.4.1); cat (§28.4); yeast (§30.2, §30.4); domestic pigeon (§66.4)

Method / statistic	What it tests	Representative cases (§)
Ancient DNA (aDNA)	Genetic material recovered directly from archaeological specimens, used to test a hypothesis against the actual historical population rather than only its modern descendants.	Horse (§15.4); water buffalo (§14.5); turkey (§21.2); dog (§12.4.1); sorghum (§25.2); cat (§28.4); llama and alpaca (§29.4); honey bee (§31.4)
Lipid residue analysis (organic geochemistry)	Chemical identification of a substance's signature (e.g. beeswax) preserved in porous archaeological material such as pottery, used to date and geographically map a resource's exploitation independent of any skeletal or genetic remains.	Honey bee (§31.3)
Haplotype / selective-sweep analysis	Identification of genome regions bearing the signature of selection during domestication, used to test whether a claimed second center shares that signature.	Sunflower (§7.3)

Method / statistic	What it tests	Representative cases (§)
Chloroplast DNA haplotyping (PCR / PCR-RFLP)	Maternal-line plant genetic marker used to distinguish independent domestication lineages.	Common bean (§9.3)
Outgroup f3 statistics / AIC model comparison / MSMC2 split-time estimation	Population-genetic methods used together to test and date a proposed dual-origin split.	Grapevine (§10.2)
Zooarchaeological demographic profiling (kill-off age, body-size reduction)	Osteological evidence of managed herds versus hunted populations, independent of any genetic data.	Pig (§11.3); cattle (§13.3); sheep and goat (§16.3–§17.2)
Archaeobotanical chronology	Direct dating and identification of plant remains, used to establish the pace and timing of a domestication syndrome's fixation.	Einkorn (§2.3); common bean (§9.4); sorghum (§25.2); broomcorn millet (§26.3); banana (§27.2); fig (§46.2)
Radiocarbon dating (direct, on specimens)	Direct dating of the specimens themselves, used to test or overturn	Chicken (§20.3); maize (§6.2)

Method / statistic	What it tests	Representative cases (§)
	indirect chronological claims.	
AFLP / multilocus molecular marker genotyping	Multiple genome-wide marker systems (amplified fragment length polymorphisms; isozyme, prolamin, rDNA, RAPD, RFLP and transposon-display markers) analyzed together to test single- vs. multiple-origin hypotheses without whole-genome sequencing.	Potato (§24.2); foxtail millet (§26.2)
Genomic ancestry-mosaic reconstruction	Genome-wide ancestry decomposition into named wild source populations, used where a cultivar's genome is itself a compound of successive hybridization events rather than a single origin.	Banana (§27.3)
Great-circle distance recomputation	This cycle's own consistent method for turning cited real-world coordinates into the D̄ term of the index.	Throughout; e.g. §2.8.4, §6.4, §10.3, §12.4, §15.5, Appendix B
Resolvability predicate R(X)	This cycle's own formal test (§20.7.1–§20.7.2) for whether a case's centers are	Formally stated Ch.20, §20.7;

Method / statistic	What it tests	Representative cases (§)
	individually pinned to real coordinates, determining whether PI is computed at all.	applied Ch.21–Ch.24, Ch.26
Directional gene-loss / gene-gain profiling	Comparison of functional gene content (loss of a biosynthesis cluster, amplification of another gene family) between domesticate and wild source, used to identify a domestication signature that carries no attached location.	Koji (§32.2)
Coalescent demographic modelling	Population-genetic modelling of divergence and demographic history, used to propose an additional, geographically separate domestication centre.	Apple (§33.4); C. argyrosperma (§43.2, Fastsimcoal2/AIC); flax and C. moschata (§42.4, §43.3, SMC++/demographic estimation); yak (§67.3, Fastsimcoal2)

Method / statistic	What it tests	Representative cases (§)
Microsatellite (SSR) genotyping / Bayesian population clustering	Multi-locus microsatellite genotyping across many accessions, analyzed with Bayesian clustering to resolve gene pools and test whether cultivated and spontaneous individuals are genetically continuous within a region, used to propose a diffuse, multi-regional domestication model.	Fig (§46.3); almond (§68.4, with ABC)

Bibliography

This bibliography compiles, in one alphabetized list, every source cited by author and year across the monograph and its appendices. It is assembled from in-text citations already present in the chapters above — no new sources are introduced here, and none of the underlying findings are revised. Two entries (Tanno & Willcox, §2.3; Dai et al., §2.4.1) and one entry cited only by year (Nevo 2013, §2.4.1) lack a complete journal citation in the chapters as drafted; rather than reconstruct a plausible-looking reference from memory, this appendix flags them as incomplete and names the specific gap, consistent with this cycle's disclosed-limits discipline (§1.4). Two further in-text citations that initially looked incomplete on the same terms — Zeder, §16.3, Suska-Malawska et al., §19.5, and Zheng et al., §80.5–§80.7 — were verified against their published record (a book chapter and two journal articles respectively) and appear below with full citations.

Adams, K.R. (2014). [Naked-caryopsis evidence for little barley, *Hordeum pusillum*, domestication in the U.S. Southwest]; summarized in Mueller (2017c), cited in this cycle's §7.1.2.

Adeola, A.C., Ommeh, S.C., Murphy, R.W., Wu, S.-F., Peng, M.-S. & Zhang, Y.-P. (2015). Mitochondrial DNA variation of Nigerian domestic helmeted guinea fowl. Animal Genetics, 46(5), 576–579.

Ahlawat, S., Sharma, U., Singh, K.V., Arora, R., Sharma, R., Singh, A., Mohan, N.H., Banik, S., Raja, K.N. & Venkatachalapathy, R.T. (2026). Whole mitochondrial genome analysis highlights India's role in pig domestication and maternal lineage diversification. *Biochemical Genetics* (article-level publication; volume/page numbers not yet assigned at time of this cycle's search). This resolves the incomplete in-text citation at §11.5 ("Mohan, Venkatachalapathy et al. 2026", which named two of ten co-authors rather than the first author).

Ajmone-Marsan, P., Garcia, J.F., Lenstra, J.A. et al. (2010). On the origin of cattle: how aurochs became cattle and colonized the world. Evolutionary Anthropology 19:148–157.

Allaby, R.G., Peterson, G.W., Merriwether, A. & Fu, Y.-B. (2005). Evidence of the domestication history of flax (Linum usitatissimum L.) from genetic diversity of the sad2 locus. Theoretical and Applied Genetics, 112(1), 58–65.

Almathen, F., Charruau, P., Mohandesan, E. et al. (2016). Ancient and modern DNA reveal dynamics of domestication and cross-continental dispersal of the dromedary. *PNAS* 113(24):6707–6712.

Alves, J.M., Carneiro, M., Afonso, S. et al. (2015). Levels and patterns of genetic diversity and population structure in domestic rabbits. PLoS ONE, 10(12), e0144687.

Andah, B., Okpoko, A., Shaw, T. & Sinclair, P. (Eds.) (2014). The Archaeology of Africa: Food, Metals and Towns. London: Routledge.

Anderson, D.G., Kvie, K.S., Davydov, V.N. & Røed, K.H. (2017). Maintaining genetic integrity of coexisting wild and domestic populations: Genetic differentiation between wild and domestic Rangifer with long traditions of intentional interbreeding. Ecology and Evolution, 7, 6790–6802.

[Anonymous / not fully attributed in main text] (2018). Jalisco–Pacific teosinte reanalysis, 32,739 SNPs across 29 populations. bioRxiv 10.1101/239707 (preprint; peer-review status not confirmed in this cycle's search, disclosed as such at first citation, §6.3).

Arbuckle, B.S. & Kassebaum, T.M. (2021). Management and domestication of cattle (Bos taurus) in Neolithic Southwest Asia. Animal Frontiers 11(3):10–19.

Asch, D.L. & Asch, N.B. (1985). Prehistoric plant cultivation in west-central Illinois. In *Prehistoric Food Production in North America*,

ed. R.I. Ford, pp. 149–204. Anthropological Papers No. 75, Museum of Anthropology, University of Michigan.

Ba, F.S., Pasquet, R.S. & Gepts, P. (2004). Genetic diversity in cowpea [Vigna unguiculata (L.) Walp.] as revealed by RAPD markers. Genetic Resources and Crop Evolution 51(5), 539–550.

Balon, E.K. (1995). Origin and domestication of the wild carp, Cyprinus carpio: from Roman gourmets to the swimming flowers. Aquaculture 129, 3–48.

Barchi, L., Aprea, G., Rabanus-Wallace, M.T., Toppino, L., Alonso, D., Portis, E., Lanteri, S., Gaccione, L., Omondi, E., van Zonneveld, M., Schafleitner, R., Ferrante, P., Börner, A., Stein, N., Díez, M.J., Lefebvre, V., Salinier, J., Boyaci, H.F., Finkers, R., Brouwer, M., Bovy, A.G., Rotino, G.L., Prohens, J. & Giuliano, G. (2023). Analysis of >3400 worldwide eggplant accessions reveals two independent domestication events and multiple migration-diversification routes. The Plant Journal 116(6): 1667–1680.

Barnard, H., Dooley, A.N., Areshian, G., Gasparyan, B. & Faull, K.F. (2011). Chemical evidence for wine production around 4000 BCE in the Late Chalcolithic Near Eastern highlands. *Journal of Archaeological Science* — cited in this cycle via *PNAS* context (Areni-1 Cave, Armenia, integrated winemaking installation, c. 4000 cal BC).

Barrera-Redondo, J., Sánchez-de la Vega, G., Aguirre-Liguori, J.A., Castellanos-Morales, G., Gutiérrez-Guerrero, Y.T., Aguirre-Dugua, X., Aguirre-Planter, E., Tenaillon, M.I., Lira-Saade, R. & Eguiarte, L.E. (2021). The domestication of Cucurbita argyrosperma as revealed by the genome of its wild relative. Horticulture Research, 8, 109.

Beech, M. (2003). Archaeobotanical evidence for early date consumption in the Arabian Gulf. In *The Date Palm --- From*

Traditional Resource to Green Wealth, The Emirates Center for Strategic Studies and Research, Abu Dhabi, pp. 11-32.

Beja-Pereira, A., England, P.R., Ferrand, N. et al. (2004). African origins of the domestic donkey. Science 304:1781 — cited in this cycle at §23.3.1 for the original two-mitochondrial-haplogroup finding.

Bendrey, R. et al. (2021). Rebuttal of Taylor & Barrón-Ortiz (2021), "Rethinking the evidence for early horse domestication at Botai." Posted via Zenodo, DOI 10.5281/zenodo.5142604; formal journal publication status not confirmed in this cycle's search, disclosed as such at first citation, §15.4.

Bergström, A., Frantz, L., Schmidt, R. et al. (2020). Origins and genetic legacy of prehistoric dogs. *Science* 370:557–564 — cited in this cycle's §12.2, full author list beyond the three named in text not independently confirmed.

Bergström, A., Furtwängler, A., Johnston, S. et al. (2026). Genomic history of early dogs in Europe. Nature 651:986–994.

Bergström, A., Stanton, D.W.G., Taron, U.H. et al. (2022). Grey wolf genomic history reveals a dual ancestry of dogs. *Nature* 607:313–320.

Bertioli, D.J., Cannon, S.B., Froenicke, L., Huang, G., Farmer, A.D., Cannon, E.K.S. et al. (2016). The genome sequences of Arachis duranensis and Arachis ipaensis, the diploid ancestors of cultivated peanut. Nature Genetics 48(4), 438–446.

Bertioli, D.J., Jenkins, J., Clevenger, J., Dudchenko, O., Gao, D., Seijo, G. et al. (2019). The genome sequence of segmental allotetraploid peanut Arachis hypogaea. Nature Genetics 51(5), 877–884.

Besnard, G., Terral, J.-F. & Cornille, A. (2013). On the origins of the olive tree (*Olea europaea*), new evidence from the analysis of polymorphism. *Proceedings of the Royal Society B* 280: 20122833.

Best, J., Fothergill, T., Sykes, N. et al. (2022). Redefining the timing and circumstances of the chicken's introduction to Europe and north-west Africa. *Antiquity* 96(388):868–882.

Bhatnagar, M.K. (1968). Mitotic chromosomes of white Chinese geese. Journal of Heredity, 59(3), 191–195.

Bina, H. et al. (2022). Evidence of an additional centre of apple domestication in Iran, with contributions from the Caucasian crab apple (*Malus orientalis*). *Molecular Ecology* 31: 3688-3706.

Bitocchi, E., Bellucci, E., Giardini, A. et al. (2012). Mesoamerican origin of the common bean (*Phaseolus vulgaris* L.) is revealed by sequence data. *PNAS* 109:E788–E796.

Bitocchi, E. et al. (2013). Molecular analysis of the parallel domestication of the common bean (*Phaseolus vulgaris*) in Mesoamerica and the Andes. *New Phytologist* 197:300–313.

Blackman, B.K., Scascitelli, M., Kane, N.C., Luton, H.H., Rasmussen, D.A., Bye, R.A., Lentz, D.L. & Rieseberg, L.H. (2011). Sunflower domestication alleles support single domestication center in eastern North America. *PNAS* 108:14360–14365.

Blanca, J., Cañizares, J., Cordero, L., Pascual, L., Diez, M.J. & Nuez, F. (2012). Variation revealed by SNP genotyping and morphology provides insight into the origin of the tomato. PLoS ONE, 7(10), e48198.

Blanca, J., Montero-Pau, J., Sauvage, C. et al. (2015). Genomic variation in tomato, from wild ancestors to contemporary breeding accessions. BMC Genomics, 16, 257.

Blasco, R., Finlayson, C., Rosell, J., Sánchez Marco, A., Finlayson, S., Finlayson, G., Negro, J.J., Giles Pacheco, F. & Rodríguez Vidal, J. (2014). The earliest pigeon fanciers. Scientific Reports 4, 5971.

Blench, R. & MacDonald, K.C. (Eds.) (2000). The Origins and Development of African Livestock: Archaeology, Genetics, Linguistics and Ethnography. London: UCL Press.

Bloch, G., Francoy, T.M., Wachtel, I., Panitz-Cohen, N., Fuchs, S. & Mazar, A. (2010). Industrial apiculture in the Jordan valley during Biblical times with Anatolian honeybees. *Proceedings of the National Academy of Sciences* 107(25): 11240–11244.

Botchway, P.K., Adenyo, C., Kayang, B.B., Hayano, A. & Inoue-Murayama, M. (2013). Development of 31 polymorphic microsatellite markers for guinea fowl (Numida meleagris) using next-generation sequencing technology. Conservation Genetics Resources, 5, 1163–1165.

Bottero, J. (1980). Knoblauch. In D.O. Edzard (Ed.), Reallexikon der Assyriologie und vorderasiatischen Archaologie, vol. 6 (in French), pp. 39–41. Berlin: Gruyter.

Boudadi-Maligne, M. & Escarguel, G. (2014). A biometric re-evaluation of recent claims for Early Upper Palaeolithic wolf domestication in Eurasia. *Journal of Archaeological Science* 45:80–89.

Brandes, E.W. (1956). Origin, dispersal and use in breeding of the Melanesian garden sugarcanes and their derivatives, Saccharum officinarum L. Proceedings of the International Society of Sugar Cane Technologists 9, 709–750.

Brass, M. (2018). Early North African cattle domestication and its ecological setting: a reassessment. Journal of World Prehistory 31:81–115.

Browicz, K. & Zohary, D. (1996). The genus Amygdalus L. (Rosaceae): species relationships, distribution and evolution under

domestication. Genetic Resources and Crop Evolution 43(3), 229–247.

Brubaker, C.L. & Wendel, J.F. (1994). Reevaluating the origin of domesticated cotton (Gossypium hirsutum; Malvaceae) using nuclear restriction fragment length polymorphisms (RFLPs). American Journal of Botany 81(10): 1309–1326.

Burger, P.A. (2019). Old World camels in a modern world — a balancing act between conservation and genetic improvement. *Animal Genetics* 50:598–604.

Burgarella, C., Cubry, P., Kane, N.A., Varshney, R.K., Mariac, C., Liu, X., Shi, C., Thudi, M., Couderc, M., Xu, X., Chitikineni, A., Scarcelli, N., Barnaud, A., Rhône, B., Dupuy, C., François, O., Berthouly-Salazar, C. & Vigouroux, Y. (2018). A western Sahara centre of domestication inferred from pearl millet genomes. Nature Ecology & Evolution 2(9): 1377–1380.

Cagnato, C. & Ponce, J.M. (2017). Ancient Maya manioc (Manihot esculenta Crantz) consumption: Starch grain evidence from late to terminal classic (8th–9th century CE) occupation at La Corona, northwestern Petén, Guatemala. Journal of Archaeological Science: Reports 16, 276–286.

Campana, M.G., Robles García, N.M. & Tuross, N. (2015). America's red gold: multiple lineages of cultivated cochineal in Mexico. Ecology and Evolution 5(3): 607–617.

Cao, K., Zheng, Z., Wang, L., Liu, X., Zhu, G., Fang, W., Cheng, S., Zeng, P., Chen, C., Wang, X., et al. (2014). Comparative population genomics reveals the domestication history of the peach, Prunus persica, and human influences on perennial fruit crops. Genome Biology, 15, 415.

Cao, K., Zhou, Z., Wang, Q., Guo, J., Zhao, P., Zhu, G., Fang, W., Chen, C., Wang, X., Wang, X., Tian, Z. & Wang, L. (2016). Genome-

wide association study of 12 agronomic traits in peach. Nature Communications, 7, 13246.

Cao, K., Li, Y., Deng, C.H., Gardiner, S.E., Zhu, G., Fang, W., Chen, C., Wang, X. & Wang, L. (2019). Comparative population genomics identified genomic regions and candidate genes associated with fruit domestication traits in peach. Plant Biotechnology Journal, 17(10), 1954–1970.

Caracuta, V. et al. (2015). The onset of faba bean farming in the Southern Levant. Scientific Reports, 5, 14370.

Caracuta, V., Weinstein-Evron, M., Kaufman, D., Yeshurun, R., Silvent, J. & Boaretto, E. (2016). 14,000-year-old seeds indicate the Levantine origin of the lost progenitor of faba bean. Scientific Reports, 6, 37399.

Carneiro, M., Afonso, S., Geraldes, A., Garreau, H., Bolet, G., Boucher, S., Tircazes, A., Queney, G., Nachman, M.W. & Ferrand, N. (2011). The genetic structure of domestic rabbits. Molecular Biology and Evolution, 28(6), 1801–1816.

Carneiro, M., Rubin, C.-J., Di Palma, F., Albert, F.W., Alföldi, J., Martinez Barrio, A., Pielberg, G., Rafati, N., Sayyab, S., Turner-Maier, J., Younis, S., Afonso, S., Aken, B., Alves, J.M., Barrell, D., Bolet, G., Boucher, S., Burbano, H.A., Campos, R., Chang, J.L., Duranthon, V., Fontanesi, L., Garreau, H., Heiman, D., Johnson, J., Mage, R.G., Peng, Z., Queney, G., Rogel-Gaillard, C., Ruffier, M., Searle, S., Villafuerte, R., Xiong, A., Young, S., Forsberg-Nilsson, K., Good, J.M., Lander, E.S., Ferrand, N., Lindblad-Toh, K. & Andersson, L. (2014). Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. Science, 345(6200), 1074–1079.

Carpenter, M.H. & Harpur, B.A. (2021). Genetic past, present, and future of the honey bee (Apis mellifera) in the United States of America. *Apidologie* 52: 63–79.

Chacón, M.I., Pickersgill, B. & Debouck, D.G. (2005). Domestication patterns in common bean (*Phaseolus vulgaris* L.) and the origin of the Mesoamerican and Andean cultivated races. *Theoretical and Applied Genetics* 110:432–444.

Chacón-Sánchez, M.I. & Martínez-Castillo, J. (2017). Testing domestication scenarios of lima bean (*Phaseolus lunatus* L.) in Mesoamerica: insights from genome-wide genetic markers. *Frontiers in Plant Science* 8:1551.

Chai, Z.-X., Xin, J.-W., Zhang, C.-F., Dawayangla, Luosang, Zhang, Q., Pingcuozhandui, Li, C., Zhu, Y., Cao, H.-W., Wang, H., Han, J.-L., Ji, Q.-M. & Zhong, J.-C. (2020). Whole-genome resequencing provides insights into the evolution and divergence of the native domestic yaks of the Qinghai–Tibet Plateau. BMC Evolutionary Biology 20, 137.

Chen, S., Lin, B.-Z., Baig, M. et al. (2010). Zebu cattle are an exclusive legacy of the South Asia Neolithic. Molecular Biology and Evolution 27:1–6.

Chalhoub, B. et al. (2014). Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. Science 345(6199), 950–953.

Chen, D. et al. (2020). The evolutionary origin and domestication history of goldfish (Carassius auratus). Proceedings of the National Academy of Sciences 117(47): 29775–29785.

Chen, D.-B., Zhang, R.-S., Bian, H.-X., Li, Q., Xia, R.-X., Li, Y.-P., Liu, Y.-Q. & Lu, C. (2019). Comparative mitochondrial genomes provide new insights into the true wild progenitor and origin of domestic silkworm Bombyx mori. International Journal of Biological Macromolecules, 131, 176–183.

Chen, N., Zhang, Z., Hou, J., Chen, J., Gao, X., Tang, L., Wangdue, S., Zhang, X., Sinding, M.-H.S., Liu, X., Han, J., Lü, H., Lei, C.,

Marshall, F. & Liu, X. (2023). Evidence for early domestic yak, taurine cattle, and their hybrids on the Tibetan Plateau. Science Advances 9(50), eadi6857.

Chen, C.-J., Pang, X.-X., Ding, Y.-M., Zhang, W.-P., Yang, Y., Liu, J., Nersesyan, A., Zhang, B.-W., Renner, S.S., Zhang, D.-Y. & Bai, W.-N. (2026). Resolving sampling and population-size biases in domestication genomics supports a South Asian origin of walnuts. Genome Biology 27: 61.

Chiou, K.L., Lira-Noriega, A. et al. (2024). Interdisciplinary insights into the cultural and chronological context of chili pepper (Capsicum annuum var. annuum L.) domestication in Mexico. Proceedings of the National Academy of Sciences, 121(47), e2413764121.

Chomicki, G. & Renner, S.S. (2015). Watermelon origin solved with molecular phylogenetics including Linnaean material: another example of museomics. New Phytologist, 205(2), 526–532.

Chomicki, G., Schaefer, H. & Renner, S.S. (2020). Origin and domestication of Cucurbitaceae crops: insights from phylogenies, genomics and archaeology. New Phytologist, 226(5), 1240–1255.

Chung, J. et al. (2014). Population genetic analysis of the domestication genes of wild soybean using targeted resequencing.

Civán, P., Craig, H., Cox, C.J. & Brown, T.A. (2015). Three geographically separate domestications of Asian rice. *Nature Plants* 1:15164.

Clark, J.D. & Stemler, A. (1975). Early domesticated sorghum from Central Sudan. Nature 254: 588–591.

Clouse, J.W., Adhikary, D., Page, J.T., Ramaraj, T., Deyholos, M.K., Udall, J.A., Fairbanks, D.J., Jellen, E.N. & Maughan, P.J. (2016). The Amaranth Genome: Genome, Transcriptome, and Physical Map Assembly. The Plant Genome 9(1): 1–14.

Colli, L., Milanesi, M., Vajana, E. et al. (2018). New insights on water buffalo genomic diversity and post-domestication migration routes from medium density SNP chip data. Frontiers in Genetics 9:53.

Cornejo, O.E. et al. (2018). Population genomic analyses of the chocolate tree, *Theobroma cacao* L., provide insights into its domestication process. *Communications Biology* 1: 167.

Cornille, A. et al. (2012). New insight into the history of domesticated apple: secondary contribution of the European wild apple to the genome of cultivated varieties. *PLoS Genetics* 8: e1002703.

Coulibaly, S., Pasquet, R.S., Papa, R. & Gepts, P. (2002). AFLP analysis of the phenetic organization and genetic diversity of Vigna unguiculata L. Walp. reveals extensive gene flow between wild and domesticated types. Theoretical and Applied Genetics 104(2–3), 358–366.

Cowan, C.W. (1978). The prehistoric use and distribution of maygrass in eastern North America: cultural and phytogeographical implications. In *The Nature and Status of Ethnobotany*, ed. R.I. Ford, pp. 263–288. Anthropological Papers No. 67, Museum of Anthropology, University of Michigan.

Crockford, S.J. & Kuzmin, Y.V. (2012). Comments on Germonpré et al., Journal of Archaeological Science 36, 2009 "Fossil dogs and wolves from Palaeolithic sites in Belgium, the Ukraine and Russia: osteometry, ancient DNA and stable isotopes." *Journal of Archaeological Science* 39:2797–2801.

Cubry, P., Tranchant-Dubreuil, C., Thuillet, A.-C. et al. (2018). The rise and fall of African rice cultivation revealed by analysis of 246 new genomes. Current Biology 28:2274-2282 — cited in this cycle at §4.7.1–§4.7.2 for the Inland Niger Delta/Jenne-Jeno anchor.

Dai, F., Nevo, E., Wu, D., Comadran, J., Zhou, M., Qiu, L., Chen, Z., Beiles, A., Chen, G. & Zhang, G. (2012). Tibet is one of the centers of domestication of cultivated barley. PNAS 109(42):16969–16973.

D'Andrea, A.C., Kahlheber, S., Logan, A.L. & Watson, D.J. (2007). Early domesticated cowpea (Vigna unguiculata) from Central Ghana. Antiquity 81(313), 686–698.

Daly, K.G., Maisano Delser, P., Mullin, V.E. et al. (2018). Ancient goat genomes reveal mosaic domestication in the Fertile Crescent. *Science* 361(6397):85–88.

Daly, K.G., Mattiangeli, V., Hare, A.J. et al. (2021). Herded and hunted goat genomes from the dawn of domestication in the Zagros Mountains. *PNAS* 118(25):e2100901118.

Daly, K.G., Mullin, V.E., Hare, A.J. et al. (2025). Ancient genomics and the origin, dispersal, and development of domestic sheep. *Science* 387(6733):492–497.

Darwin, C. (1883). The Variation of Animals and Plants under Domestication (2nd ed.). London: John Murray.

De Martino, M. et al. (2025). The dispersal of domestic cats from North Africa to Europe around 2000 years ago. *Science* 390(6776).

de Groene, D., Bendrey, R., Müldner, G., Coogan, A. & Matthews, R. (2023). Sheep and goat management in the Early Neolithic in the Zagros region (8000–5000 BC): New zooarchaeological and isotopic evidence from Ganj Dareh, Bestansur and Jarmo. *Journal of Archaeological Science: Reports* 49:103936.

Decker, J.E., Taylor, J.F. et al. (2014). Worldwide patterns of ancestry, divergence, and admixture in domesticated cattle. PLoS Genetics 10:e1004254.

Decroocq, S., Cornille, A., Dlalah, N., Duval, H., Tricon, D., Quilot, B., Khalid, W.K., Chague, A., Eduardo, I., Batlle, I., Drogoudi, P., Küden, A., Asma, B.M., Kostritsyna, T. & Decroocq, V. (2025).

Insights Into the Almond Domestication History. Evolutionary Applications 18(9), e70150.

Denham, T.P., Haberle, S.G., Lentfer, C. et al. (2003). Origins of Agriculture at Kuk Swamp in the Highlands of New Guinea. Science 301: 189–193.

Diamond, J. (2002). Evolution, consequences and future of plant and animal domestication. Nature 418, 700–707.

Díaz-Maroto, P., Rey-Iglesia, A., Cartajena, I., Núñez, L., Westbury, M.V., Varas, V., Moraga, M., Campos, P.F., Orozco-terWengel, P., Marín, J.C. & Hansen, A.J. (2021). Ancient DNA reveals the lost domestication history of South American camelids in Northern Chile and across the Andes. *eLife* 10: e63390.

Diez, C.M. et al. (2015). Olive domestication and diversification in the Mediterranean Basin, genome-wide re-analysis reviewed alongside Besnard et al. (2013). *New Phytologist* 206: 436-447.

Ding, Z.L., Oskarsson, M., Ardalan, A., Angleby, H., Dahlgren, L.G., Tepeli, C., Kirkness, E., Savolainen, P. & Zhang, Y.P. (2012). Origins of domestic dog in Southern East Asia is supported by analysis of Y-chromosome DNA. *Heredity* 108:507–514.

Ding, Y.M., Cao, Y., Zhang, W.P., Chen, J., Liu, J., Li, P. et al. (2022). Population-genomic analyses reveal bottlenecks and asymmetric introgression from Persian into iron walnut during domestication. Genome Biology 23: 145.

Ahmed, I., Lockhart, P.J., Agoo, E.M.G., Naing, K.W., Nguyen, D.V., Medhi, D.K. & Matthews, P.J. (2020). Evolutionary origins of taro (Colocasia esculenta) in Southeast Asia. Ecology and Evolution 10(24), 13530–13543.

de Candolle, A. (1885). Origin of Cultivated Plants. New York: D. Appleton and Company.

Dong, Y., Duan, S., Xia, Q. et al. (2023). Dual domestications and origin of traits in grapevine evolution. *Science* 379:892–901.

Drake, A.G., Coquerelle, M. & Colombeau, G. (2015). 3D morphometric analysis of fossil canid skulls contradicts the suggested domestication of dogs during the late Paleolithic. *Scientific Reports* 5:8299.

Dramé, D., Bodian, A., Nguepjop, J.R., Tossim, H.-A., Sambakhe, D., Seye, M., Djiboune, Y.R., Badji, R., Rami, J.-F., Diouf, D. & Fonceka, D. (2026). Genetic architecture of cowpea domestication: QTL mapping and comparison shed new light on the dual domestication events. G3: Genes|Genomes|Genetics 16(1), jkaf248.

Driscoll, C.A., Menotti-Raymond, M., Roca, A.L., Hupe, K., Johnson, W.E., Geffen, E., Harley, E.H., Delibes, M., Pontier, D., Kitchener, A.C., Yamaguchi, N., O'Brien, S.J. & Macdonald, D.W. (2007). The Near Eastern Origin of Cat Domestication. *Science* 317(5837): 519–523.

Duan, S.-F., Han, P.-J., Wang, Q.-M., Liu, W.-Q., Shi, J.-Y., Li, K., Zhang, X.-L. & Bai, F.-Y. (2018). The origin and adaptive evolution of domesticated populations of yeast from Far East Asia. Nature Communications 9: 2690.

Eda, M. (2021). Origin of the domestic chicken from modern biological and zooarchaeological approaches. *Animal Frontiers* 11(3):52–58.

Eda, M., Itahashi, Y., Kikuchi, H., Sun, G., Hsu, K.H., Gakuhari, T. et al. (2022). Multiple lines of evidence of early goose domestication in a 7,000-y-old rice cultivation village in the lower Yangtze River, China. Proceedings of the National Academy of Sciences, 119(12), e2117064119.

Endl, J., Achigan-Dako, E.G., Pandey, A.K., Monforte, A.J., Pico, B. & Schaefer, H. (2018). Repeated domestication of melon (Cucumis

melo) in Africa and Asia and a new close relative from India. American Journal of Botany 105: 1662–1671.

Erickson, D.L., Smith, B.D., Clarke, A.C., Sandweiss, D.H. & Tuross, N. (2005). An Asian origin for a 10,000-year-old domesticated plant in the Americas. Proceedings of the National Academy of Sciences 102(51): 18315–18320.

Fan, R. et al. (2020). Genomic analysis of the domestication and post-Spanish conquest evolution of the llama and alpaca. *Genome Biology* 21: 159.

Fawcett, J.A., Takeshima, R., Kikuchi, S., Yazaki, E., Katsube-Tanaka, T., Dong, Y., Li, M., Hunt, H.V., Jones, M.K., Lister, D.L., Ohsako, T., Ogiso-Tanaka, E., Fujii, K., Hara, T., Matsui, K., Mizuno, N., Nishimura, K., Nakazaki, T., Saito, H., Takeuchi, N., Ueno, M., Matsumoto, D., Norizuki, M., Shirasawa, K., Li, C., Hirakawa, H., Ota, T. & Yasui, Y. (2023). Genome sequencing reveals the genetic architecture of heterostyly and domestication history of common buckwheat. Nature Plants 9(8): 1236–1251.

Fenwick, G.R., Hanley, A.B. & Whitaker, J.R. (1985). The genus Allium—Part 1. Critical Reviews in Food Science and Nutrition, 22(3), 199–271.

Fernando, P., Pfrender, M.E., Encalada, S.E. & Lande, R. (2000). Mitochondrial DNA variation, phylogeography and population structure of the Asian elephant. Heredity 84, 362–372.

Fiscus, C.J., Herniter, I.A., Tchamba, M., Paliwal, R., Muñoz-Amatriáin, M., Roberts, P.A., Abberton, M., Alaba, O., Close, T.J., Oyatomi, O. & Koenig, D. (2024). The pattern of genetic variability in a core collection of 2,021 cowpea accessions. G3: Genes|Genomes|Genetics 14(6), jkae071.

Marsh, W.A., Scarsbrook, L., Yüncü, E. et al. (2026). Dogs were widely distributed across western Eurasia during the Palaeolithic. Nature 651:995–1003.

Frantz, L.A.F., Mullin, V.E., Pionnier-Capitan, M., Lebrasseur, O., Ollivier, M., Perri, A., Linderholm, A., Mattiangeli, V., Teasdale, M.D., Dimopoulos, E.A., Tresset, A., Duffraisse, M., McCormick, F., Bartosiewicz, L., Gál, E., Nyerges, É.A., Sablin, M.V., Bréhard, S., Mashkour, M., Bălășescu, A., Gillet, B., Hughes, S., Chassaing, O., Hitte, C., Vigne, J.-D., Dobney, K., Hänni, C., Bradley, D.G. & Larson, G. (2016). Genomic and archaeological evidence suggest a dual origin of domestic dogs. *Science* 352:1228–1231.

Fritz, G.J. (2014). Maygrass (*Phalaris caroliniana* Walt.). In *New Lives for Ancient and Extinct Crops*, ed. P.E. Minnis, pp. 12–43. University of Arizona Press.

Fu, Y.-B., Peterson, G., Diederichsen, A. & Richards, K.W. (2002). RAPD analysis of genetic relationships of seven flax species in the genus Linum L. Genetic Resources and Crop Evolution, 49, 253–259.

Fu, Y.-B. & Allaby, R.G. (2010). Phylogenetic network of Linum species as revealed by non-coding chloroplast DNA sequences. Genetic Resources and Crop Evolution, 57, 667–677.

Fu, Y.-B., Diederichsen, A. & Allaby, R.G. (2012). Locus-specific view of flax domestication history. Ecology and Evolution, 2(1), 139–152.

Fu, Y.-B. (2023). Pale flax (Linum bienne): an underexplored flax wild relative. In The Flax Genome, Compendium of Plant Genomes (eds. F.M. You & B. Fofana), pp. 37–53. Springer Cham.

Fu, Y.-B. (2025). Flax domestication processes as inferred from genome-wide SNP data. Scientific Reports, 15, 8731.

Fullagar, R., Field, J., Denham, T. & Lentfer, C. (2006). Early and mid Holocene tool-use and processing of taro (Colocasia esculenta) and yam (Dioscorea sp.) and other plants at Kuk Swamp in the Highlands of Papua New Guinea. Journal of Archaeological Science, 33, 595–614.

Fullagar, R., Field, J., Denham, T. & Lentfer, C. (2006). Early and mid Holocene tool-use and processing of taro (Colocasia esculenta), yam (Dioscorea sp.) and other plants at Kuk Swamp in the highlands of Papua New Guinea. Journal of Archaeological Science 33(5), 595–614.

Fuller, D.Q. (2006). Agricultural origins and frontiers in South Asia: a working synthesis. Journal of World Prehistory 20:1–86.

Fuller, D.Q., Qin, L., Zheng, Y., Zhao, Z., Chen, X., Hosoya, L.A. & Sun, G.-P. (2009). The domestication process and domestication rate in rice: spikelet bases from the Lower Yangtze. *Science* 323:1607–1610.

Fuller, D.Q. & Stevens, C.J. (2018). Sorghum domestication and diversification: a current archaeobotanical perspective. In Mercuri, D'Andrea, Fornaciari & Hoelzmann (eds.), Plants and People in the African Past.

Fumihito, A., Miyake, T., Sumi, S., Takada, M., Ohno, S. & Kondo, N. (1994). One subspecies of the red junglefowl (*Gallus gallus gallus*) suffices as the matriarchic ancestor of all domestic breeds. *PNAS* 91:12505–12509.

Galeta, P., Lázničková-Galetová, M., Sablin, M. & Germonpré, M. (2021). Morphological evidence for early dog domestication in the European Pleistocene: New evidence from a randomization approach to group differences. *The Anatomical Record* 304:42–62.

Gallone, B., Steensels, J., Prahl, T., Soriaga, L., Saels, V., Herrera-Malaver, B., Merlevede, A., Roncoroni, M., Voordeckers, K.,

Miraglia, L. et al. (2016). Domestication and Divergence of Saccharomyces cerevisiae Beer Yeasts. Cell 166(6): 1397–1410.

Gangwar, M., Ahmad, S.F., Ali, A.B., Kumar, A., Kumar, A., Gaur, G.K. et al. (2024). Identifying low-density, ancestry-informative SNP markers through whole genome resequencing in Indian, Chinese, and wild yak. BMC Genomics 25, 1043.

Gao, M., Soriano, S.F., Cao, Q., Yang, X. & Lu, G. (2020). Hexaploid sweetpotato (Ipomoea batatas (L.) Lam.) may not be a true type to either auto- or allopolyploid. PLoS ONE, 15(3), e0229624.

Garsmeur, O., Rio, S., Pompidor, N., Lipzen, A., Hervouet, C., Durand, T., Daum, C., Yoshinaga, Y., Butterfield, M., Sanchez, A., Piperidis, G., Lincoln, N., Hale, A., Hoarau, J.Y., Terajima, Y., Lakshmanan, P., Sacks, E., Sharma, S., Vitrac, M., Barry, K., Schmutz, J. & D'Hont, A. (2025). The genomic footprints of wild Saccharum species trace domestication, diversification, and modern breeding of sugarcane. Cell.

Gaunitz, C., Fages, A., Hanghøj, K. et al. (2018). Ancient genomes revisit the ancestry of domestic and Przewalski's horses. Science 360(6384):111–114.

Gebremichael, H. et al. (2025). Genetic diversity and population structure analysis of Pisum sativum var. abyssinicum genotypes from Northern Ethiopia using ISSR markers. Agrosystems, Geosciences & Environment, 8(1), e70151.

Germer, R. (1989). Die Pflanzenmaterialien aus dem Grab des Tutanchamun. In A. Eggebrecht & B. Schmitz (Eds.), Hildesheimer Ägyptologische Beiträge, 28th ed., pp. 1–94. Hildesheim: Pelizaeus-Museum.

Germonpré, M., Sablin, M.V., Stevens, R.E., Hedges, R.E.M., Hofreiter, M., Stiller, M. & Després, V.R. (2009). Fossil dogs and wolves from Palaeolithic sites in Belgium, the Ukraine and Russia:

osteometry, ancient DNA and stable isotopes. *Journal of Archaeological Science* 36:473–490.

Germonpré, M., Láznička-Galetová, M. & Sablin, M.V. (2012). Palaeolithic dog skulls at the Gravettian Předmostí site, the Czech Republic. *Journal of Archaeological Science* 39:184–202.

Gibbons, J.G. et al. (2012). The evolutionary imprint of domestication on genome variation and function of the filamentous fungus *Aspergillus oryzae*. *PNAS* 109: 11515-11520.

Gonçalves-Dias, J., Singh, A., Graf, C. & Stetter, M.G. (2023). Genetic incompatibilities and evolutionary rescue by wild relatives shaped grain amaranth domestication. Molecular Biology and Evolution 40(8): msad177.

Gonzalez-Ibeas, D. et al. (2021). Shaping the biology of citrus: I. Genomic determinants of evolution. The Plant Genome, 14(3), e20104.

Grassi, F., Labra, M., Imazio, S., Spada, A., Sgorbati, S., Scienza, A. & Sala, F. (2003). Evidence of a secondary grapevine domestication centre detected by SSR analysis. Theoretical and Applied Genetics 107:1315-1320 — cited in this cycle at §10.2.2 for the proposed, and since reinterpreted, Sardinian claim.

Gros-Balthazard, M. et al. (2017). The discovery of wild date palms in Oman reveals a complex domestication history involving centers in the Middle East and Africa. *Current Biology* 27: 2211-2218.

Hammons, R.O. (1994). The origin and history of the groundnut. In: Smartt, J. (ed.), The Groundnut Crop: A Scientific Basis for Improvement, Chapman & Hall, London; cited in the Arachis duranensis overview consulted at §80.4.

Hampton, R., Nickerson, G., Whitney, P. & Haunold, A. (2001). Hop stability and diversity in wild populations. Journal of the American Society of Brewing Chemists 59(3), 97–102.

Han, F., Wallberg, A. & Webster, M.T. (2012). From where did the Western honeybee (Apis mellifera) originate? *Ecology and Evolution* 2(8): 1949–1957.

Harding, E.A., Fernie, A.R. et al. (2026). Domestication and genome evolution in Allium crops: from hybrid origins to breeding perspectives. Plant Communications 7(5), 101877.

Hazzouri, K.M. et al. (2015). Whole genome re-sequencing of date palms yields insights into diversification of a fruit tree crop. *Nature Communications* 6: 8824.

He, K., Yu, X., Shen, C. & Lu, H. (2022). Coupled and decoupled legumes and cereals in prehistoric northern and southern China. Frontiers in Plant Science, 13:1013480.

Heikkinen, M.E., Ruokonen, M., White, T.A., Alexander, M.M., Gunduz, I., Dobney, K.M. et al. (2020). Long-term reciprocal gene flow in wild and domestic geese reveals complex domestication history. G3, 10(9), 3061–3070.

Dorji, T., Mannen, H., Namikawa, T., Inamura, T. & Kawamoto, Y. (2010). Diversity and phylogeny of mitochondrial DNA isolated from mithun Bos frontalis located in Bhutan. Animal Genetics 41: 554–556.

Heiser, C.B. (2008). [Re-examination and reclassification of the San Andrés, Tabasco achene as *Lagenaria siceraria* rather than sunflower]; cited via Smith (2006) and Blackman et al. (2011).

Hellwig, T., Abbo, S. & Ophir, R. (2022). Phylogeny and disparate selection signatures suggest two genetically independent domestication events in pea (Pisum L.). The Plant Journal, 110, 419–439.

Helmer, D., Gourichon, L. & Stordeur, D. (2004). À l'aube de la domestication animale. Anthropozoologica 39(1):143–163 — Near East cattle domestication chronology cited in §13.3.

Her, C., Rezaei, H.-R., Hughes, S., Naderi, S., Duffraisse, M., Mashkour, M. et al. (2022). Broad maternal geographic origin of domestic sheep in Anatolia and the Zagros. *Animal Genetics* 53:452–459.

Hernández-Alonso, G., Ramos-Madrigal, J., van Grouw, H., Ciucani, M.M., Cavill, E.L., Sinding, M.-H.S., Gopalakrishnan, S., Pacheco, G. & Gilbert, M.T.P. (2023). Redefining the evolutionary history of the Rock Dove, Columba livia, using whole genome sequences. Molecular Biology and Evolution 40(11), msad243.

Heun, M. et al. (1997). Site of einkorn wheat domestication identified by DNA fingerprinting. *Science* 278:1312–1314.

Hillman, G. (1975). The plant remains from Tell Abu Hureyra: a preliminary report. Proceedings of the Prehistoric Society, 41, 70–73.

Hillman, G.C. (1978). On the origins of domestic rye—Secale cereale: the finds from Aceramic Can Hasan III in Turkey. Anatolian Studies 28, 157–174.

Hongo, H., Pearson, J., Öksüz, B. & Ilgezdi, G. (2009). The process of ungulate domestication at Çayönü, southeastern Turkey: a multidisciplinary approach focusing on Bos sp. and Cervus elaphus. Anthropozoologica 44(1):63–78 — cited via Arbuckle & Kassebaum (2021) in §13.3.

Hou, S. et al. (2022). Whole-genome sequencing reveals the artificial selection and local environmental adaptability of pigeons (Columba livia). Evolutionary Applications 15(9), 1355–1369.

Huang, X. et al. (2012). A map of rice genome variation reveals the origin of cultivated rice. *Nature* 490:497–501.

Hunt, H.V., Rudzinski, A., Jones, M.K. et al. Genetic evidence for a western Chinese origin of broomcorn millet (Panicum miliaceum).

Hunt, H.V., Shang, X. & Jones, M.K. (2018). Buckwheat: a crop from outside the major Chinese domestication centres? A review of the archaeobotanical, palynological and genetic evidence. Vegetation History and Archaeobotany 27(3): 493–506.

Hunter, A.A. (1992). [Morphometric analysis of archaeological little barley, *Hordeum pusillum*, from eastern North American sites]; cited via Mueller (2017c), this cycle's §7.1.2.

Huynh, B.L., Close, T.J., Roberts, P.A., Hu, Z., Wanamaker, S., Lucas, M.R., Chiulele, R., Cissé, N., David, A., Hearne, S., Fatokun, C., Diop, N.N. & Ehlers, J.D. (2013). Gene pools and the genetic architecture of domesticated cowpea. The Plant Genome 6(3), 1–8.

[IMA Fungus, 2025]. Global population-genomic survey of *Aspergillus oryzae* reporting potential evidence for multiple independent domestication events from wild *A. flavus* [author attribution not fully resolved from the abstract/results reviewed for this chapter; cited here by venue and year rather than invented].

Ioannidis, A.G., Blanco-Portillo, J., Sandoval, K., Hagelberg, E., Miquel-Poblete, J.F., Moreno-Mayar, J.V., Rodríguez-Rodríguez, J.E., Quinto-Cortés, C.D., Auckland, K., Parks, T., Robson, K., Hill, A.V.S., Avila-Arcos, M.C., Sockell, A., Homburger, J.R., Wojcik, G.L., Barnes, K.C., Herrera, L., Berríos, S., Acuña, M., Llop, E., Eng, C., Huntsman, S., Burchard, E.G., Gignoux, C.R., Cifuentes, L., Verdugo, R.A., Moraga, M., Mentzer, A.J., Bustamante, C.D. & Moreno-Estrada, A. (2020). Native American gene flow into Polynesia predating Easter Island settlement. Nature, 583(7817), 572–577.

Irving-Pease, E.K., Frantz, L.A.F., Sykes, N., Callou, C. & Larson, G. (2018). Rabbits and the Specious Origins of Domestication. Trends in Ecology & Evolution, 33(3), 149–152.

Janssens, L., Perri, A., Crombé, P., Van Dongen, S. & Lawler, D. (2019). An evaluation of classical morphologic and morphometric

parameters reported to distinguish wolves and dogs. *Journal of Archaeological Science: Reports* 23:501–533.

Jarvis, D.E., Ho, Y.S., Lightfoot, D.J., Schmöckel, S.M., Li, B., Borm, T.J.A., Ohyanagi, H., Mineta, K., Michell, C.T., Saber, N., Kharbatia, N.M., Rupper, R.R., Sharp, A.R., Dally, N., Boughton, B.A., Woo, Y.H., Gao, G., Schijlen, E.G.W.M., Guo, X., Momin, A.A., Negrão, S., Al-Babili, S., Gehring, C., Roessner, U., Jung, C., Murphy, K., Arold, S.T., Gojobori, T., van der Linden, C.G., van Loo, E.N., Jellen, E.N., Maughan, P.J. & Tester, M. (2017). The genome of Chenopodium quinoa. Nature, 542, 307–312.

Jayakodi, M. et al. (2023). The giant diploid faba genome unlocks variation in a global protein crop. Nature (published online 8 March 2023).

Ji, R., Cui, P., Ding, F., Geng, J. & Meng, H. (2009). Monophyletic origin of domestic bactrian camel (*Camelus bactrianus*) and its evolutionary relationship with the extant wild camel (*Camelus bactrianus ferus*). *Animal Genetics* 40(4):377–382.

Jing, Zhang, Wang et al. (2023). [Large-scale resequencing study of rice domestication, 1,578 genomes]. *Nature Plants* 9:1221–1235.

Johannessen, S. (1981). [Report of a single instance of increased maygrass caryopsis size in an ENA archaeobotanical assemblage]; cited via the standard paleoethnobotanical laboratory guide to eastern North American plant remains, this cycle's §7.1.2.

Johnston, R.F. (1992). Evolution in the Rock Dove: skeletal morphology. The Auk 109(3), 530–542.

Johnston, R.F. & Janiga, M. (1995). Feral Pigeons. Oxford University Press.

Kadwell, M., Fernandez, M., Stanley, H.F., Baldi, R., Wheeler, J.C., Rosadio, R. & Bruford, M.W. (2001). Genetic analysis reveals the

wild ancestors of the llama and the alpaca. *Proceedings of the Royal Society B* 268(1485): 2575–2584.

Kamalakkannan, R., Arjun, M.S., Bhavana, K., Prabhu, V.R. & Nagarajan, M. (2020). The complete mitochondrial genome of Indian gaur, Bos gaurus and its phylogenetic implications. Scientific Reports 10: 11936.

Kamenetsky, R., Shafir, I.L., Baizerman, M., Khassanov, F., Kik, C. & Rabinowitch, H.D. (2004). Garlic (Allium sativum L.) and its wild relatives from Central Asia: evaluation for fertility potential. Acta Horticulturae 637, 65–73.

Kanginakudru, S., Metta, M., Jakati, R. D. & Nagaraju, J. (2008). Genetic evidence from Indian red jungle fowl corroborates multiple domestication of modern day chicken. BMC Evolutionary Biology 8: 174.

Kanginakudru, S., Metta, M., Jakati, R.D. & Nagaraju, J. (2008). Genetic evidence from Indian red jungle fowl corroborates multiple domestication of modern day chicken. *BMC Evolutionary Biology* 8:174.

Kaplan, L. & Lynch, T.F. (1999). Phaseolus (Fabaceae) in archaeology: AMS radiocarbon dates and their significance for pre-Columbian agriculture. *Economic Botany* 53:261–272.

Kates, H.R., Soltis, P.S. & Soltis, D.E. (2017). Evolutionary and domestication history of Cucurbita (pumpkin and squash) species inferred from 44 nuclear loci. Molecular Phylogenetics and Evolution, 111, 98–109.

Kawase, M. & Sakamoto, S. Origins and geographic differentiation of foxtail millet (as reviewed in later syntheses of foxtail millet crop evolution).

Kayang, B.B., Youssao, I., Inoue, E., Naazie, A., Abe, H., Ito, S. & Inoue-Murayama, M. (2010). Genetic diversity of Helmeted

Guineafowl (Numida meleagris) based on microsatellite analysis. Journal of Poultry Science, 47, 120–124.

Khadari, B., Kakenov, S., Achtak, H., Charafi, J., Chalak, L., Santoni, S., Kjellberg, F. & Cornille, A. (2025/2026). Diffuse and regionally structured domestication of the common fig (Ficus carica L.) in the Mediterranean Basin. Posted to bioRxiv September 2025; published in Horticulture Research, 2026, uhag113.

Kharzinova, V.R., Dotsev, A.V., Deniskova, T.E., Solovieva, A.D., Fedorov, V.I., Layshev, K.A., Romanenko, T.M., Okhlopkov, I.M., Wimmers, K., Reyer, H., Brem, G. & Zinovieva, N.A. (2018). Genetic diversity and population structure of domestic and wild reindeer (Rangifer tarandus L. 1758): A novel approach using BovineHD BeadChip. PLOS ONE, 13(11), e0207944.

Kilian, B. et al. (2007). [Independent resequencing/SNP confirmation of einkorn's Karacadağ origin, complementing Heun et al. 1997].

Kimber, C.T. (2000). Origins of domesticated sorghum and its early diffusion to India and China. In Smith, C.W. & Frederiksen, R.A. (eds.), Sorghum: Origin, History, Technology, and Production.

Kimura, B., Marshall, F.B., Chen, S. et al. (2011). Ancient DNA from Nubian and Somali wild ass provides insights into donkey ancestry and domestication. Proceedings of the Royal Society B 278:50-57 — cited in this cycle at §23.3.1 for confirming the Nubian wild ass as ancestor of Clade I and excluding the Somali wild ass as Clade II's source.

Kinder, D.H., Adams, K.R. & Wilson, H.J. (2017). Solanum jamesii: Evidence for Cultivation of Wild Potato Tubers by Ancestral Puebloan Groups. Journal of Ethnobiology 37(2): 218–240.

Kislev, M.E. (1985). Early Neolithic horsebean from Yiftah'el, Israel. Science, 228(4698), 319–320.

Kislev, M.E., Hartmann, A. & Bar-Yosef, O. (2006). Early domesticated fig in the Jordan Valley. Science, 312(5778), 1372–1374.

Kislev, M.E., Hartmann, A. & Bar-Yosef, O. (2006). Response to Comment on "Early Domesticated Fig in the Jordan Valley". Science, 314(5806), 1683.

Kistler, L., Montenegro, Á., Smith, B.D., Gifford, J.A., Green, R.E., Newsom, L.A. & Shapiro, B. (2014). Transoceanic drift and the domestication of African bottle gourds in the Americas. Proceedings of the National Academy of Sciences 111(8): 2937–2941.

Kistler, L., Thakar, H.B., VanDerwarker, A.M., Domic, A., Bergström, A., George, R.J. et al. (2018). Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. *Science* 362:1309–1313.

Kitchen, A., Ehret, C., Assefa, S. & Mulligan, C.J. (2009). Bayesian phylogenetic analysis of Semitic languages identifies an Early Bronze Age origin of Semitic in the Near East. *Proceedings of the Royal Society B* 276:2703–2710.

Kraft, K.H., Brown, C.H., Nabhan, G.P., Luedeling, E., de Jesús Luna Ruiz, J., Coppens d'Eeckenbrugge, G., Hijmans, R.J. & Gepts, P. (2014). Multiple lines of evidence for the origin of domesticated chili pepper, Capsicum annuum, in Mexico. Proceedings of the National Academy of Sciences, 111(17), 6165–6170.

Kroonen, G., Jakob, A., Palmér, A.I., van Sluis, P. & Wigman, A. (2022). Indo-European cereal terminology suggests a Northwest Pontic homeland for the core Indo-European languages. *PLOS ONE* 17(10):e0275744.

Kumar, S., Nagarajan, M., Sandhu, J.S., Kumar, N. & Behl, V. (2007). Phylogeography and domestication of Indian river buffalo. BMC Evolutionary Biology 7:186.

Kundu, A., Topdar, N., Sarkar, D., Sinha, M.K., Ghosh, A., Banerjee, S., Das, M., Balyan, H.S., Mahapatra, B.S. & Gupta, P.K. (2013). Origins of white (Corchorus capsularis L.) and dark (C. olitorius L.) jute: a reevaluation based on nuclear and chloroplast microsatellites. Journal of Plant Biochemistry and Biotechnology 22(4): 372–381.

Kyriakidou, M., Achakkagari, S.R., Tai, H.H. et al. (2025). Genomic and pangenomic resources for potato improvement: harnessing diversity from wild relatives. Canadian Journal of Plant Science.

Lado, S., Elbers, J.P., Doskocil, A. et al. (2020). Genome-wide diversity and global migration patterns in dromedaries follow ancient caravan routes. Communications Biology 3:387 — cited in this cycle at §18.3.1 for post-domestication trade-route gene flow and the absence of a domestication-era bottleneck.

Lapham, H.A., Feinman, G.M. & Nicholas, L.M. (2016). Turkey husbandry and use in Oaxaca, Mexico: A contextual study of turkey remains and SEM analysis of eggshell from the Mitla Fortress. Journal of Archaeological Science: Reports 10: 534–546.

Larson, G., Dobney, K., Albarella, U., Fang, M., Matisoo-Smith, E., Robins, J., Lowden, S., Finlayson, H., Brand, T., Willerslev, E., Rowley-Conwy, P., Andersson, L. & Cooper, A. (2005). Worldwide phylogeography of wild boar reveals multiple centers of pig domestication. *Science* 307:1618–1621.

Larson, G. et al. (2007). Ancient DNA, pig domestication, and the spread of the Neolithic into Europe. *PNAS* 104:15276–15281.

Larson, G. et al. (2010). Patterns of East Asian pig domestication, migration, and turnover revealed by modern and ancient DNA. *PNAS* 107:7686–7691.

Le Neün, M., Dufour, E., Goepfert, N., Wheeler, J.C. & Cucchi, T. (2023). Documenting past South American camelid diversity at

Telarmachay (Puna of Junín, Peru) using first phalanges morphometrics. *Revista de Arqueologia* 36(3): 26–37; follow-up study, *Quaternary Science Reviews* (2026), New insights into the domestication process of South American camelids at Telarmachay (Peru) from 9,000 to 4,500 years BP.

Lee, G.-A. et al. (2011). Archaeological soybean (Glycine max) in East Asia: does size matter?

Lema, V.S. (2011). The possible influence of post-harvest objectives on Cucurbita maxima ssp. maxima and ssp. andreana evolution under cultivation at the Argentinean Northwest: an archaeological example. Archaeological and Anthropological Sciences, 3(2), 113–139.

Lentz, D.L. et al. (2001). [Candidate sunflower achene, San Andrés, Tabasco, Mexico, 4,130 BP — later reclassified, see Heiser 2008].

Lentz, D.L. et al. (2008). [Candidate sunflower achenes, Cueva del Gallo, Morelos, Mexico, ~2,600 BP; specimens destroyed during dating, precluding independent confirmation].

Lev-Yadun, S., Gopher, A. & Abbo, S. (2000). The cradle of agriculture. *Science* 288:1602–1603.

Lev-Yadun, S., Ne'eman, G., Abbo, S. & Flaishman, M.A. (2006). Comment on "Early Domesticated Fig in the Jordan Valley". Science, 314(5806), 1683.

Li, G., Luo, J., Wang, F., Xu, D., Ahmed, Z., Chen, S. & Ma, Z. (2023). Whole-genome resequencing reveals genetic diversity, differentiation, and selection signatures of yak breeds/populations in Qinghai, China. Frontiers in Genetics 13, 1034094.

Li, N., Zhang, X., Sun, X., Zhu, S., Cheng, Y., Liu, M., Gao, S. et al. (2022). Genomic insights into the evolutionary history and diversification of bulb traits in garlic. Genome Biology 23, 188.

Li, H.F., Zhu, W.Q., Chen, K.W.H.Y., Xu, W.J. & Song, W. (2011). Two maternal origins of Chinese domestic goose. Poultry Science, 90(12), 2705–2710.

Li, X.-W., Meng, X.-Q., Jia, H.-J., Yu, M.-L., Ma, R.-J., Wang, L.-R., et al. (2013). Peach genetic resources: diversity, population structure and linkage disequilibrium. BMC Genetics, 14(1), 84.

Liber, M., Duarte, I., Maxted, N. & Rubio Teso, M.L. (2021). The history of lentil (*Lens culinaris* subsp. *culinaris*) domestication and spread as revealed by genotyping-by-sequencing of wild and landrace accessions. *Frontiers in Plant Science* 12:628439.

Librado, P., Khan, N., Fages, A. et al. (2021). The origins and spread of domestic horses from the Western Eurasian steppes. Nature 598(7882):634–640.

Lin, T., Zhu, G., Zhang, J. et al. (2014). Genomic analyses provide insights into the history of tomato breeding. Nature Genetics, 46, 1220–1226.

Lin, Z., Zhu, Z., Zhuang, M., Wang, Z., Zhang, Y., Gao, F., Niu, Q. & Ji, T. (2023). Effects of local domestication warrant attention in honey bee population genetics. *Science Advances* 9(18): eade7917.

Liu, Y.-P., Wu, G.-S., Yao, Y.-G., Li, Y., Luo, S.-J., Andersson, L. & Zhang, Y.-P. (2006). Multiple maternal origins of chickens: out of the Asian jungles. *Molecular Phylogenetics and Evolution* 38:12–19.

Liu, F., Zhao, J., Sun, H., Xiong, C., Sun, X., Wang, X., Wang, Z., Jarret, R., Wang, J., Tang, B., Xu, H., Hu, B., Suo, H., Yang, B., Ou, L., Li, X., Zhou, S., Yang, S., Liu, Z., Yuan, F., Pei, Z., Ma, Y., Dai, X., Wu, S., Fei, Z. & Zou, X. (2023). Genomes of cultivated and wild Capsicum species provide insights into pepper domestication and population differentiation. Nature Communications, 14, 5487.

Loftus, R.T., MacHugh, D.E., Bradley, D.G., Sharp, P.M. & Cunningham, P. (1994). Evidence for two independent domestications of cattle. PNAS 91(7):2757–2761.

Lombardo, U., Iriarte, J., Hilbert, L., Ruiz-Pérez, J., Capriles, J.M. & Veit, H. (2020). Early Holocene crop cultivation and landscape modification in Amazonia. Nature 581(7807), 190–193.

Long, J.-R., Qiu, X.-P., Zeng, F.-T., Tang, L.-M. & Zhang, Y.-P. (2003). Origin of rabbit (Oryctolagus cuniculus) in China: evidence from mitochondrial DNA control region sequence analysis. Animal Genetics, 34(2), 82–87.

Lord, E., Collins, C., deFrance, S., LeFebvre, M.J., Pigière, F., Eeckhout, P., Erauw, C., Fitzpatrick, S.M., Healy, P.F., Martínez-Polanco, M.F., Garcia, J.L., Ramos Roca, E., Delgado, M., Sánchez Urriago, A., Peña León, G.A., Toyne, J.M., Dahlstedt, A., Moore, K.M., Laguer Diaz, C., Zori, C. & Matisoo-Smith, E. (2020). Ancient DNA of guinea pigs (Cavia spp.) indicates a probable new center of domestication and pathways of global distribution. Scientific Reports, 10, 8901.

Losey, R.J. et al. (2020). Domestication as Enskilment: Harnessing Reindeer in Arctic Siberia. Journal of Archaeological Method and Theory, published online May 12, 2020.

Lu, H., Zhang, J., Wu, N., Zhu, K.B., Yang, X., Weng, D., Huang, T., Ge, Y., Wang, J. & Chen, Y. (2009). Earliest domestication of common millet (Panicum miliaceum) in East Asia extended to 10,000 years ago. Proceedings of the National Academy of Sciences 106(18): 7367–7372.

Lubinsky, P. et al. (2006). Neotropical roots of a Polynesian spice: the hybrid origin of Tahitian vanilla, *Vanilla tahitensis* (Orchidaceae); native-pollinator question for *V. planifolia* reviewed in the same discussion. *American Journal of Botany* 93: 1198-1210.

Luo, X., Zhou, H., Cao, D., Yan, F., Chen, P., Wang, J., Woeste, K., Chen, X., Fei, Z., An, H., Malvolti, M., Ma, K., Liu, C., Ebrahimi, A., Qiao, C., Ye, H., Li, M., Lu, Z., Xu, J., Cao, S. & Zhao, P. (2022). Domestication and selection footprints in Persian walnuts (Juglans regia). PLOS Genetics 18: e1010513.

Mace, E.S., Tai, S., Gilding, E.K. et al. (2013). Whole-genome sequencing reveals untapped genetic potential in Africa's indigenous cereal crop sorghum. Nature Communications 4: 2320.

Machado, R.S.R., Bonhomme, V., Soteras, R., Jeanty, A., Bouby, L., Evin, A., Fernandes Martins, M.J., Gonçalves, S., Antolín, F., Salavert, A. & Oliveira, H.R. (2025). The origins and spread of the opium poppy (Papaver somniferum L.) revealed by genomics and seed morphometrics. Philosophical Transactions of the Royal Society B 380(1926): 20240198.

Magee, P. (2015). When was the dromedary domesticated in the ancient Near East? *Zeitschrift für Orient-Archäologie* 8:253–278.

Magris, G., Jurman, I., Fornasiero, A., Paparelli, E., Schwope, R., Marroni, F., Di Gaspero, G. & Morgante, M. (2021). The genomes of 204 *Vitis vinifera* accessions reveal the origin of European wine grapes. *Nature Communications* 12:7240.

Manin, A., Corona-M, E., Alexander, M., Craig, A., Thornton, E.K., Yang, D.Y., Richards, M. & Speller, C.F. (2018). Diversity of management strategies in Mesoamerican turkeys: archaeological, isotopic and genetic evidence. Royal Society Open Science 5(1): 171613.

Manning, K., Pelling, R., Higham, T., Schwenniger, J.-L. & Fuller, D.Q. (2011). 4500-year old domesticated pearl millet (Pennisetum glaucum) from the Tilemsi Valley, Mali: new insights into an alternative cereal domestication pathway. Journal of Archaeological Science 38(2): 312–322.

Martin, G., Baurens, F.C., Cenci, A. et al. (2020, and 2023 Interspecific introgression patterns reveal the origins of worldwide cultivated bananas in New Guinea). The Plant Journal.

Mathew, B. (1996). A Review of Allium Section Allium. Kew: Royal Botanic Gardens.

Mathew, L.S. et al. (2015). A genome-wide survey of date palm cultivars supports two major subpopulations in *Phoenix dactylifera*. *G3: Genes, Genomes, Genetics* 5: 1429-1438.

Matsuoka, Y. et al. (2002). A single domestication for maize shown by multilocus microsatellite genotyping. *PNAS* 99:6080–6084.

Maxted, N. & Ambrose, M. (2001). Peas (Pisum L.). In: Plant Genetic Resources of Legumes in the Mediterranean, Kluwer, 181–190.

Mazar, A. & Panitz-Cohen, N. (2007). It Is the Land of Honey: Beekeeping at Tel Rehov. *Near Eastern Archaeology* 70(4): 202–219.

McAlvay, A.C., Ragsdale, A.P., Mabry, M.E., Qi, X., Bird, K.A., Velasco, P., An, H., Pires, J.C. & Emshwiller, E. (2021). Brassica rapa domestication: untangling wild and feral forms and convergence of crop morphotypes. Molecular Biology and Evolution 38(8), 3358–3372.

McGovern, P.E. et al. (1996). Neolithic resinated wine. *Nature* 381:480–481 — cited in this cycle via the Hajji Firuz Tepe tartaric-acid residue evidence (c. 5400–5000 BC).

Meegahakumbura, M.K. et al. (2016). Indications for three independent domestication events for the tea plant (*Camellia sinensis*) and new insights into the origin of tea germplasm in China and India revealed by nuclear microsatellites. *PLoS ONE* 11: e0155369.

Mei, C., Wang, H., Zhu, W., Wang, H., Cheng, G., Qu, K., Guang, X., Li, A., Zhao, C., Yang, W., Wang, C., Xin, Y. & Zan, L. (2016). Whole-genome sequencing of the endangered bovine species Gayal

(Bos frontalis) provides new insights into its genetic features. Scientific Reports 6: 19787.

Mekonnen, D.Z., Gomes, A.I., Machado, R.S.R. & Oliveira, H.R. (2025). The genomics of t'ef and finger millet domestication and spread. Philosophical Transactions of the Royal Society B 380(1926): 20240196.

Mengoni-Goñalons, G.L. & Yacobaccio, H.D. (2006). The domestication of South American camelids: a view from the South-Central Andes. In *Documenting Domestication*, ed. Zeder, Bradley, Emshwiller & Smith.

Meyer, R.S., Karol, K.G., Little, D.P., Nee, M.H. & Litt, A. (2012). Phylogeographic relationships among Asian eggplants and new perspectives on eggplant domestication. Molecular Phylogenetics and Evolution 63(3): 685–701.

Mikić, A. (2012). Origin of the words denoting some of the most ancient Old World pulse crops and their diversity in modern European languages. *PLOS ONE* 7(9):e44512.

Ming, L., Yuan, L., Yi, L. et al. (2020). Whole-genome sequencing of 128 camels across Asia reveals origin and migration of domestic Bactrian camels. *Communications Biology* 3:1.

Mizuno, N., Toyoshima, M., Fujita, M., Fukuda, S., Kobayashi, Y., Ueno, M., Tanaka, K., Tanaka, T., Nishihara, E., Mizukoshi, H., Yasui, Y. & Fujita, Y. (2020). The genotype-dependent phenotypic landscape of quinoa in salt tolerance and key growth traits. DNA Research, 27(4), dsaa022.

Mohandesan, E., Fitak, R.R., Corander, J., Yadamsuren, A., Chuluunbat, B., Abdelhadi, O., Raziq, A., Nagy, P., Stalder, G., Walzer, C., Faye, B. & Burger, P.A. (2017). Mitogenome sequencing in the genus *Camelus* reveals evidence for purifying selection and

long-term divergence between wild and domestic Bactrian camels. *Scientific Reports* 7:9970.

Molina, J. et al. (2011). Molecular evidence for a single evolutionary origin of domesticated rice. *PNAS* 108:8351–8356.

Montagnon, C., Mahyoub, A., Solano, W. & Sheibani, F. (2021). Unveiling a unique genetic diversity of cultivated Coffea arabica L. in its main domestication center: Yemen. Genetic Resources and Crop Evolution, 68, 2411–2422.

Montagnon, C., Sheibani, F., Benti, T., Daniel, D. & Bote, A.D. (2022). Deciphering early movements and domestication of Coffea arabica through a comprehensive genetic diversity study covering Ethiopia and Yemen. Agronomy, 12(12), 3203.

Morrell, P.L. & Clegg, M.T. (2007). Genetic evidence for a second domestication of barley (*Hordeum vulgare*) east of the Fertile Crescent. *PNAS* 104:3289–3294.

Motamayor, J.C. et al. (2008). Geographic and genetic population differentiation of the Amazonian chocolate tree (*Theobroma cacao* L.). *PLoS ONE* 3: e3311.

Motta-Aldana, J.R. et al. (2010). Multiple origins of lima bean landraces in the Americas: evidence from chloroplast and nuclear DNA polymorphisms. *Crop Science* 50:1773–1787.

Moulherat, C., Tengberg, M., Haquet, J.-F. & Mille, B. (2002). First evidence of cotton at Neolithic Mehrgarh, Pakistan: analysis of mineralized fibres from a copper bead. Journal of Archaeological Science 29(12): 1393–1401.

Mueller, N.G. (2017a). Documenting domestication in a lost crop (*Polygonum erectum* L.): evolutionary bet-hedgers under cultivation. *Novon* 25(2):166–179.

Mueller, N.G. (2017b). Evolutionary 'bet-hedgers' under cultivation: investigating the domestication of erect knotweed

(*Polygonum erectum*) using growth experiments. *Journal of Anthropological Archaeology* 49:39–50.

Mueller, N.G. (2017c). Seeds as artifacts of communities: the domestication of erect knotweed in ancient eastern North America. *Human Ecology* 45(2):189–203.

Muñoz-Rodríguez, P., Carruthers, T., Wood, J.R.I., Williams, B.R.M., Weitemier, K., Kronmiller, B., Ellis, D., Anglin, N.L., Longway, L., Harris, S.A., Rausher, M.D., Kelly, S., Liston, A. & Scotland, R.W. (2018). Reconciling conflicting phylogenies in the origin of sweet potato and dispersal to Polynesia. Current Biology, 28(8), 1246–1256.

Muñoz-Rodríguez, P., Wells, T., Wood, J.R.I., Carruthers, T., Anglin, N.L., Jarret, R.L. & Scotland, R.W. (2022). Discovery and characterization of sweetpotato's closest tetraploid relative. New Phytologist, 234(4), 1185–1194.

Murunga, P., Kennedy, G.M., Imboma, T., Malaki, P., Kariuki, D., Ndiema, E., Obanda, V., Agwanda, B., Lichoti, J.K. & Ommeh, S.C. (2018). Mitochondrial DNA D-loop diversity of the helmeted guinea fowls in Kenya and its implications on HSP70 gene functional polymorphism. BioMed Research International, 2018, 7314038.

Naderi, S., Rezaei, H.-R., Taberlet, P., Zundel, S., Rafat, S.-A. et al. (2007). Large-scale mitochondrial DNA analysis of the domestic goat reveals six haplogroups with high diversity. *PLoS ONE* 2(10):e1012.

Naderi, S., Rezaei, H.-R., Pompanon, F., Blum, M.G.B., Negrini, R. et al. (2008). The goat domestication process inferred from large-scale mitochondrial DNA analysis of wild and domestic individuals. *PNAS* 105(46):17659–17664.

Nee, M. (1990). The domestication of Cucurbita (Cucurbitaceae). Economic Botany, 44(3, Supplement), 56–68.

Nevo, E. (2013). [A distinct 2013 Nevo work is co-cited alongside Dai et al. 2012/2014 for the Tibetan-center position in later secondary literature (e.g. PMC4588695); its own full bibliographic form was not independently confirmed and remains an open gap rather than a completed citation].

Ng, N.Q. & Maréchal, R. (1985). Cowpea taxonomy, origin and germplasm, in Singh, S.R. & Rachie, K.O. (eds), Cowpea Research, Production and Utilization, pp. 11–21. New York: Wiley.

Malzew, A.I. (1930). Wild and Cultivated Oats, Section Euavena Griseb. Bulletin of Applied Botany, Genetics and Plant Breeding, Supplement 38 (Leningrad).

Matthews, P.J. (1991). A possible tropical wildtype taro: Colocasia esculenta var. aquatilis. Man and Culture in Oceania 7, 31–55.

Matthews, P.J. & Nguyen, D.V. (2014). Origins and development of taro. In: Smith, C. (ed.), Encyclopedia of Global Archaeology, pp. 419–426. Berlin: Springer.

Miyasaka, S.C. et al. (2019). Genetic Diversity in Taro (Colocasia esculenta). In: Genetic Diversity and Erosion in Plants, pp. 191–215. Cham: Springer.

Olsen, K.M. & Schaal, B.A. (1999). Evidence on the origin of cassava: Phylogeography of Manihot esculenta. Proceedings of the National Academy of Sciences 96(10), 5586–5591.

Olsen, K.M. & Schaal, B.A. (2001). Microsatellite variation in cassava (Manihot esculenta, Euphorbiaceae) and its wild relatives: further evidence for a southern Amazonian origin of domestication. American Journal of Botany 88(1), 131–142.

Osypińska, M., Osypiński, P., Wiktorowicz, P. et al. (2025). Cattle domestication revisited: Middle Nile evidence suggests

independent origins in Africa 10,000 years ago. Journal of Archaeological Science 177:106202.

Ottoni, C. et al. (2017). The palaeogenetics of cat dispersal in the ancient world. *Nature Ecology & Evolution* 1: 0139.

Outram, A.K., Stear, N.A., Bendrey, R. et al. (2009). The earliest horse harnessing and milking. Science 323(5919):1332–1335.

Ovodov, N.D., Crockford, S.J., Kuzmin, Y.V., Higham, T.F.G., Hodgins, G.W.L. & van der Plicht, J. (2011). A 33,000-year-old incipient dog from the Altai Mountains of Siberia: evidence of the earliest domestication disrupted by the Last Glacial Maximum. *PLOS ONE* 6:e22821.

Özkan, H. et al. (2002). AFLP analysis of a collection of tetraploid wheats indicates the origin of emmer and hard wheat domestication in southeast Turkey. *Molecular Biology and Evolution* 19:1797–1801.

Page, A., Gibson, J., Meyer, R.S. & Chapman, M.A. (2019). Eggplant Domestication: Pervasive Gene Flow, Feralization, and Transcriptomic Divergence. Molecular Biology and Evolution 36(7): 1359–1372.

Palombo, N.E., Weiss-Schneeweiss, H. & Carrizo García, C. (2024). Evolutionary relationships, hybridization and diversification under domestication of the locoto chile (Capsicum pubescens) and its wild relatives. Frontiers in Plant Science, 15, 1353991.

Panziera, D., Requier, F., Chantawannakul, P., Pirk, C.W.W. & Blacquière, T. (2022). The Diversity Decline in Wild and Managed Honey Bee Populations Urges for an Integrated Conservation Approach. *Frontiers in Ecology and Evolution* 10: 767950.

Patiranage, D.S.R., Rey, E., Emrani, N., Wellman, G., Schmid, K., Jarvis, D.E., Rey, E. & Maughan, P.J. et al. (2022). Genome-wide

association study in quinoa reveals selection pattern typical for crops with a short breeding history. eLife, 11, e66873.

Pavlik, B.M., del Rio, A., Bamberg, J. & Louderback, L.A. (2024). Evidence for human-caused founder effect in populations of Solanum jamesii at archaeological sites: II. Genetic sequencing establishes ancient transport across the Southwest USA. American Journal of Botany.

Penmetsa, R.V. et al. (2016). Multiple post-domestication origins of kabuli chickpea through allelic variation in a diversification-associated transcription factor. *New Phytologist* — cited in this cycle's Chapter 2 discussion of chickpea diversification (post-domestication, not a second domestication center).

Pérez-Escobar, O.A., Tusso, S., Przelomska, N.A.S., Wu, S., Ryan, P., Nesbitt, M., Silber, M.V., Preick, M., Fei, Z., Hofreiter, M., Chomicki, G. & Renner, S.S. (2022). Genome sequencing of up to 6,000-year-old Citrullus seeds reveals use of a bitter-fleshed species prior to watermelon domestication. Molecular Biology and Evolution, 39(8), msac168.

Prabhu, V.R., Arjun, M.S., Bhavana, K., Kamalakkannan, R. & Nagarajan, M. (2019). Complete mitochondrial genome of Indian mithun, Bos frontalis and its phylogenetic implications. Molecular Biology Reports 46(2): 2561–2566.

Perry, L., Dickau, R., Zarrillo, S., Holst, I., Pearsall, D.M., Piperno, D.R., Berman, M.J., Cooke, R.G., Rademaker, K., Ranere, A.J., Raymond, J.S., Sandweiss, D.H., Scaramelli, F., Tarble, K. & Zeidler, J.A. (2007). Starch fossils and the domestication and dispersal of chili peppers (Capsicum spp. L.) in the Americas. Science, 315, 986–988.

Peter, J. et al. (2018). Genome evolution across 1,011 Saccharomyces cerevisiae isolates. Nature 556(7701): 339–344.

Peters, J. & von den Driesch, A. (1997). The two-humped camel (*Camelus bactrianus*): new light on its distribution, management and medical treatment in the past. *Journal of Zoology* 242:651–679 — cited in-text (§19.4) as volume 243; the published record gives volume 242, disclosed here rather than silently altered in the chapter itself.

Peters, J., Lebrasseur, O., Irving-Pease, E. K., Paxinos, P. D., Best, J., Smallman, R. et al. (2022). The biocultural origins and dispersal of domestic chickens. Proceedings of the National Academy of Sciences USA 119(24): e2121978119.

Peters, J., Lebrasseur, O., Irving-Pease, E.K., Paxinos, P.D., Best, J., Smallman, R. et al. (2022). The biocultural origins and dispersal of domestic chickens. *PNAS* 119(24):e2121978119.

Pickersgill, B. (1969). The archaeological record of chili peppers (Capsicum spp.) and the sequence of plant domestication in Peru. American Antiquity, 34, 54–61.

Pintaud, J.-C. et al. (2010). Species delimitation in the genus *Phoenix* (Arecaceae) based on SSR markers, with emphasis on the identity of the date palm (*P. dactylifera*). *Fruits* 65: 205-214.

Piperno, D.R., Ranere, A.J., Holst, I. & Hansell, P. (2000). Starch grains reveal early root crop horticulture in the Panamanian tropical forest. Nature 407, 894–897.

Piperno, D.R. et al. (2009). [Companion archaeobotanical/starch-grain paper to Ranere et al. 2009, same issue]. *PNAS* 106.

Piperno, D.R., Ranere, A.J., Holst, I., Iriarte, J. & Dickau, R. (2009). Starch grain and phytolith evidence for early ninth millennium B.P. maize from the Central Balsas River Valley, Mexico. Proceedings of the National Academy of Sciences USA, 106(13), 5019–5024.

Pokharel, K., Weldenegodguad, M., Dudeck, S., Honkatukia, M., Lindeberg, H., Mazzullo, N., Paasivaara, A., Peippo, J., Soppela, P., Stammler, F. & Kantanen, J. (2023). Whole-genome sequencing

provides novel insights into the evolutionary history and genetic adaptation of reindeer populations in northern Eurasia. Scientific Reports, 13, 23019.

Pooler, M.R. & Simon, P.W. (1994). Garlic flowering in response to clone, photoperiod, growth temperature and cold storage. HortScience 29(11), 1341–1342.

Portères, R. (1962). Berceaux agricoles primaires sur le continent africain. Journal of African History 3:195-210 — cited in this cycle at §4.7.1 for the original centric hypothesis of O. glaberrima domestication in the inland Niger delta.

Quezada-Martinez, D., Addo Nyarko, C.P., Schiessl, S.V. & Mason, A.S. (2021). Using wild relatives and related species to build climate resilience in Brassica crops. Theoretical and Applied Genetics 134(6), 1711–1728.

Ramos-Madrigal, J., Smith, B.D., Moreno-Mayar, J.V., Gopalakrishnan, S., Ross-Ibarra, J., Gilbert, M.T.P. & Wales, N. (2016). Genome sequence of a 5,310-year-old maize cob provides insights into the early stages of maize domestication. *Current Biology* 26:3195–3201.

Qiu, Q., Wang, L., Wang, K., Yang, Y., Ma, T., Wang, Z., Zhang, X., Ni, Z., Hou, F., Long, R., Abbott, R., Lenstra, J. & Liu, J. (2015). Yak whole-genome resequencing reveals domestication signatures and prehistoric population expansions. Nature Communications 6, 10283.

Ranere, A.J., Piperno, D.R., Holst, I., Dickau, R. & Iriarte, J. (2009). The cultural and chronological context of early Holocene maize and squash domestication in the Central Balsas River Valley, Mexico. *PNAS* 106:5014–5018.

Rangel, J., Traver, B., Stoner, M., Hatter, A., Trevelline, B., Garza, C., Shepherd, T., Seeley, T.D. & Wenzel, J. (2020). Genetic diversity

of wild and managed honey bees (Apis mellifera) in Southwestern Pennsylvania, and prevalence of the microsporidian gut pathogens Nosema ceranae and N. apis. *Apidologie* 51: 802–814.

Raviv, L., Jacobson, S.L., Plotnik, J.M., Bowman, J., Lynch, V. & Benítez-Burraco, A. (2023). Elephants as an animal model for self-domestication. Proceedings of the National Academy of Sciences 120(15), e2208607120.

Razifard, H. et al. (2020). Genomic Evidence for Complex Domestication History of the Cultivated Tomato in Latin America. Molecular Biology and Evolution, 37(4), 1118–1132.

Røed, K.H., Flagstad, Ø., Nieminen, M., Holand, Ø., Dwyer, M.J., Røv, N. & Vilà, C. (2008). Genetic analyses reveal independent domestication origins of Eurasian reindeer. Proceedings of the Royal Society B: Biological Sciences, 275, 1849–1855.

Røed, K.H., Bjørklund, I. & Olsen, B.J. (2018). From wild to domestic reindeer – Genetic evidence of a non-native origin of reindeer pastoralism in northern Fennoscandia. Journal of Archaeological Science: Reports, 19, 279–286.

Røed, K.H., Kvie, K.S., Losey, R.J. et al. (2020). Temporal and structural genetic variation in reindeer (Rangifer tarandus) associated with the pastoral transition in Northwestern Siberia. Ecology and Evolution, published online 2020.

Ren, G. et al. (2021). Large-scale whole-genome resequencing unravels the domestication history of *Cannabis sativa*. *Science Advances* 7: eabg2286.

Renner, S.S., Sousa, A. & Chomicki, G. (2017). Chromosome numbers, Sudanese wild forms, and classification of the watermelon genus Citrullus, with 50 names allocated to seven biological species. Taxon, 66(6), 1393–1405.

Renner, S.S., Pérez-Escobar, O.A., Silber, M.V., Nesbitt, M., Preick, M., Hofreiter, M. & Chomicki, G. (2019). A 3500-year-old leaf from a Pharaonic tomb reveals that New Kingdom Egyptians were cultivating domesticated watermelon. bioRxiv 642785 (preprint).

Renner, S.S., Wu, S., Pérez-Escobar, O.A., Silber, M.V., Fei, Z. & Chomicki, G. (2021). A chromosome-level genome of a Kordofan melon illuminates the origin of domesticated watermelons. Proceedings of the National Academy of Sciences USA, 118(23), e2101486118.

Renny-Byfield, S., Page, J.T., Udall, J.A., Sanders, W.S., Peterson, D.G., Arick, M.A., Grover, C.E. & Wendel, J.F. (2016). Independent Domestication of Two Old World Cotton Species. Genome Biology and Evolution 8(6): 1940–1947.

Rick, C.M. & Holle, M. (1990). Andean Solanum lycopersicum var. cerasiforme: genetic variation and its evolutionary significance. Economic Botany, 44(3 Supplement), 69–78.

Riehl, S., Zeidi, M. & Conard, N.J. (2013). Emergence of agriculture in the foothills of the Zagros Mountains of Iran. Science, 341, 65–67.

Rodríguez, L.C., Méndez, M.A. & Niemeyer, H.M. (2001). Direction of dispersion of cochineal (Dactylopius coccus Costa) within the Americas. Antiquity 75(287): 73–77.

Roffet-Salque, M., Regert, M., Evershed, R.P. et al. (2015). Widespread exploitation of the honeybee by early Neolithic farmers. *Nature* 527: 226–230.

Rouard, M., Martin, G., Chase, R. et al. (2025). Unravelling genomic drivers of speciation in Musa through genome assemblies of wild banana ancestors. Nature Communications.

Roullier, C., Benoit, L., McKey, D.B. & Lebot, V. (2013). Historical collections reveal patterns of diffusion of sweet potato in Oceania obscured by modern plant movements and recombination.

Proceedings of the National Academy of Sciences, 110(6), 2205–2210.

Roullier, C., Duputié, A., Wennekes, P., Benoit, L., Fernández Bringas, V.M., Rossel, G., Tay, D., McKey, D. & Lebot, V. (2013). Disentangling the origins of cultivated sweet potato (Ipomoea batatas (L.) Lam.). PLoS ONE, 8(5), e62707.

Ryan, S.E., Dabrowski, V., Dapoigny, A., Gauthier, C., Douville, E., Tengberg, M., Kerfant, C., Mouton, M., Desormeau, X., Zazzo, A. & Bouchaud, C. (2021). Strontium isotope evidence for a trade network between southeastern Arabia and India during Antiquity. Scientific Reports 11: 303.

Sánchez-Pérez, R., Pavan, S., Mazzeo, R., Moldovan, C., Aiese Cigliano, R., Del Cueto, J., Ricciardi, F., Lotti, C., Ricciardi, L., Dicenta, F., López-Marqués, R.L. & Møller, B.L. (2019). Mutation of a bHLH transcription factor allowed almond domestication. Science 364(6445), 1095–1098.

Sanjur, O.I., Piperno, D.R., Andres, T.C. & Wessel-Beaver, L. (2002). Phylogenetic relationships among domesticated and wild species of Cucurbita (Cucurbitaceae) inferred from a mitochondrial gene: implications for crop plant evolution and areas of origin. Proceedings of the National Academy of Sciences USA, 99(1), 535–540.

Sardos, J., Perrier, X., Doutrelepont, H. et al. Genome ancestry mosaics reveal multiple and cryptic contributors to cultivated banana.

Sauer, J.D. (1993). Historical Geography of Crop Plants: A Select Roster. CRC Press.

Savolainen, P., Zhang, Y.P., Luo, J., Lundeberg, J. & Leitner, T. (2002). Genetic evidence for an East Asian origin of domestic dogs. *Science* 298:1610–1613.

Scalabrin, S. et al. (2020). A single polyploidization event at the origin of the tetraploid genome of Coffea arabica is responsible for the extremely low genetic variation in wild and cultivated germplasm.

Scarcelli, N., Cubry, P., Akakpo, R., Thuillet, A.-C., Obidiegwu, J., Baco, M.N., Otoo, E., Sonké, B., Dansi, A., Djedatin, G., Mariac, C. et al. (2019). Yam genomics supports West Africa as a major cradle of crop domestication. Science Advances, 5(5), eaaw1947.

Schick, T. (1988). Nahal Hemar cave: cordage, basketry and fabrics. 'Atiqot (English Series), 18, 31–43.

Schmutz, J., McClean, P.E., Mamidi, S. et al. (2014). A reference genome for common bean and genome-wide analysis of dual domestications. *Nature Genetics* 46:707–713.

Sebastian, P., Schaefer, H., Telford, I.R. & Renner, S.S. (2010). Cucumber (Cucumis sativus) and melon (C. melo) have numerous wild relatives in Asia and Australia, and the sister species of melon is from Australia. Proceedings of the National Academy of Sciences USA 107: 14269–14273.

Sedivy, E.J., Wu, F. & Hanzawa, Y. (2017). Soybean domestication: the origin, genetic architecture and molecular bases. New Phytologist, 214(2), 539–553.

Shamir, O. & Rast-Eicher, A. (2020). Continuity and discontinuity in Neolithic and Chalcolithic linen textile production in the southern Levant. In The Competition of Fibres: Early Textile Production in Western Asia, South-East and Central Europe (10,000–500 BC), Ancient Textile Series Vol. 32 (eds. W. Schier & S. Pollock), pp. 27–37. Oxbow Books.

Shannon, L.M., Boyko, R.H., Castelhano, M. et al. (2015). Genetic structure in village dogs reveals a Central Asian domestication origin. *PNAS* 112:13639–13644.

Shapiro, M.D. & Domyan, E.T. (2013). Domestic pigeons. Current Biology 23(8), R302–R303.

Shapiro, M.D., Kronenberg, Z., Li, C., Domyan, E.T., Pan, H., Campbell, M., Tan, H., Huff, C.D., Hu, H., Vickrey, A.I., Nielsen, S.C.A. et al. (2013). Genomic diversity and evolution of the head crest in the rock pigeon. Science 339(6123), 1063–1067.

Sharif, B.M. et al. (2020). Genome-wide genotyping elucidates the geographical diversification and dispersal of the polyploid and clonally propagated yam (Dioscorea alata). Annals of Botany, 126(6), 1029.

Shemesh-Mayer, E. & Kamenetsky-Goldstein, R. (2018). Garlic (Allium sativum L.) fertility: transition from vegetative to reproductive growth. Frontiers in Plant Science 9, 1553.

Shen, Q.-K., Peng, M.-S., Adeola, A.C., Kui, L., Duan, S., Miao, Y.-W., Eltayeb, N.M., Lichoti, J.K., Otecko, N.O., Strillacci, M.G., Gorla, E., Bagnato, A., Charles, O.S., Sanke, O.J., Dawuda, P.M., Okeyoyin, A.O., Musina, J., Njoroge, P., Agwanda, B., Kusza, S., Nanaei, H.A., Pedar, R., Xu, M.-M., Du, Y., Nneji, L.M., Murphy, R.W., Wang, M.-S., Esmailizadeh, A., Dong, Y., Ommeh, S.C. & Zhang, Y.-P. (2021). Genomic analyses unveil helmeted guinea fowl (Numida meleagris) domestication in West Africa. Genome Biology and Evolution, 13(6), evab090.

Shi, X.W., Zeng, F.T., Qiu, X.P. & Zhang, Y.P. (1998). Mitochondrial DNA polymorphism and origin differentiation in major Chinese goose breeds. Journal of Genetics, 25(6), 499–507.

Shi, X.W., Wang, J.W., Zeng, F.T. & Qiu, X.P. (2006). Mitochondrial DNA cleavage patterns distinguish independent origin of Chinese domestic geese and Western domestic geese. Biochemical Genetics, 44(5–6), 237–245.

Small, E. (1980). The relationships of hop cultivars and wild variants of Humulus lupulus. Canadian Journal of Botany 58(6), 676–686.

Small, E. (2006). Molecular phylogeny of wild hops, Humulus lupulus L. Heredity 96, 391–401.

Smith, B.D. (2006). Eastern North America as an independent center of plant domestication. *PNAS* 103:12223–12228.

Smith, B.D. & Yarnell, R.A. (2009). Initial formation of an indigenous crop complex in eastern North America at 3800 B.P. *PNAS* 106:6561–6566.

Smith, O., Nicholson, W.V., Kistler, L., Mace, E., Clapham, A., Rose, P., Stevens, R., Ware, R., Samavedam, S., Barker, G., Jordan, D., Fuller, D.Q. & Allaby, R.G. (2019). A domestication history of dynamic adaptation and genomic deterioration in Sorghum. Nature Plants 5: 369–379.

Smýkal, P., Trněný, O., Brus, J., Hanáček, P., Rathore, A., Das Roma, R., Pechanec, V., Duchoslav, M., Bhattacharyya, D., Bariotakis, M., Pirintsos, S., Berger, J. & Toker, C. (2018). Genetic structure of wild pea (Pisum sativum subsp. elatius) populations in the northern part of the Fertile Crescent reflects moderate cross-pollination and strong effect of geographic but not environmental distance. PLoS ONE, 13(3), e0194056.

Solares, E., Morales-Cruz, A., Figueroa Balderas, R., Focht, E., Ashworth, V.E.T.M., Wyant, S., Minio, A., Cantu, D., Arpaia, M.L. & Gaut, B.S. (2023). Insights into the domestication of avocado and potential genetic contributors to heterodichogamy. G3 Genes|Genomes|Genetics 13(2), jkac323.

Speller, C.F., Kemp, B.M., Wyatt, S.D., Monroe, C., Lipe, W.D., Arndt, U.M. & Yang, D.Y. (2010). Ancient mitochondrial DNA analysis reveals complexity of indigenous North American turkey

domestication. Proceedings of the National Academy of Sciences USA 107(7): 2807–2812.

Spooner, D.M., McLean, K., Ramsay, G., Waugh, R. & Bryan, G.J. (2005). A single domestication for potato based on multilocus amplified fragment length polymorphism genotyping. Proceedings of the National Academy of Sciences 102(41): 14694–14699.

Spotorno, A.E. et al. (2004, 2006). Molecular diversity among domestic guinea-pigs (Cavia porcellus) and their close phylogenetic relationship with the Andean wild species Cavia tschudii.

Stephens, S.G. (1975). A reexamination of the cotton remains from Huaca Prieta, north coastal Peru. American Antiquity 40(4): 406–419.

Stetter, M.G. & Schmid, K.J. (2017). Analysis of phylogenetic relationships and genome size evolution of the Amaranthus genus using GBS indicates the ancestors of an ancient crop. Molecular Phylogenetics and Evolution 109: 80–92.

Stetter, M.G., Müller, T. & Schmid, K.J. (2017). Genomic and phenotypic evidence for an incomplete domestication of South American grain amaranth (Amaranthus caudatus). Molecular Ecology 26(3): 871–886.

Stiner, M.C., Munro, N.D., Buitenhuis, H., Duru, G. & Özbaşaran, M. (2022). An endemic pathway to sheep and goat domestication at Aşıklı Höyük (Central Anatolia, Turkey). *PNAS* 119(4):e2110930119.

Sugihara, Y., Darkwa, K., Yaegashi, H., Natsume, S., Shimizu, M. et al. (2020). Genome analyses reveal the hybrid origin of the staple crop white Guinea yam (Dioscorea rotundata). Proceedings of the National Academy of Sciences, 117(50), 31987–31992.

Sugihara, Y., Kudoh, A., Oli, M.T., Takagi, H., Natsume, S., Shimizu, M., Abe, A., Asiedu, R., Asfaw, A., Adebola, P. &

Terauchi, R. (2021). Population genomics of yams: evolution and domestication of Dioscorea species. In P. Rajora (Ed.), Population Genomics: Crop Plants (pp. 1–28). Springer, Cham.

Sun, W., Yu, H., Shen, Y. et al. (2012). Phylogeny and evolutionary history of the silkworm. Science China Life Sciences, 55, 483–496.

Sun, X. et al. (2020). [Genomic reanalysis of Tian Shan *Malus sieversii* as apple's primary domestication source, reviewed alongside Cornille et al. 2012 and Zhang et al. 2024].

Sun, Y., Shen, E., Hu, Y., Wu, D., Feng, Y., Lao, S., Dong, C., Du, T., Hua, W., Ye, C.-Y., Zhu, J., Zhu, Q.-H., Cai, D., Skuza, L., Qiu, J. & Fan, L. (2022). Population genomic analysis reveals domestication of cultivated rye from weedy rye. Molecular Plant 15(3), 552–561.

Suska-Malawska, M., Kot, M., Gręzak, A., Mętrak, M., Khudjanazarov, M. & Szymczak, K. (2022). Potential impact of Holocene climate changes on camel breeding practices of Neolithic pastoralists in the Central Asian drylands: a preliminary assessment. *The Holocene* 32(11):1132–1143.

Talavera, A., Soorni, A., Bombarely, A., Matas, A.J. & Hormaza, J.I. (2019). Genome-Wide SNP discovery and genomic characterization in avocado (Persea americana Mill.). Scientific Reports 9, 20137.

Tanno, K. & Willcox, G. (2012). Distinguishing wild and domestic wheat and barley spikelets from early Holocene sites in the Near East. Vegetation History and Archaeobotany 21:107–115.

Taylor, W.T.T. & Barrón-Ortiz, C.I. (2021). Rethinking the evidence for early horse domestication at Botai. Scientific Reports 11:7440.

The International Peach Genome Initiative, Verde, I., Abbott, A.G., Scalabrin, S., Jung, S., Shu, S., et al. (2013). The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. Nature Genetics, 45, 487–494.

Thornton, E.K. et al. (2012). Earliest Mexican turkeys (Meleagris gallopavo) in the Maya region: implications for pre-Hispanic animal trade and the timing of turkey domestication. PLoS ONE 7(8): e42630.

Todd, E.T., Tonasso-Calvière, L., Chauvey, L. et al. (2022). The genomic history and global expansion of domestic donkeys. Science 377(6611): 1172–1180.

Trněný, O., Brus, J., Hradilová, I., Rathore, A., Das, R.R., Kopecký, P., Coyne, C.J., Reeves, P., Richards, C. & Smýkal, P. (2018). Molecular evidence for two domestication events in the pea crop. Genes, 9(11), 535.

U, N. (1935). Genome analysis in Brassica with special reference to the experimental formation of B. napus and peculiar mode of fertilization. Japanese Journal of Botany 7, 389–452.

Uerpmann, H. & Uerpmann, M. (2002). The appearance of the domestic camel in south-east Arabia. *Journal of Oman Studies* 12:235–260.

Uysal, H., Fu, Y.-B., Kurt, O., Peterson, G.W., Diederichsen, A. & Kusters, P. (2010). Genetic diversity of cultivated flax (Linum usitatissimum L.) and its wild progenitor pale flax (Linum bienne Mill.) as revealed by ISSR markers. Genetic Resources and Crop Evolution, 57, 1109–1119.

Uysal, H., Kurt, O., Fu, Y.-B., Diederichsen, A. & Kusters, P. (2012). Variation in phenotypic characters of pale flax (Linum bienne Mill.) from Turkey. Genetic Resources and Crop Evolution, 59, 19–30.

Vallebueno-Estrada, M., Rodríguez-Arévalo, I., Rougon-Cardoso, A., Martínez González, J., García Cook, A., Montiel, R. & Vielle-Calzada, J.-P. (2016). The earliest maize from San Marcos Tehuacán is a partial domesticate with genomic evidence of inbreeding. *PNAS* 113:14151–14156.

Van Dam, A.R., Portillo Martinez, L., Jeri Chavez, A. & May, B.P. (2015). Range Wide Phylogeography of Dactylopius coccus (Hemiptera: Dactylopiidae). Annals of the Entomological Society of America 108(3): 299–310.

Van Heerwaarden, J. et al. (2011). Genetic signals of origin, spread, and introgression in a large sample of maize landraces. *PNAS* 108:1088–1092.

van Oss, R., Abbo, S., Eshed, R., Sherman, A., Coyne, C.J., Vandemark, G.J., Zhang, H.-B. & Peleg, Z. (2015). Genetic relationship in *Cicer* sp. expose evidence for geneflow between the cultigen and its wild progenitor. *PLOS ONE* 10(10):e0139789.

van Zeist, W. & Bakker-Heeres, J.A.H. (1975). Evidence for linseed cultivation before 6000 BC. Journal of Archaeological Science, 2, 215–219.

Van Zeist, W. & de Roller, G.J. (1993). Plant remains from Maadi, a Predynastic site in Lower Egypt. Vegetation History and Archaeobotany 2: 1–14.

VanDerwarker, A.M., Thakar, H.B., Hirth, K., Domic, A.I., Harper, T.K., George, R.J., Johnson, E.S., Newhall, V., Scheffler, T.E., McCool, W.C., Wann, K., Gaut, B.S., Kistler, L. & Kennett, D.J. (2025). Early evidence of avocado domestication from El Gigante Rockshelter, Honduras. Proceedings of the National Academy of Sciences 122(10), e2417072122.

Varshney, R.K., Roorkiwal, M., Sun, S. et al. (2021). A chickpea genetic variation map based on the sequencing of 3,171 genomes. *Nature* 599:622–627.

Verdugo, M.P., Mullin, V.E., Scheu, A. et al. (2019). Ancient cattle genomics, origins, and rapid turnover in the Fertile Crescent. Science 365(6449):173–176.

Vignal, A., Boitard, S., Thébault, N., Dayo, G.-K., Yapi-Gnaore, V., Youssao Abdou Karim, I., Berthouly-Salazar, C., Pálinkás-Bodzsár, N., Guémené, D., Thibaud-Nissen, F., Warren, W.C., Tixier-Boichard, M. & Rognon, X. (2019). A guinea fowl genome assembly provides new evidence on evolution following domestication and selection in galliformes. Molecular Ecology Resources, 19, 997–1014.

Vigne, J.-D., Guilaine, J., Debue, K., Haye, L. & Gérard, P. (2004). Early taming of the cat in Cyprus. *Science* 304(5668): 259.

von Wettberg, E.J.B., Chang, P.L., Başdemir, F., Carrasquila-Garcia, N., Korbu, L.B., Moenga, S.M. et al. (2018). Ecology and genomics of an important crop wild relative as a prelude to agricultural innovation. *Nature Communications* 9:649.

Sun, Z. et al. (2022). Extensive genomic analyses reveal the complex evolutionary history of cultivated and weedy rye (Secale cereale L.). BMC Biology.

Tidemann, B.D. & Beckie, H.J. (2021). Avena fatua L. In: Biology and Management of Problematic Crop Weed Species (chapter). Academic Press.

Tinker, N.A. et al. (2022). Genome analysis in Avena sativa reveals hidden breeding barriers and opportunities for oat improvement. Communications Biology 5, 474.

Tokenova, A., Sitpayeva, G., Gemejiyeva, N., Suleimenova, S., Friesen, N. & Batayeva, D. (2023). Wild Allium longicuspis Regel is a feral form of Allium sativum L. in Kazakhstan: a comparative molecular genetic analysis. OnLine Journal of Biological Sciences 23(1), 33–43.

Wallberg, A., Han, F., Wellhagen, G., Dahle, B., Kawata, M., Haddad, N. et al. (2014). A worldwide survey of genome sequence

variation provides insight into the evolutionary history of the honeybee Apis mellifera. *Nature Genetics* 46(10): 1081–1088.

Wang, M., Yu, Y., Haberer, G. et al. (2014). The genome sequence of African rice (Oryza glaberrima) and evidence for independent domestication. Nature Genetics 46:982-988 — cited in this cycle at §4.7.1 for the single-region domestication model.

Wang, G.-D., Zhai, W., Yang, H.-C., Wang, L., Zhong, L., Liu, Y.-H., Fan, R.-X., Yin, T.-T., Zhu, C.-L., Poyarkov, A.D., Irwin, D.M., Hytönen, M.K., Lohi, H., Wu, C.-I., Savolainen, P. & Zhang, Y.-P. (2016). Out of southern East Asia: the natural history of domestic dogs across the world. *Cell Research* 26:21–33.

Wang, L.-X. et al. (2016). Genetic diversity center of cultivated soybean (Glycine max) in China — new insight and evidence for the diversity center of Chinese cultivated soybean. Journal of Integrative Agriculture, 15(11), 2481–2487.

Wang, M.-S., Thakur, M., Peng, M.-S. et al. (2020). 863 genomes reveal the origin and domestication of chicken. *Cell Research* 30:693–701.

Wang, M.-S., Zeng, Y., Wang, X., Nie, W.-H., Wang, J.-H., Su, W.-T., Otecko, N.O., Xiong, Z.-J., Wang, S., Qu, K.-X., Yan, S.-Q., Yang, M.-M., Wang, W., Dong, Y., Wu, D.-D. & Zhang, Y.-P. (2017). Draft genome of the gayal, Bos frontalis. GigaScience 6(11): 1–7.

Wang, P., Luo, Y., Huang, J., Gao, S., Zhu, G., Dang, Z., Gai, J., Yang, M., Zhu, M., Zhang, H., Ye, X., Gao, A., Tan, X., Wang, S., Wu, S., Cahoon, E.B., Bai, B., Zhao, Z., Li, Q., Wei, J., Chen, H., Luo, R., Gong, D., Tang, K., Zhang, B., Ni, Z., Huang, G., Hu, S. & Chen, Y. (2020). The genome evolution and domestication of tropical fruit mango. Genome Biology 21(1): 60.

Wang, S.-Y., Luo, J., Murphy, R.W., Wu, S.-F., Zhu, C.-L., Gao, Y. & Zhang, Y.-P. (2013). Origin of Chinese Goldfish and Sequential Loss

of Genetic Diversity Accompanies New Breeds. PLoS ONE 8(3): e59571.

Warschefsky, E.J. & von Wettberg, E.J.B. (2019). Population genomic analysis of mango (Mangifera indica) suggests a complex history of domestication. New Phytologist 222(4): 2023–2037.

Wasylikowa, K. & van der Veen, M. (2004). An archaeobotanical contribution to the history of watermelon, Citrullus lanatus (Thunb.) Matsum. et Nakai (syn. C. vulgaris Schrad.). Vegetation History and Archaeobotany, 13(4), 213–217.

Weber, S.A. (1991). Plants and Harappan Subsistence: An Example of Stability and Change from Rojdi. Boulder, CO: Westview Press.

Weeden, N.F. (2018). Domestication of pea (Pisum sativum L.): The case of the Abyssinian pea. Frontiers in Plant Science, 9, 515.

Weldenegodguad, M. et al. (2020). Genome sequence and comparative analysis of reindeer (Rangifer tarandus) in northern Eurasia. Scientific Reports, 10, 8980.

Wen, J., Li, H., Wang, H., Yu, J., Zhu, T., Zhang, J., Li, X., Jiang, Z., Ning, Z. & Qu, L. (2023). Origins, timing and introgression of domestic geese revealed by whole genome data. Journal of Animal Science and Biotechnology, 14, 26.

Westengen, O.T., Huamán, Z. & Heun, M. (2005). Genetic diversity and geographic pattern in early South American cotton domestication. Theoretical and Applied Genetics 110: 392–402.

Wheeler, J.C. (1984, 1985). Publications on the Telarmachay faunal sequence; reviewed in Wheeler (1995) and in Le Neün et al. (2023, 2026).

Whitfield, C.W., Behura, S.K., Berlocher, S.H., Clark, A.G., Johnston, J.S., Sheppard, W.S., Smith, D.R., Suarez, A.V., Weaver, D. & Tsutsui, N.D. (2006). Thrice out of Africa: ancient and recent

expansions of the honey bee, Apis mellifera. *Science* 314(5799): 642–645.

Winchell, F., Brass, M., Manzo, A., Beldados, A., Perna, V., Murphy, C., Stevens, C. & Fuller, D.Q. (2018). On the Origins and Dissemination of Domesticated Sorghum and Pearl Millet across Africa and into India: a View from the Butana Group of the Far Eastern Sahel. African Archaeological Review 35(4): 483–505.

Winchell, F., Stevens, C.J., Murphy, C., Champion, L. & Fuller, D.Q. (2017). Evidence for Sorghum Domestication in Fourth Millennium BC Eastern Sudan: Spikelet Morphology from Ceramic Impressions of the Butana Group. Current Anthropology 58(5): 673–683.

Wolcott, K.A., Chomicki, G., Staedler, Y.M., Wasylikowa, K., Nesbitt, M., Schönenberger, J. & Renner, S.S. (2021). Three-dimensional X-ray-computed tomography of 3300- to 6000-year-old Citrullus seeds from Libya and Egypt compared to extant seeds throws doubts on species assignments. Plants, People, Planet, 3(6), 694–702.

Wright, R.P., Lentz, D.L., Beaubien, H.F. & Kimbrough, C.K. (2012). New evidence for jute (Corchorus capsularis L.) in the Indus civilization. Archaeological and Anthropological Sciences 4(2): 137–143.

Wu, D.-D., Ding, X.-D., Wang, S., Wójcik, J.M., Zhang, Y., Tokarska, M., Li, Y., Wang, M.-S., Faruque, O., Nielsen, R. et al. (2018). Pervasive introgression facilitated domestication and adaptation in the Bos species complex. Nature Ecology & Evolution 2: 1139–1145.

Wu, G.A., Prochnik, S., Jenkins, J. et al. (2014). Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. Nature Biotechnology, 32, 656–662.

Wu, G.A., Terol, J., Ibanez, V. et al. (2018). Genomics of the origin and evolution of Citrus. Nature, 554(7692), 311–316.

Wu, Y., Choi, J.Y., Ware, D. et al. (2019). The complex geography of domestication of the African rice Oryza glaberrima. PLOS Genetics 15:e1007414 — cited in this cycle at §4.7.1–§4.7.2 for the noncentric, multiregional alternative model.

Wu, G.A. et al. (2021). Diversification of mandarin citrus by hybrid speciation and apomixis. Nature Communications.

Wu, S. et al. (2023). A Citrullus genus super-pangenome reveals extensive variations in wild and cultivated watermelons and sheds light on watermelon evolution and domestication. Plant Biotechnology Journal (advance online / PMC10502741).

Wu, B., Ren, Q., Yan, X., Zhao, F., Qin, T., Xin, P., Cui, X., Wang, K., Du, R., Røed, K.H., Côté, S.D., Yannic, G., Li, Z. & Qiu, Q. (2024). Resequencing of reindeer genomes provides clues to their docile habits. Evolution Letters, 8, 494–504.

Wu, S., Sun, H., Zhao, X., Hamilton, J.P., Mollinari, M., De Siqueira Gesteira, G., Kitavi, M., Yan, M., Wang, H., Yang, J., Yencho, G.C., Buell, C.R. & Fei, Z. (2025). Phased chromosome-level assembly provides insight into the genome architecture of hexaploid sweetpotato. Nature Plants, 11, 1951–1959.

Xia, Q., Guo, Y., Zhang, Z., Li, D., Xuan, Z., Li, Z., Dai, F., Li, Y., Cheng, D., Li, R. et al. (2009). Complete resequencing of 40 genomes reveals domestication events and genes in silkworm (Bombyx). Science, 326(5951), 433–436.

Xia, E.-H. et al. (2020). The reference genome of tea plant and resequencing of 81 diverse accessions supports the mainland origin. *Molecular Plant* 13: 1013-1026.

Xie, K., Song, Z., Wang, Y., Di, Y., Li, W., Wang, Y.B., Yang, A., Qiao, X., Wang, B., Li, M., Xie, X.P., Xie, X.H., Liu, L., Ning, C., Tang, H.,

Li, X.Y., Wu, X., Zhang, Q., Wang, D. & Fan, X. (2024). Whole-genome resequencing revealed the origin and domestication of Chinese domestic rabbits. bioRxiv 2024.03.26.586758 (preprint; peer-reviewed publication status not confirmed in this cycle's search, disclosed as such at first citation, §51.2).

Xiong, H., Shi, A., Mou, B., Qin, J., Motes, D., Lu, W., Ma, J., Weng, Y., Yang, W. & Wu, D. (2016). Genetic diversity and population structure of cowpea (Vigna unguiculata L. Walp). PLoS ONE 11(8), e0160941.

Xu, P., Zhang, X., Wang, X., Li, J., Liu, G., Kuang, Y., Xu, J., Zheng, X., Ren, L., Wang, G., Zhang, Y., Huo, L., Zhao, Z., Cao, D., Lu, C., Li, C., Zhou, Y., Liu, Z., Fan, Z., Shan, G., Li, X., Wu, S., Song, L., Hou, G., Jiang, Y., Jeney, Z., Yu, D., Wang, L., Shao, C., Song, L., Sun, J., Ji, P., Wang, J., Li, Q., Xu, L., Sun, F., Feng, J., Wang, C., Wang, S., Wang, B., Li, Y., Zhu, Y., Xue, W., Zhao, L., Wang, J., Gu, Y., Lv, W., Wu, K., Xiao, J., Wu, J., Zhang, Z., Yu, J. & Sun, X. (2014). Genome sequence and genetic diversity of the common carp, Cyprinus carpio. Nature Genetics 46(11), 1212–1219.

Wang, X., Aninta, S.G., Garcia-Erill, G., Li, Z., Khan, A., Liu, X., Bertola, L.D., Dharmayanthi, A.B., Yulianto, Yonathan, Rossi, C., Cauble-Sims, R., Rosen, B.D., Hagen, D.E., Heaton, M.P., Smith, T.P.L., Lenstra, J.A., Martins, N.F.G., Sinding, M.-H.S., Agil, M., Purwantara, B., Hvilsom, C., Semiadi, G. & Heller, R. (2026). Population structure and domestication history of the Javan banteng. Current Biology 36(2): 458–473.

Yan, M., Li, M., Wang, Y., Wang, X., Moeinzadeh, M.-H., Quispe-Huamanquispe, D.G., Fan, W., Fang, Y., Wang, Y., Nie, H., Wang, Z., Tanaka, A., Heider, B., Kreuze, J.F., Gheysen, G., Wang, H., Vingron, M., Bock, R. & Yang, J. (2024). Haplotype-based phylogenetic analysis and population genomics uncover the origin and domestication of sweetpotato. Molecular Plant, 17(2), 277–296.

Yang, D.Y., Liu, L., Chen, X. & Speller, C.F. (2008). Wild or domesticated: DNA analysis of ancient water buffalo remains from north China. Journal of Archaeological Science 35(10):2778–2785.

Yang, J., Liu, D., Wang, X., Ji, C., Cheng, F., Liu, B., Hu, Z., Chen, S., Pental, D., Ju, Y., Yao, P., Li, X., Xie, K., Zhang, J., Wang, J., Liu, F., Ma, W., Shopan, J., Zheng, H., Mackenzie, S.A. & Zhang, M. (2016). The genome sequence of allopolyploid Brassica juncea and analysis of differential homoeolog gene expression influencing selection. Nature Genetics 48(10), 1225–1232.

Yang, N., Wang, Y., Liu, X., Jin, M., Vallebueno-Estrada, M., Calfee, E. et al. (2023). Two-way gene flow between teosinte and maize contributed to genetic diversity in maize domestication. *Science* 382:eadg8940 (highland *mexicana* admixture result).

Yang, Z., Tian, S., Li, X. et al. (2022). Multi-omics provides new insights into the domestication and improvement of dark jute (Corchorus olitorius). Plant Journal 112: 1–18.

Yin, J. et al. (2021). A high-quality genome of taro (Colocasia esculenta (L.) Schott), one of the world's oldest crops. Molecular Ecology Resources 21(1), 68–77.

Yindee, M. et al. (2010). Y-chromosomal variation confirms independent domestications of swamp and river buffalo. Animal Genetics 41(4):433–435.

Yuan, D., Grover, C.E., Hu, G., Pan, M., Miller, E.R., Conover, J.L., Hunt, S.P., Udall, J.A. & Wendel, J.F. (2021). Parallel and Intertwining Threads of Domestication in Allopolyploid Cotton. Advanced Science 8: 2003634.

Zarrillo, S. et al. (2018). The use and domestication of *Theobroma cacao* during the mid-Holocene in the upper Amazon. *Nature Ecology & Evolution* 2: 1879-1888.

Zecca, G., De Mattia, F., Lovicu, G., Labra, M., Sala, F. & Grassi, F. (2010). Wild grapevine: silvestris, hybrids or cultivars that escaped from vineyards? Molecular evidence in Sardinia. Plant Biology 12:558-562 — cited in this cycle at §10.2.2 for the reinterpretation of Grassi et al. (2003) as cultivar introgression rather than independent domestication.

Zeder, M.A. & Hesse, B. (2000). The initial domestication of goats (*Capra hircus*) in the Zagros Mountains 10,000 years ago. *Science* 287:2254–2257.

Zeder, M.A. (2008). Animal domestication in the Zagros: an update and directions for future research. In E. Vila, L. Gourichon, A.M. Choyke & H. Buitenhuis (eds.), *Archaeozoology of the Near East VIII*, pp. 243–278 — verified against the published proceedings record; cited in-text at §16.3 without full bibliographic detail.

Zehdi-Azouzi, S. et al. (2015). Genetic structure of the date palm (*Phoenix dactylifera*) in the Old World reveals a strong differentiation between eastern and western populations. *Annals of Botany* 116: 101-112.

Zhang, L., Ma, X., Zhang, X., Xu, Y., Ibrahim, A.K., Yao, J., Huang, H., Chen, S., Liao, Z., Zhang, Q., Niyitanga, S., Yu, J., Liu, Y., Xu, X., Wang, J., Tao, A., Xu, J., Chen, S., Yang, X., He, Q., Lin, L., Fang, P., Zhang, L., Ming, R. & Qi, J. (2021). Reference genomes of the two cultivated jute species. Plant Biotechnology Journal 19(11): 2235–2248.

Zhang, Y., Bao, Q., Cao, Z., Bian, Y., Zhang, Y., Cao, Z., Chen, G. & Xu, Q. (2023). Chinese domestic ducks evolved from mallard duck (Anas platyrhynchos) and spot-billed duck (A. zonorhyncha). Animals 13(7), 1156.

Zheng, Z., Sun, Z., Qi, F., Fang, Y., Lin, K., Pavan, S. et al. (2024). Chloroplast and whole-genome sequencing shed light on the

evolutionary history and phenotypic diversification of peanuts. Nature Genetics 56, 1975–1984.

Zhang, Y., Colli, L. & Barker, J.S.F. (2020). Asian water buffalo: domestication, history and genetics. Animal Genetics 51(2):177–191.

Zhang, W. et al. (2021). [Population-genomic support for a multi-centre reading of *Camellia sinensis* domestication]. *Nature Communications* 12.

Zhang, et al. (2024). [Further genomic confirmation of the Tian Shan/*M. sieversii* apple domestication centre, reviewed alongside Cornille et al. 2012 and Sun et al. 2020].

Zhang, C. et al. (2025). A genomic variation map provides insights into potato evolution and key agronomic traits. Plant Communications / ScienceDirect.

Zheng, Y.-F., Crawford, G.W. & Chen, X.-G. (2014). Archaeological evidence for peach (Prunus persica) cultivation and domestication in China. PLoS ONE, 9(9), e106595.

Zheng, Y., Crawford, G.W., Jiang, L. & Chen, X. (2016). Rice domestication revealed by reduced shattering of archaeological rice from the Lower Yangtze valley. *Scientific Reports* 6:28136.

Zhao, G., Lian, Q., Zhang, Z., Fu, Q., He, Y., Ma, S. et al. (2019). A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. Nature Genetics 51: 1607–1615.

Zhou, Z. et al. (2015). Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean.

Zohary, D. & Hopf, M. (2000). Domestication of Plants in the Old World, 3rd edn. Oxford University Press.

Zohary, D., Hopf, M. & Weiss, E. (2012). Domestication of Plants in the Old World, 4th edn. Oxford University Press, pp. 254–261.

Zou, C., Chen, A., Xiao, L., Muller, H.M., Ache, P., Haberer, G., Zhang, M., Jia, W., Deng, P., Huang, R., Fahlgren, N., Ilut, D.C., Chow, J., Bilinski, P., Katz, E., Denolf, P., Bakker, E.-J., Schranz, M.E., Mockler, T.C., Bergelson, J., Nagler, J.E., Schilling, M. & Zhang, J. (2017). A high-quality genome assembly of quinoa provides insights into the molecular basis of salt bladder-based salinity tolerance and the exceptional nutritional value. Cell Research, 27, 1327–1340.